

Mattias Rantalainen

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

5,737
citations

172457

29
h-index

155660

55
g-index

57
all docs

57
docs citations

57
times ranked

11561
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-wide prediction of prostate cancer gene expression from histopathology images using co-expression-based convolutional neural networks. <i>Bioinformatics</i> , 2022, 38, 3462-3469.	4.1	9
2	Using deep learning to detect patients at risk for prostate cancer despite benign biopsies. <i>IScience</i> , 2022, 25, 104663.	4.1	5
3	Challenging conventional karyotyping by next-generation karyotyping in 281 intensively treated patients with AML. <i>Blood Advances</i> , 2021, 5, 1003-1016.	5.2	12
4	Biological and therapeutic implications of a unique subtype of NPM1 mutated AML. <i>Nature Communications</i> , 2021, 12, 1054.	12.8	29
5	Artificial Intelligence for Diagnosis and Gleason Grading of Prostate Cancer in Biopsies—Current Status and Next Steps. <i>European Urology Focus</i> , 2021, 7, 687-691.	3.1	18
6	Predicting Molecular Phenotypes from Histopathology Images: A Transcriptome-Wide Expression—Morphology Analysis in Breast Cancer. <i>Cancer Research</i> , 2021, 81, 5115-5126.	0.9	32
7	An investigation of attention mechanisms in histopathology whole-slide-image analysis for regression objectives. , 2021, , .		7
8	Artificial intelligence for diagnosis and grading of prostate cancer in biopsies: a population-based, diagnostic study. <i>Lancet Oncology</i> , The, 2020, 21, 222-232.	10.7	364
9	Integrated transcriptomic and genomic analysis improves prediction of complete remission and survival in elderly patients with acute myeloid leukemia. <i>Blood Cancer Journal</i> , 2020, 10, 67.	6.2	6
10	Artificial intelligence as the next step towards precision pathology. <i>Journal of Internal Medicine</i> , 2020, 288, 62-81.	6.0	212
11	<i>TP53</i> Outperforms Other Androgen Receptor Biomarkers to Predict Abiraterone or Enzalutamide Outcome in Metastatic Castration-Resistant Prostate Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 1766-1773.	7.0	117
12	Development and Validation of a Novel RNA Sequencing—Based Prognostic Score for Acute Myeloid Leukemia. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1094-1101.	6.3	15
13	Isoform-level gene expression patterns in single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2018, 34, 2392-2400.	4.1	15
14	Prognostic value of Ki67 analysed by cytology or histology in primary breast cancer. <i>Journal of Clinical Pathology</i> , 2018, 71, 787-794.	2.0	21
15	Application of single-cell sequencing in human cancer. <i>Briefings in Functional Genomics</i> , 2018, 17, 273-282.	2.7	34
16	Digital image analysis of Ki67 in hot spots is superior to both manual Ki67 and mitotic counts in breast cancer. <i>Histopathology</i> , 2018, 72, 974-989.	2.9	70
17	Cell-free DNA profiling of metastatic prostate cancer reveals microsatellite instability, structural rearrangements and clonal hematopoiesis. <i>Genome Medicine</i> , 2018, 10, 85.	8.2	94
18	Expression levels of long non-coding RNAs are prognostic for AML outcome. <i>Journal of Hematology and Oncology</i> , 2018, 11, 52.	17.0	43

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19	Validation of risk stratification models in acute myeloid leukemia using sequencing-based molecular profiling. <i>Leukemia</i> , 2017, 31, 2029-2036.	7.2	54
20	E-Science technologies in a workflow for personalized medicine using cancer screening as a case study. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 950-957.	4.4	4
21	Assessment of Breast Cancer Risk Factors Reveals Subtype Heterogeneity. <i>Cancer Research</i> , 2017, 77, 3708-3717.	0.9	87
22	Molecular Differences between Screen-Detected and Interval Breast Cancers Are Largely Explained by PAM50 Subtypes. <i>Clinical Cancer Research</i> , 2017, 23, 2584-2592.	7.0	15
23	Intra-tumor heterogeneity in breast cancer has limited impact on transcriptomic-based molecular profiling. <i>BMC Cancer</i> , 2017, 17, 802.	2.6	10
24	Sequencing-based breast cancer diagnostics as an alternative to routine biomarkers. <i>Scientific Reports</i> , 2016, 6, 38037.	3.3	17
25	Study design requirements for RNA sequencing-based breast cancer diagnostics. <i>Scientific Reports</i> , 2016, 6, 20200.	3.3	2
26	Reprogramming Tumor-Associated Macrophages by Antibody Targeting Inhibits Cancer Progression and Metastasis. <i>Cell Reports</i> , 2016, 15, 2000-2011.	6.4	452
27	Beta-Poisson model for single-cell RNA-seq data analyses. <i>Bioinformatics</i> , 2016, 32, 2128-2135.	4.1	151
28	Determining breast cancer histological grade from RNA-sequencing data. <i>Breast Cancer Research</i> , 2016, 18, 48.	5.0	34
29	Digital image analysis outperforms manual biomarker assessment in breast cancer. <i>Modern Pathology</i> , 2016, 29, 318-329.	5.5	144
30	Robust Linear Models for Cis-eQTL Analysis. <i>PLoS ONE</i> , 2015, 10, e0127882.	2.5	7
31	An Integrated Bioinformatics Approach for Identifying Genetic Markers that Predict Cerebrospinal Fluid Biomarker p-tau181/A β ²¹⁻⁴² Ratio in ApoE4-Negative Mild Cognitive Impairment Patients. <i>Journal of Alzheimer's Disease</i> , 2015, 45, 1061-1076.	2.6	6
32	Integrative Transcriptomic and Metabonomic Molecular Profiling of Colonic Mucosal Biopsies Indicates a Unique Molecular Phenotype for Ulcerative Colitis. <i>Journal of Proteome Research</i> , 2015, 14, 479-490.	3.7	13
33	Combining Metabonomics and Other -omics Data. <i>Methods in Molecular Biology</i> , 2015, 1277, 147-159.	0.9	2
34	Integration of transcriptomics and metabonomics: improving diagnostics, biomarker identification and phenotyping in ulcerative colitis. <i>Metabolomics</i> , 2014, 10, 280-290.	3.0	24
35	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	2.5	83
36	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. <i>PLoS Genetics</i> , 2012, 8, e1002704.	3.5	48

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37	Systems Responses of Rats to Mequindox Revealed by Metabolic and Transcriptomic Profiling. <i>Journal of Proteome Research</i> , 2012, 11, 4712-4721.	3.7	24
38	Accounting for Control Mislabeling in Caseâ€“Control Biomarker Studies. <i>Journal of Proteome Research</i> , 2011, 10, 5562-5567.	3.7	5
39	MicroRNA Expression in Abdominal and Gluteal Adipose Tissue Is Associated with mRNA Expression Levels and Partly Genetically Driven. <i>PLoS ONE</i> , 2011, 6, e27338.	2.5	46
40	Non-linear modeling of 1H NMR metabonomic data using kernel-based orthogonal projections to latent structures optimized by simulated annealing. <i>Analytica Chimica Acta</i> , 2011, 705, 72-80.	5.4	13
41	Variance decomposition of protein profiles from antibody arrays using a longitudinal twin model. <i>Proteome Science</i> , 2011, 9, 73.	1.7	19
42	Human metabolic profiles are stably controlled by genetic and environmental variation. <i>Molecular Systems Biology</i> , 2011, 7, 525.	7.2	158
43	A Genome-Wide Metabolic QTL Analysis in Europeans Implicates Two Loci Shaped by Recent Positive Selection. <i>PLoS Genetics</i> , 2011, 7, e1002270.	3.5	132
44	Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	2.7	44
45	Analytic Properties of Statistical Total Correlation Spectroscopy Based Information Recovery in 1H NMR Metabolic Data Sets. <i>Analytical Chemistry</i> , 2009, 81, 2075-2084.	6.5	56
46	Top-Down Systems Biology Modeling of Host Metabotypeâ€“Microbiome Associations in Obese Rodents. <i>Journal of Proteome Research</i> , 2009, 8, 2361-2375.	3.7	228
47	Piecewise multivariate modelling of sequential metabolic profiling data. <i>BMC Bioinformatics</i> , 2008, 9, 105.	2.6	24
48	K-OPLS package: Kernel-based orthogonal projections to latent structures for prediction and interpretation in feature space. <i>BMC Bioinformatics</i> , 2008, 9, 106.	2.6	71
49	Symbiotic gut microbes modulate human metabolic phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2117-2122.	7.1	994
50	Topographical Variation in Metabolic Signatures of Human Gastrointestinal Biopsies Revealed by High-Resolution Magic-Angle Spinning ¹ H NMR Spectroscopy. <i>Journal of Proteome Research</i> , 2007, 6, 3944-3951.	3.7	72
51	Statistical Correlation and Projection Methods for Improved Information Recovery from Diffusion-Edited NMR Spectra of Biological Samples. <i>Analytical Chemistry</i> , 2007, 79, 5682-5689.	6.5	87
52	Kernelâ€“based orthogonal projections to latent structures (Kâ€“OPLS). <i>Journal of Chemometrics</i> , 2007, 21, 376-385.	1.3	55
53	The comparative metabonomics of age-related changes in the urinary composition of male Wistar-derived and Zucker (fa/fa) obese rats. <i>Molecular BioSystems</i> , 2006, 2, 193.	2.9	54
54	Statistically Integrated Metabonomicâ€“Proteomic Studies on a Human Prostate Cancer Xenograft Model in Mice. <i>Journal of Proteome Research</i> , 2006, 5, 2642-2655.	3.7	146

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55	OPLS discriminant analysis: combining the strengths of PLS-DA and SIMCA classification. Journal of Chemometrics, 2006, 20, 341-351.	1.3	1,134
56	The metabonomics of aging and development in the rat: an investigation into the effect of age on the profile of endogenous metabolites in the urine of male rats using ¹ H NMR and HPLC-TOF MS. Molecular BioSystems, 2005, 1, 166.	2.9	119