Jari HÃ¤kkinen

List of Publications by Year
in descending order

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	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	2.5	361
2	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
3	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
4	Microenvironmental control of breast cancer subtype elicited through paracrine platelet-derived growth factor-CC signaling. Nature Medicine, 2018, 24, 463-473.	30.7	120
5	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
6	The Proteios Software Environment: An Extensible Multiuser Platform for Management and Analysis of Proteomics Data. Journal of Proteome Research, 2009, 8, 3037-3043.	3.7	88
7	Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDIâ€'MS Mass Spectra. Journal of Proteome Research, 2006, 5, 785-792.	3.7	68
8	The X-Linked DDX3X RNA Helicase Dictates Translation Reprogramming and Metastasis in Melanoma. Cell Reports, 2019, 27, 3573-3586.e7.	6.4	66
9	Proteomic Variation Is as Large within as between Strawberry Varieties. Journal of Proteome Research, 2007, 6, 3011-3020.	3.7	58
10	Molecular and genetic diversity in the metastatic process of melanoma. Journal of Pathology, 2014, 233, 39-50.	4.5	58
11	Î“-polarization in e+eâ€'-annihilation at the Z0-pole. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1993, 303, 350-354.	4.1	57
12	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53
13	BASE - 2nd generation software for microarray data management and analysis. BMC Bioinformatics, 2009, 10, 330.	2.6	45
14	Colour interference and confinement effects in W-pair production. Zeitschrift Für Physik C-Particles and Fields, 1994, 64, 659-664.	1.5	42
15	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
16	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
17	The mutational landscape of the <scp>SCAN</scp> â€B realâ€world primary breast cancer transcriptome. EMBO Molecular Medicine, 2020, 12, e12118.	6.9	36
18	PROTEIOS: an open source proteomics initiative. Bioinformatics, 2005, 21, 2085-2087.	4.1	32

#	ARTICLE	IF	CITATIONS
19	Colour connections in e+eâˆ' annihilation. Nuclear Physics B, 1997, 490, 289-305.	2.5	30
20	Automated reporting from gel-based proteomics experiments using the open source Proteios database application. Proteomics, 2007, 7, 668-674.	2.2	30
21	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
22	Improving missing value imputation of microarray data by using spot quality weights. BMC Bioinformatics, 2006, 7, 306.	2.6	24
23	Frequent miRNA-convergent fusion gene events in breast cancer. Nature Communications, 2017, 8, 788.	12.8	24
24	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
25	Molecular analyses of triple-negative breast cancer in the young and elderly. Breast Cancer Research, 2021, 23, 20.	5.0	23
26	Tumor genetic heterogeneity analysis of chronic sunâ€damaged melanoma. Pigment Cell and Melanoma Research, 2020, 33, 480-489.	3.3	22
27	Preexisting Somatic Mutations of Estrogen Receptor Alpha (*ESR1*) in Early-Stage Primary Breast Cancer. JNCI Cancer Spectrum, 2021, 5, pkab028.	2.9	20
28	ACID: a database for microarray clone information. Bioinformatics, 2004, 20, 2305-2306.	4.1	18
29	Molecular microheterogeneity of prostate specific antigen in seminal fluid by mass spectrometry. Clinical Biochemistry, 2012, 45, 331-338.	1.9	17
30	Getting a grip on proteomics data â€" Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	2.2	15
31	The Mass Distance Fingerprint: A statistical framework for de novo detection of predominant modifications using high-accuracy mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 854, 173-182.	2.3	13
32	A Potts Neuron Approach to Communication Routing. Neural Computation, 1998, 10, 1587-1599.	2.2	12
33	Is there screwiness at the end of the QCD cascades?. Journal of High Energy Physics, 1998, 1998, 014-014.	4.7	10
34	Colour: a computer program for QCD colour factor calculations. Computer Physics Communications, 1997, 100, 311-321.	7.5	9
35	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
36	Improving automatic peptide mass fingerprint protein identification by combining many peak sets. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2004, 807, 209-215.	2.3	6

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37	Local routing algorithms based on Potts neural networks. IEEE Transactions on Neural Networks, 2000, 11, 970-977.	4.2	5
38	Regulatory networks and 5â€² partner usage of <scp>miRNA</scp> host gene fusions in breast cancer. International Journal of Cancer, 2022, 151, 95-106.	5.1	5
39	Laboratory Data and Sample Management for Proteomics. Methods in Molecular Biology, 2011, 696, 79-92.	0.9	4
40	Proteomics Data Collection â€" 4th ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. Proteomics, 2009, 9, 218-222.	2.2	3
41	Bioinformatic strategies for unambiguous identification of prostate specific antigen in clinical samples. Journal of Proteomics, 2011, 75, 202-210.	2.4	2
42	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
43	${m bar b}$ -fragmentation and B pi correlations. Zeitschrift Für Physik C-Particles and Fields, 1997, 75, 35-40.	1.5	0