

Jari HÄÄKkinen

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

2,000
citations

304743

22
h-index

254184

43
g-index

52
all docs

52
docs citations

52
times ranked

4008
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulatory networks and 5â€™ partner usage of <sc>miRNA</sc> host gene fusions in breast cancer. International Journal of Cancer, 2022, 151, 95-106.	5.1	5
2	Molecular analyses of triple-negative breast cancer in the young and elderly. Breast Cancer Research, 2021, 23, 20.	5.0	23
3	Preexisting Somatic Mutations of Estrogen Receptor Alpha (<i>ESR1</i>) in Early-Stage Primary Breast Cancer. JNCI Cancer Spectrum, 2021, 5, pkab028.	2.9	20
4	Tumor genetic heterogeneity analysis of chronic sunâ€damaged melanoma. Pigment Cell and Melanoma Research, 2020, 33, 480-489.	3.3	22
5	Prognostic implications of the expression levels of different immunoglobulin heavy chain-encoding RNAs in early breast cancer. Npj Breast Cancer, 2020, 6, 28.	5.2	25
6	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53
7	Analysis of fusion transcripts indicates widespread deregulation of snoRNAs and their host genes in breast cancer. International Journal of Cancer, 2020, 146, 3343-3353.	5.1	8
8	The mutational landscape of the <sc>SCAN</sc> â€ realâ€world primary breast cancer transcriptome. EMBO Molecular Medicine, 2020, 12, e12118.	6.9	36
9	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.	1.6	2
10	Prediction of Lymph Node Metastasis in Breast Cancer by Gene Expression and Clinicopathological Models: Development and Validation within a Population-Based Cohort. Clinical Cancer Research, 2019, 25, 6368-6381.	7.0	37
11	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. Scientific Reports, 2019, 9, 12184.	3.3	39
12	Agreement between molecular subtyping and surrogate subtype classification: a contemporary population-based study of ER-positive/HER2-negative primary breast cancer. Breast Cancer Research and Treatment, 2019, 178, 459-467.	2.5	23
13	The X-Linked DDX3X RNA Helicase Dictates Translation Reprogramming and Metastasis in Melanoma. Cell Reports, 2019, 27, 3573-3586.e7.	6.4	66
14	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
15	Microenvironmental control of breast cancer subtype elicited through paracrine platelet-derived growth factor-CC signaling. Nature Medicine, 2018, 24, 463-473.	30.7	120
16	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. JCO Precision Oncology, 2018, 2, 1-18.	3.0	101
17	Frequent miRNA-convergent fusion gene events in breast cancer. Nature Communications, 2017, 8, 788.	12.8	24
18	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. Genome Medicine, 2015, 7, 20.	8.2	129

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19	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	4.5	58
20	Molecular microheterogeneity of prostate specific antigen in seminal fluid by mass spectrometry. <i>Clinical Biochemistry</i> , 2012, 45, 331-338.	1.9	17
21	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. <i>PLoS ONE</i> , 2011, 6, e17911.	2.5	361
22	Bioinformatic strategies for unambiguous identification of prostate specific antigen in clinical samples. <i>Journal of Proteomics</i> , 2011, 75, 202-210.	2.4	2
23	Laboratory Data and Sample Management for Proteomics. <i>Methods in Molecular Biology</i> , 2011, 696, 79-92.	0.9	4
24	BASE - 2nd generation software for microarray data management and analysis. <i>BMC Bioinformatics</i> , 2009, 10, 330.	2.6	45
25	Proteomics Data Collection – ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009, 9, 218-222.	2.2	3
26	Getting a grip on proteomics data – Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933.	2.2	15
27	The Proteios Software Environment: An Extensible Multiuser Platform for Management and Analysis of Proteomics Data. <i>Journal of Proteome Research</i> , 2009, 8, 3037-3043.	3.7	88
28	Proteomic Variation Is as Large within as between Strawberry Varieties. <i>Journal of Proteome Research</i> , 2007, 6, 3011-3020.	3.7	58
29	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 854, 173-182.	2.3	13
30	Automated reporting from gel-based proteomics experiments using the open source Proteios database application. <i>Proteomics</i> , 2007, 7, 668-674.	2.2	30
31	Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDI-MS Mass Spectra. <i>Journal of Proteome Research</i> , 2006, 5, 785-792.	3.7	68
32	Improving missing value imputation of microarray data by using spot quality weights. <i>BMC Bioinformatics</i> , 2006, 7, 306.	2.6	24
33	PROTEIOS: an open source proteomics initiative. <i>Bioinformatics</i> , 2005, 21, 2085-2087.	4.1	32
34	ACID: a database for microarray clone information. <i>Bioinformatics</i> , 2004, 20, 2305-2306.	4.1	18
35	Improving automatic peptide mass fingerprint protein identification by combining many peak sets. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2004, 807, 209-215.	2.3	6
36	Local routing algorithms based on Potts neural networks. <i>IEEE Transactions on Neural Networks</i> , 2000, 11, 970-977.	4.2	5

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37	A Potts Neuron Approach to Communication Routing. <i>Neural Computation</i> , 1998, 10, 1587-1599.	2.2	12
38	Is there screwiness at the end of the QCD cascades?. <i>Journal of High Energy Physics</i> , 1998, 1998, 014-014.	4.7	10
39	Colour connections in $e+e^{-}$ annihilation. <i>Nuclear Physics B</i> , 1997, 490, 289-305.	2.5	30
40	\bar{b} -fragmentation and $B \rightarrow \pi$ correlations. <i>Zeitschrift für Physik C-Particles and Fields</i> , 1997, 75, 35-40.	1.5	0
41	Colour: a computer program for QCD colour factor calculations. <i>Computer Physics Communications</i> , 1997, 100, 311-321.	7.5	9
42	Colour interference and confinement effects in W -pair production. <i>Zeitschrift für Physik C-Particles and Fields</i> , 1994, 64, 659-664.	1.5	42
43	$\hat{\Gamma}$ -polarization in $e+e^{-}$ -annihilation at the Z^0 -pole. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1993, 303, 350-354.	4.1	57