Jaak Vilo

List of Publications by Year
in descending order

91 papers	20,291 citations	66234 42 h-index	46693 89 g-index
103 all docs	103 docs citations	103 times ranked	35636 citing authors

#	Article	IF	Citations
1	Minimum information about a microarray experiment (MIAME)â€"toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
2	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	6.5	3,302
3	ClustVis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap. Nucleic Acids Research, 2015, 43, W566-W570.	6.5	2,762
4	g:Profilerâ€"a web-based toolset for functional profiling of gene lists from large-scale experiments. Nucleic Acids Research, 2007, 35, W193-W200.	6.5	1,203
5	g:Profilerâ€"a web server for functional interpretation of gene lists (2016 update). Nucleic Acids Research, 2016, 44, W83-W89.	6.5	1,179
6	Robust rank aggregation for gene list integration and meta-analysis. Bioinformatics, 2012, 28, 573-580.	1.8	875
7	ArrayExpress--a public repository for microarray gene expression data at the EBI. Nucleic Acids Research, 2003, 31, 68-71.	6.5	727
8	Gene expression data analysis. FEBS Letters, 2000, 480, 17-24.	1.3	472
9	g:Profilerâ€"a web server for functional interpretation of gene lists (2011 update). Nucleic Acids Research, 2011, 39, W307-W315.	6.5	454
10	MethSurv: a web tool to perform multivariable survival analysis using DNA methylation data. Epigenomics, 2018, 10, 277-288.	1.0	381
11	A first-generation linkage disequilibrium map of human chromosome 22. Nature, 2002, 418, 544-548.	13.7	376
12	gprofiler2 -- an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	0.8	331
13	DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns. Genome Biology, 2014, 15, r54.	3.8	325
14	Predicting Gene Regulatory Elements in Silico on a Genomic Scale. Genome Research, 1998, 8, 1202-1215.	2.4	294
15	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. Archives of Toxicology, 2013, 87, 123-143.	1.9	222
16	Protein Interaction Verification and Functional Annotation by Integrated Analysis of Genome-Scale Data. Molecular Cell, 2002, 9, 1133-1143.	4.5	221
17	Metaâ€analysis of microRNA expression in lung cancer. International Journal of Cancer, 2013, 132, 2884-2893.	2.3	195
18	A Preclinical Model for ERÎ±-Positive Breast Cancer Points to the Epithelial Microenvironment as Determinant of Luminal Phenotype and Hormone Response. Cancer Cell, 2016, 29, 407-422.	7.7	168

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19	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. Scientific Reports, 2015, 5, 13107.	1.6	148
20	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. Genome Biology, 2009, 10, R139.	13.9	133
21	Mechanisms of IFN-Î³â€"induced apoptosis of human skin keratinocytes in patients with atopic dermatitis. Journal of Allergy and Clinical Immunology, 2012, 129, 1297-1306.	1.5	128
22	gprofiler2 -- an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. F1000Research, 2020, 9, 709.	0.8	128
23	MicroRNA Expression Profiles of Human Blood Monocyte-derived Dendritic Cells and Macrophages Reveal miR-511 as Putative Positive Regulator of Toll-like Receptor 4. Journal of Biological Chemistry, 2011, 286, 26487-26495.	1.6	121
24	Identification of miRâ€374a as a prognostic marker for survival in patients with earlyâ€stage nonsmall cell lung cancer. Genes Chromosomes and Cancer, 2011, 50, 812-822.	1.5	116
25	Research Resource: Interactome of Human Embryo Implantation: Identification of Gene Expression Pathways, Regulation, and Integrated Regulatory Networks. Molecular Endocrinology, 2012, 26, 203-217.	3.7	107
26	Expression Profiler: next generation--an online platform for analysis of microarray data. Nucleic Acids Research, 2004, 32, W465-W470.	6.5	105
27	Comprehensive reanalysis of transcription factor knockout expression data in Saccharomyces cerevisiae reveals many new targets. Nucleic Acids Research, 2010, 38, 4768-4777.	6.5	102
28	Gene Expression Profiles of Non-Small Cell Lung Cancer: Survival Prediction and New Biomarkers. Oncology, 2010, 79, 283-292.	0.9	98
29	A new way to protect privacy in large-scale genome-wide association studies. Bioinformatics, 2013, 29, 886-893.	1.8	98
30	ASTD: The Alternative Splicing and Transcript Diversity database. Genomics, 2009, 93, 213-220.	1.3	87
31	GOsummaries: an R Package for Visual Functional Annotation of Experimental Data. F1000Research, 2015, 4, 574.	0.8	86
32	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. Nucleic Acids Research, 2008, 36, W452-W459.	6.5	81
33	A Data Integration Approach to Mapping OCT4 Gene Regulatory Networks Operative in Embryonic Stem Cells and Embryonal Carcinoma Cells. PLoS ONE, 2010, 5, e10709.	1.1	81
34	Using RNA sequencing for identifying gene imprinting and random monoallelic expression in human placenta. Epigenetics, 2014, 9, 1397-1409.	1.3	74
35	Prediction of the coupling specificity of G protein coupled receptors to their G proteins. Bioinformatics, 2001, 17, S174-S181.	1.8	73
36	ArrayExpress: a public database of gene expression data at EBI. Comptes Rendus - Biologies, 2003, 326, 1075-1078.	0.1	69

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37	Translating genotype data of 44,000 biobank participants into clinical pharmacogenetic recommendations: challenges and solutions. Genetics in Medicine, 2019, 21, 1345-1354.	1.1	68
38	Comparing distributions of polygenic risk scores of type 2 diabetes and coronary heart disease within different populations. PLoS ONE, 2017, 12, e0179238.	1.1	67
39	Characterization of the Phosphoinositide 3-Kinase-Dependent Transcriptome in Murine Embryonic Stem Cells: Identification of Novel Regulators of Pluripotency. Stem Cells, 2009, 27, 764-775.	1.4	66
40	Gene expression data analysis#1Abridged version of article in FEBS Lett. 480 (2000) 17â€"24; with permission from Elsevier Science. PII of original article: S0014-5793(00)01772-5. Microbes and Infection, 2001, 3, 823-829.	1.0	56
41	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. PLoS ONE, 2009, 4, e6804.	1.1	54
42	From genomes to vaccines:Leishmaniaas a model. Philosophical Transactions of the Royal Society B: Biological Sciences, 2002, 357, 5-11.	1.8	49
43	Autoantibody Repertoire in APECED Patients Targets Two Distinct Subgroups of Proteins. Frontiers in Immunology, 2017, 8, 976.	2.2	48
44	Fast fully dynamic landmark-based estimation of shortest path distances in very large graphs. , 2011, , .		47
45	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. Molecular Biology of the Cell, 2014, 25, 2522-2536.	0.9	44
46	DNA methylation changes in endometrium and correlation with gene expression during the transition from pre-receptive to receptive phase. Scientific Reports, 2017, 7, 3916.	1.6	37
47	Autoimmune regulator is acetylated by transcription coactivator CBP/p300. Experimental Cell Research, 2012, 318, 1767-1778.	1.2	36
48	Comprehensive Meta-analysis of MicroRNA Expression Using a Robust Rank Aggregation Approach. Methods in Molecular Biology, 2014, 1182, 361-373.	0.4	36
49	HENA, heterogeneous network-based data set for Alzheimerâ€™s disease. Scientific Data, 2019, 6, 151.	2.4	34
50	KEGGanim: pathway animations for high-throughput data. Bioinformatics, 2008, 24, 588-590.	1.8	31
51	Three LIF-dependent signatures and gene clusters with atypical expression profiles, identified by transcriptome studies in mouse ES cells and early derivatives. BMC Genomics, 2009, 10, 73.	1.2	29
52	Genome-wide promoter analysis of histone modifications in human monocyte-derived antigen presenting cells. BMC Genomics, 2010, 11, 642.	1.2	29
53	Comprehensive transcriptome analysis of mouse embryonic stem cell adipogenesis unravels new processes of adipocyte development. Genome Biology, 2010, 11, R80.	13.9	29
54	seqlm: an MDL based method for identifying differentially methylated regions in high density methylation array data. Bioinformatics, 2016, 32, 2604-2610.	1.8	29

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55	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. European Journal of Human Genetics, 2019, 27, 442-454.	1.4	29
56	Validating Fitbit Zip for monitoring physical activity of children in school: a cross-sectional study. BMC Public Health, 2018, 18, 858.	1.2	28
57	Relicensing of Transcriptionally Inactivated Replication Origins in Budding Yeast. Journal of Biological Chemistry, 2010, 285, 40004-40011.	1.6	27
58	Pattern discovery in biosequences. Lecture Notes in Computer Science, 1998, , 257-270.	1.0	23
59	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	15.2	23
60	Gene Expression Signatures Defining Fundamental Biological Processes in Pluripotent, Early, and Late Differentiated Embryonic Stem Cells. Stem Cells and Development, 2012, 21, 2471-2484.	1.1	21
61	Prostaglandin D2 Receptor DP1 Antibodies Predict Vaccine-induced and Spontaneous Narcolepsy Type 1: Large-scale Study of Antibody Profiling. EBioMedicine, 2018, 29, 47-59.	2.7	21
62	Microarray Data Representation, Annotation and Storage. Advances in Biochemical Engineering/Biotechnology, 2002, 77, 113-139.	0.6	21
63	Regulatory sequence analysis: application to the interpretation of gene expression. European Neuropsychopharmacology, 2001, 11, 399-411.	0.3	20
64	TRIB3 enhances cell viability during glucose deprivation in HEK293-derived cells by upregulating IGFBP2, a novel nutrient deficiency survival factor. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 2492-2505.	1.9	17
65	Correlating gene promoters and expression in gene disruption experiments. Bioinformatics, 2002, 18, S172-S180.	1.8	16
66	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. Frontiers in Physiology, 2013, 4, 303.	1.3	15
67	DosOpt: A Tool for Personalized Bayesian Dose Adjustment of Vancomycin in Neonates. Therapeutic Drug Monitoring, 2017, 39, 604-613.	1.0	15
68	Fast approximate hierarchical clustering using similarity heuristics. BioData Mining, 2008, 1, 9.	2.2	14
69	Estimating differential expression from multiple indicators. Nucleic Acids Research, 2014, 42, e72-e72.	6.5	13
70	Healthspan pathway maps in C. elegans and humans highlight transcription, proliferation/biosynthesis and lipids. Aging, 2020, 12, 12534-12581.	1.4	12
71	Ranking Genes by Their Co‐expression to Subsets of Pathway Members. Annals of the New York Academy of Sciences, 2009, 1158, 1-13.	1.8	11
72	FUN-L: gene prioritization for RNAi screens: Fig. 1.. Bioinformatics, 2015, 31, 2052-2053.	1.8	9

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73	An exploratory phenome wide association study linking asthma and liver disease genetic variants to electronic health records from the Estonian Biobank. PLoS ONE, 2019, 14, e0215026.	1.1	8
74	VisHiC--hierarchical functional enrichment analysis of microarray data. Nucleic Acids Research, 2009, 37, W587-W592.	6.5	7
75	m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. Genome Biology, 2012, 13, R55.	13.9	7
76	Peripheral gene expression profiling of CCKâ€4â€induced panic in healthy subjects. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 269-274.	1.1	6
77	Fast probabilistic file fingerprinting for big data. BMC Genomics, 2013, 14, S8.	1.2	6
78	Expression Profiler. Statistics in the Health Sciences, 2003, , 142-162.	0.2	5
79	Global transcriptomic analysis of murine embryonic stem cellâ€derived brachyury^{+} (T) cells. Genes To Cells, 2010, 15, 209-228.	0.5	5
80	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. BMC Genomics, 2018, 19, 817.	1.2	5
81	Trajectories: a framework for detecting temporal clinical event sequences from health data standardized to the Observational Medical Outcomes Partnership (OMOP) Common Data Model. JAMIA Open, 2022, 5, ooac021.	1.0	5
82	Fraud Detection: Methods of Analysis for Hypergraph Data. , 2012, , .		4
83	PAWER: protein array web exploreR. BMC Bioinformatics, 2020, 21, 411.	1.2	4
84	Gene Expression Data Mining and Analysis. Principles and Practice, 2001, , 105-129.	0.3	3
85	Gene Expression-Based Approaches in Differentiation of Metastases and Second Primary Tumour. Case Reports in Oncology, 2010, 3, 255-261.	0.3	2
86	POSTER VIEWING SESSION - ENDOMETRIOSIS, ENDOMETRIUM, IMPLANTATION AND FALLOPIAN TUBE. Human Reproduction, 2011, 26, i202-i223.	0.4	2
87	Gâ€Š=â€ŠMAT: Linking Transcription Factor Expression and DNA Binding Data. PLoS ONE, 2011, 6, e14559.	1.1	1
88	Comparison of variation in frequency for SNPs associated with asthma or liver disease between Estonia, HapMap populations and the 1000 genome project populations. International Journal of Immunogenetics, 2019, 46, 49-58.	0.8	0
89	An Evolutionary Model of DNA Substring Distribution. Lecture Notes in Computer Science, 2010, , 147-157.	1.0	0
90	Graphs in Bioinformatics and Social Networks. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 99, 3-4.	0.8	0

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91	Abstract 1698: Systems pathology for characterization of cancer model systems in a multicenter IMI-PREDECT project. , 2015, , .		0