

Johan Vallon-Christersson

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.

61
papers

4,475
citations

31
h-index

66
g-index

68
ext. papers

5,525
ext. citations

10.7
avg, IF

4.83
L-index

#	Paper	IF	Citations
61	Interval breast cancer is associated with interferon immune response.. <i>European Journal of Cancer</i> , 2022 , 162, 194-205	7.5	1
60	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	1
59	Autoimmunity to selenoprotein P predicts breast cancer recurrence. <i>Redox Biology</i> , 2022 , 102346	11.3	0
58	Preexisting Somatic Mutations of Estrogen Receptor Alpha () in Early-Stage Primary Breast Cancer. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkab028	4.6	1
57	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. <i>Molecular Cell</i> , 2021 , 81, 1453-1468.e12	17.6	7
56	Association between breast cancer risk and disease aggressiveness: Characterizing underlying gene expression patterns. <i>International Journal of Cancer</i> , 2021 , 148, 884-894	7.5	2
55	Molecular analyses of triple-negative breast cancer in the young and elderly. <i>Breast Cancer Research</i> , 2021 , 23, 20	8.3	3
54	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
53	Analysis of fusion transcripts indicates widespread deregulation of snoRNAs and their host genes in breast cancer. <i>International Journal of Cancer</i> , 2020 , 146, 3343-3353	7.5	2
52	Tertiary lymphoid structures improve immunotherapy and survival in melanoma. <i>Nature</i> , 2020 , 577, 561-565	56.4	542
51	The mutational landscape of the SCAN-B real-world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 2020 , 12, e12118	12	11
50	Tumor genetic heterogeneity analysis of chronic sun-damaged melanoma. <i>Pigment Cell and Melanoma Research</i> , 2020 , 33, 480-489	4.5	7
49	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
48	Methylation Patterns and Chromatin Accessibility in Neuroendocrine Lung Cancer. <i>Cancers</i> , 2020 , 12,	6.6	3
47	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. <i>Nature Communications</i> , 2020 , 11, 3747	17.4	18
46	Performance of gene expression-based single sample predictors for assessment of clinicopathological subgroups and molecular subtypes in cancers: a case comparison study in non-small cell lung cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 729-740	13.4	8
45	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

44	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
43	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. <i>Journal of Medical Genetics</i> , 2019 , 56, 453-460	5.8	10
42	Glucocorticoid-resistant B cell acute lymphoblastic leukemia displays receptor tyrosine kinase activation. <i>Npj Genomic Medicine</i> , 2019 , 4, 7	6.2	9
41	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
40	An independent poor-prognosis subtype of breast cancer defined by a distinct tumor immune microenvironment. <i>Nature Communications</i> , 2019 , 10, 5499	17.4	55
39	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
38	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
37	Frequent miRNA-convergent fusion gene events in breast cancer. <i>Nature Communications</i> , 2017 , 8, 788	17.4	16
36	Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. <i>Nature Communications</i> , 2017 , 8, 1738	17.4	172
35	Multiregion Whole-Exome Sequencing Uncovers the Genetic Evolution and Mutational Heterogeneity of Early-Stage Metastatic Melanoma. <i>Cancer Research</i> , 2016 , 76, 4765-74	10.1	70
34	An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. <i>Breast Cancer Research</i> , 2016 , 18, 27	8.3	51
33	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
32	The HER2-encoded miR-4728-3p regulates ESR1 through a non-canonical internal seed interaction. <i>PLoS ONE</i> , 2014 , 9, e97200	3.7	20
31	High expression of ZNF703 independent of amplification indicates worse prognosis in patients with luminal B breast cancer. <i>Cancer Medicine</i> , 2013 , 2, 437-46	4.8	33
30	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. <i>Breast Cancer Research and Treatment</i> , 2012 , 133, 583-94	4.4	37
29	The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. <i>Cancer Research</i> , 2012 , 72, 4028-36	10.1	37
28	Molecular profiling reveals low- and high-grade forms of primary melanoma. <i>Clinical Cancer Research</i> , 2012 , 18, 4026-36	12.9	81
27	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

26	Identification of new microRNAs in paired normal and tumor breast tissue suggests a dual role for the ERBB2/Her2 gene. <i>Cancer Research</i> , 2011 , 71, 78-86	10.1	160
25	Identification of subtypes in human epidermal growth factor receptor 2--positive breast cancer reveals a gene signature prognostic of outcome. <i>Journal of Clinical Oncology</i> , 2010 , 28, 1813-20	2.2	130
24	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2010 , 12, R25	8.3	103
23	Tasquinimod (ABR-215050), a quinoline-3-carboxamide anti-angiogenic agent, modulates the expression of thrombospondin-1 in human prostate tumors. <i>Molecular Cancer</i> , 2010 , 9, 107	42.1	69
22	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010 , 12, R36	8.3	216
21	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. <i>Breast Cancer Research</i> , 2010 , 12, R42	8.3	141
20	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010 , 20, 381-391	3.3	27
19	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010 , 20, 381-91	3.3	22
18	BASE--2nd generation software for microarray data management and analysis. <i>BMC Bioinformatics</i> , 2009 , 10, 330	3.6	42
17	The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. <i>Nature Cell Biology</i> , 2009 , 11, 1268-71	23.4	127
16	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
15	High-resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 2007 , 46, 543-58	5	162
14	Non-coding antisense transcription detected by conventional and single-stranded cDNA microarray. <i>BMC Genomics</i> , 2007 , 8, 295	4.5	8
13	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007 , 8, 382	4.5	56
12	Recruitment of HIF-1alpha and HIF-2alpha to common target genes is differentially regulated in neuroblastoma: HIF-2alpha promotes an aggressive phenotype. <i>Cancer Cell</i> , 2006 , 10, 413-23	24.3	532
11	Gene expression profiles relate to SS18/SSX fusion type in synovial sarcoma. <i>International Journal of Cancer</i> , 2006 , 118, 1165-72	7.5	45
10	An introduction to BioArray Software Environment. <i>Methods in Enzymology</i> , 2006 , 411, 99-119	1.7	9
9	Distinct genomic profiles in hereditary breast tumors identified by array-based comparative genomic hybridization. <i>Cancer Research</i> , 2005 , 65, 7612-21	10.1	141

8	Staf50 is a novel p53 target gene conferring reduced clonogenic growth of leukemic U-937 cells. <i>Oncogene</i> , 2004 , 23, 4050-9	9.2	59
7	Nonsense-mediated mRNA decay in barley mutants allows the cloning of mutated genes by a microarray approach. <i>Plant Physiology and Biochemistry</i> , 2004 , 42, 681-5	5.4	17
6	Human neuroblastoma cells exposed to hypoxia: induction of genes associated with growth, survival, and aggressive behavior. <i>Experimental Cell Research</i> , 2004 , 295, 469-87	4.2	103
5	Characterization of a novel breast carcinoma xenograft and cell line derived from a BRCA1 germ-line mutation carrier. <i>Laboratory Investigation</i> , 2003 , 83, 387-96	5.9	39
4	A naturally occurring allele of BRCA1 coding for a temperature-sensitive mutant protein. <i>Cancer Biology and Therapy</i> , 2002 , 1, 497-501	4.6	15
3	BioArray Software Environment (BASE): a platform for comprehensive management and analysis of microarray data. <i>Genome Biology</i> , 2002 , 3, SOFTWARE0003	18.3	316
2	Implementation of an Open Source Software solution for Laboratory Information Management and automated RNAseq data analysis in a large-scale Cancer Genomics initiative using BASE with extension package Reggie		3
1	Multidimensional transcriptomics provides detailed information about immune cell distribution and identity in HER2+ breast tumors		15