

Johan Vallon-Christersson

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

6,431
citations

126708

33
h-index

118652

62
g-index

68
all docs

68
docs citations

68
times ranked

11097
citing authors

#	ARTICLE	IF	CITATIONS
1	Tertiary lymphoid structures improve immunotherapy and survival in melanoma. <i>Nature</i> , 2020, 577, 561-565.	13.7	1,209
2	Recruitment of HIF-1 α and HIF-2 α to common target genes is differentially regulated in neuroblastoma: HIF-2 α promotes an aggressive phenotype. <i>Cancer Cell</i> , 2006, 10, 413-423.	7.7	624
3	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
4	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
5	Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. <i>Nature Communications</i> , 2017, 8, 1738.	5.8	310
6	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010, 12, R36.	2.2	251
7	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
8	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.	0.4	191
9	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, 543-558.	1.5	176
10	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
11	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.	2.2	167
12	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. <i>Cancer Research</i> , 2005, 65, 7612-7621.	0.4	147
13	The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. <i>Nature Cell Biology</i> , 2009, 11, 1268-1271.	4.6	147
14	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2 α -Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. <i>Journal of Clinical Oncology</i> , 2010, 28, 1813-1820.	0.8	145
15	An independent poor-prognosis subtype of breast cancer defined by a distinct tumor immune microenvironment. <i>Nature Communications</i> , 2019, 10, 5499.	5.8	132
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	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R25.	2.2	123
18	Human neuroblastoma cells exposed to hypoxia: induction of genes associated with growth, survival, and aggressive behavior. <i>Experimental Cell Research</i> , 2004, 295, 469-487.	1.2	114

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19	Clinical Value of RNA Sequencingâ€”Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis Networkâ€”Breast Initiative. <i>JCO Precision Oncology</i> , 2018, 2, 1-18.	1.5	101
20	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. <i>Clinical Cancer Research</i> , 2012, 18, 4026-4036.	3.2	96
21	Multiregion Whole-Exome Sequencing Uncovers the Genetic Evolution and Mutational Heterogeneity of Early-Stage Metastatic Melanoma. <i>Cancer Research</i> , 2016, 76, 4765-4774.	0.4	86
22	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.	7.9	77
23	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.	2.2	67
24	Staf50 is a novel p53 target gene conferring reduced clonogenic growth of leukemic U-937 cells. <i>Oncogene</i> , 2004, 23, 4050-4059.	2.6	66
25	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007, 8, 382.	1.2	57
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	Gene expression profiles relate to SS18/SSX fusion type in synovial sarcoma. <i>International Journal of Cancer</i> , 2006, 118, 1165-1172.	2.3	52
28	BASE - 2nd generation software for microarray data management and analysis. <i>BMC Bioinformatics</i> , 2009, 10, 330.	1.2	45
29	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, 583-594.	1.1	44
30	Characterization of a Novel Breast Carcinoma Xenograft and Cell Line Derived from a BRCA1 Germ-Line Mutation Carrier. <i>Laboratory Investigation</i> , 2003, 83, 387-396.	1.7	43
31	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
32	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
33	High expression of <sc><i>ZNF703</i></sc> independent of amplification indicates worse prognosis in patients with luminal B breast cancer. <i>Cancer Medicine</i> , 2013, 2, 437-446.	1.3	39
34	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
35	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
36	The mutational landscape of the <sc>SCAN</sc> â€” realâ€”world primary breast cancer transcriptome. <i>EMBO Molecular Medicine</i> , 2020, 12, e12118.	3.3	36

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37	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. <i>Molecular Cell</i> , 2021, 81, 1453-1468.e12.	4.5	31
38	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.	1.5	30
39	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010, 20, 381-391.	0.6	30
40	The HER2-Encoded miR-4728-3p Regulates ESR1 through a Non-Canonical Internal Seed Interaction. <i>PLoS ONE</i> , 2014, 9, e97200.	1.1	27
41	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
42	Frequent miRNA-convergent fusion gene events in breast cancer. <i>Nature Communications</i> , 2017, 8, 788.	5.8	24
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	Molecular analyses of triple-negative breast cancer in the young and elderly. <i>Breast Cancer Research</i> , 2021, 23, 20.	2.2	23
45	Tumor genetic heterogeneity analysis of chronic sun-damaged melanoma. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 480-489.	1.5	22
46	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010, 20, 381-91.	0.6	22
47	A Naturally Occurring Allele of BRCA1 Coding for a Temperature-Sensitive Mutant Protein. <i>Cancer Biology and Therapy</i> , 2002, 1, 497-501.	1.5	20
48	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
49	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, 681-685.	2.8	18
50	Glucocorticoid-resistant B cell acute lymphoblastic leukemia displays receptor tyrosine kinase activation. <i>Npj Genomic Medicine</i> , 2019, 4, 7.	1.7	18
51	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.	3.2	17
52	[7] An Introduction to BioArray Software Environment. <i>Methods in Enzymology</i> , 2006, 411, 99-119.	0.4	12
53	Sample Preparation Approach Influences PAM50 Risk of Recurrence Score in Early Breast Cancer. <i>Cancers</i> , 2021, 13, 6118.	1.7	10
54	Non-coding antisense transcription detected by conventional and single-stranded cDNA microarray. <i>BMC Genomics</i> , 2007, 8, 295.	1.2	9

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55	Autoimmunity to selenoprotein P predicts breast cancer recurrence. <i>Redox Biology</i> , 2022, 53, 102346.	3.9	9
56	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.	2.3	8
57	Methylation Patterns and Chromatin Accessibility in Neuroendocrine Lung Cancer. <i>Cancers</i> , 2020, 12, 2003.	1.7	5
58	Regulatory networks and 5â€™ partner usage of <sc>miRNA</sc> host gene fusions in breast cancer. <i>International Journal of Cancer</i> , 2022, 151, 95-106.	2.3	5
59	Association between breast cancer risk and disease aggressiveness: Characterizing underlying gene expression patterns. <i>International Journal of Cancer</i> , 2021, 148, 884-894.	2.3	3
60	Interval breast cancer is associated with interferon immune response. <i>European Journal of Cancer</i> , 2022, 162, 194-205.	1.3	3
61	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.	0.4	0