

Jaak Vilo

List of Publications by Year in descending order

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Version: 2024-02-01

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	Trajectories: a framework for detecting temporal clinical event sequences from health data standardized to the Observational Medical Outcomes Partnership (OMOP) Common Data Model. <i>JAMIA Open</i> , 2022, 5, ooac021.	1.0	5
2	PAWER: protein array web exploreR. <i>BMC Bioinformatics</i> , 2020, 21, 411.	1.2	4
3	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	15.2	23
4	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. <i>F1000Research</i> , 2020, 9, 709.	0.8	128
5	gprofiler2 – an R package for gene list functional enrichment analysis and namespace conversion toolset g:Profiler. <i>F1000Research</i> , 2020, 9, 709.	0.8	331
6	Healthspan pathway maps in <i>C. elegans</i> and humans highlight transcription, proliferation/biosynthesis and lipids. <i>Aging</i> , 2020, 12, 12534-12581.	1.4	12
7	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	2.4	34
8	Comparison of variation in frequency for SNPs associated with asthma or liver disease between Estonia, HapMap populations and the 1000 genome project populations. <i>International Journal of Immunogenetics</i> , 2019, 46, 49-58.	0.8	0
9	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq1 1 0.784314 rgBT /Overlock 1 6.58 3,302	6.58	3,302
10	An exploratory phenome wide association study linking asthma and liver disease genetic variants to electronic health records from the Estonian Biobank. <i>PLoS ONE</i> , 2019, 14, e0215026.	1.1	8
11	Genetic variation in the Estonian population: pharmacogenomics study of adverse drug effects using electronic health records. <i>European Journal of Human Genetics</i> , 2019, 27, 442-454.	1.4	29
12	Translating genotype data of 44,000 biobank participants into clinical pharmacogenetic recommendations: challenges and solutions. <i>Genetics in Medicine</i> , 2019, 21, 1345-1354.	1.1	68
13	MethSurv: a web tool to perform multivariable survival analysis using DNA methylation data. <i>Epigenomics</i> , 2018, 10, 277-288.	1.0	381
14	Prostaglandin D2 Receptor DP1 Antibodies Predict Vaccine-induced and Spontaneous Narcolepsy Type 1: Large-scale Study of Antibody Profiling. <i>EBioMedicine</i> , 2018, 29, 47-59.	2.7	21
15	funcExplorer: a tool for fast data-driven functional characterisation of high-throughput expression data. <i>BMC Genomics</i> , 2018, 19, 817.	1.2	5
16	Validating Fitbit Zip for monitoring physical activity of children in school: a cross-sectional study. <i>BMC Public Health</i> , 2018, 18, 858.	1.2	28
17	DNA methylation changes in endometrium and correlation with gene expression during the transition from pre-receptive to receptive phase. <i>Scientific Reports</i> , 2017, 7, 3916.	1.6	37
18	DosOpt: A Tool for Personalized Bayesian Dose Adjustment of Vancomycin in Neonates. <i>Therapeutic Drug Monitoring</i> , 2017, 39, 604-613.	1.0	15

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19	Autoantibody Repertoire in APECED Patients Targets Two Distinct Subgroups of Proteins. <i>Frontiers in Immunology</i> , 2017, 8, 976.	2.2	48
20	Comparing distributions of polygenic risk scores of type 2 diabetes and coronary heart disease within different populations. <i>PLoS ONE</i> , 2017, 12, e0179238.	1.1	67
21	A Preclinical Model for ER α -Positive Breast Cancer Points to the Epithelial Microenvironment as Determinant of Luminal Phenotype and Hormone Response. <i>Cancer Cell</i> , 2016, 29, 407-422.	7.7	168
22	g:Profiler—a web server for functional interpretation of gene lists (2016 update). <i>Nucleic Acids Research</i> , 2016, 44, W83-W89.	6.5	1,179
23	seqm: an MDL based method for identifying differentially methylated regions in high density methylation array data. <i>Bioinformatics</i> , 2016, 32, 2604-2610.	1.8	29
24	Age-related profiling of DNA methylation in CD8+ T cells reveals changes in immune response and transcriptional regulator genes. <i>Scientific Reports</i> , 2015, 5, 13107.	1.6	148
25	FUN-L: gene prioritization for RNAi screens: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2052-2053.	1.8	9
26	ClustVis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap. <i>Nucleic Acids Research</i> , 2015, 43, W566-W570.	6.5	2,762
27	TRIB3 enhances cell viability during glucose deprivation in HEK293-derived cells by upregulating IGFBP2, a novel nutrient deficiency survival factor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 2492-2505.	1.9	17
28	GOsummaries: an R Package for Visual Functional Annotation of Experimental Data. <i>F1000Research</i> , 2015, 4, 574.	0.8	86
29	Abstract 1698: Systems pathology for characterization of cancer model systems in a multicenter IMI-PREDECT project. , 2015, , .		0
30	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. <i>Molecular Biology of the Cell</i> , 2014, 25, 2522-2536.	0.9	44
31	Using RNA sequencing for identifying gene imprinting and random monoallelic expression in human placenta. <i>Epigenetics</i> , 2014, 9, 1397-1409.	1.3	74
32	Estimating differential expression from multiple indicators. <i>Nucleic Acids Research</i> , 2014, 42, e72-e72.	6.5	13
33	DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns. <i>Genome Biology</i> , 2014, 15, r54.	3.8	325
34	Comprehensive Meta-analysis of MicroRNA Expression Using a Robust Rank Aggregation Approach. <i>Methods in Molecular Biology</i> , 2014, 1182, 361-373.	0.4	36
35	Fast probabilistic file fingerprinting for big data. <i>BMC Genomics</i> , 2013, 14, S8.	1.2	6
36	Human embryonic stem cell-derived test systems for developmental neurotoxicity: a transcriptomics approach. <i>Archives of Toxicology</i> , 2013, 87, 123-143.	1.9	222

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37	Meta-analysis of microRNA expression in lung cancer. <i>International Journal of Cancer</i> , 2013, 132, 2884-2893.	2.3	195
38	Qualitative modeling identifies IL-11 as a novel regulator in maintaining self-renewal in human pluripotent stem cells. <i>Frontiers in Physiology</i> , 2013, 4, 303.	1.3	15
39	A new way to protect privacy in large-scale genome-wide association studies. <i>Bioinformatics</i> , 2013, 29, 886-893.	1.8	98
40	Research Resource: Interactome of Human Embryo Implantation: Identification of Gene Expression Pathways, Regulation, and Integrated Regulatory Networks. <i>Molecular Endocrinology</i> , 2012, 26, 203-217.	3.7	107
41	Robust rank aggregation for gene list integration and meta-analysis. <i>Bioinformatics</i> , 2012, 28, 573-580.	1.8	875
42	m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. <i>Genome Biology</i> , 2012, 13, R55.	13.9	7
43	Mechanisms of IFN- γ -induced apoptosis of human skin keratinocytes in patients with atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1297-1306.	1.5	128
44	Gene Expression Signatures Defining Fundamental Biological Processes in Pluripotent, Early, and Late Differentiated Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2012, 21, 2471-2484.	1.1	21
45	Fraud Detection: Methods of Analysis for Hypergraph Data. , 2012, , .		4
46	Autoimmune regulator is acetylated by transcription coactivator CBP/p300. <i>Experimental Cell Research</i> , 2012, 318, 1767-1778.	1.2	36
47	G α S-MAT: Linking Transcription Factor Expression and DNA Binding Data. <i>PLoS ONE</i> , 2011, 6, e14559.	1.1	1
48	Identification of miR-374a as a prognostic marker for survival in patients with early-stage nonsmall cell lung cancer. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 812-822.	1.5	116
49	Fast fully dynamic landmark-based estimation of shortest path distances in very large graphs. , 2011, , .		47
50	MicroRNA Expression Profiles of Human Blood Monocyte-derived Dendritic Cells and Macrophages Reveal miR-511 as Putative Positive Regulator of Toll-like Receptor 4. <i>Journal of Biological Chemistry</i> , 2011, 286, 26487-26495.	1.6	121
51	POSTER VIEWING SESSION - ENDOMETRIOSIS, ENDOMETRIUM, IMPLANTATION AND FALLOPIAN TUBE. <i>Human Reproduction</i> , 2011, 26, i202-i223.	0.4	2
52	g:Profiler—a web server for functional interpretation of gene lists (2011 update). <i>Nucleic Acids Research</i> , 2011, 39, W307-W315.	6.5	454
53	Peripheral gene expression profiling of CCK α -induced panic in healthy subjects. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 269-274.	1.1	6
54	Genome-wide promoter analysis of histone modifications in human monocyte-derived antigen presenting cells. <i>BMC Genomics</i> , 2010, 11, 642.	1.2	29

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55	Global transcriptomic analysis of murine embryonic stem cell-derived brachyury ⁺ (T) cells. <i>Genes To Cells</i> , 2010, 15, 209-228.	0.5	5
56	Comprehensive reanalysis of transcription factor knockout expression data in <i>Saccharomyces cerevisiae</i> reveals many new targets. <i>Nucleic Acids Research</i> , 2010, 38, 4768-4777.	6.5	102
57	Relicensing of Transcriptionally Inactivated Replication Origins in Budding Yeast. <i>Journal of Biological Chemistry</i> , 2010, 285, 40004-40011.	1.6	27
58	Gene Expression-Based Approaches in Differentiation of Metastases and Second Primary Tumour. <i>Case Reports in Oncology</i> , 2010, 3, 255-261.	0.3	2
59	Gene Expression Profiles of Non-Small Cell Lung Cancer: Survival Prediction and New Biomarkers. <i>Oncology</i> , 2010, 79, 283-292.	0.9	98
60	Comprehensive transcriptome analysis of mouse embryonic stem cell adipogenesis unravels new processes of adipocyte development. <i>Genome Biology</i> , 2010, 11, R80.	13.9	29
61	A Data Integration Approach to Mapping OCT4 Gene Regulatory Networks Operative in Embryonic Stem Cells and Embryonal Carcinoma Cells. <i>PLoS ONE</i> , 2010, 5, e10709.	1.1	81
62	An Evolutionary Model of DNA Substring Distribution. <i>Lecture Notes in Computer Science</i> , 2010, , 147-157.	1.0	0
63	VisHiC-hierarchical functional enrichment analysis of microarray data. <i>Nucleic Acids Research</i> , 2009, 37, W587-W592.	6.5	7
64	Three LIF-dependent signatures and gene clusters with atypical expression profiles, identified by transcriptome studies in mouse ES cells and early derivatives. <i>BMC Genomics</i> , 2009, 10, 73.	1.2	29
65	Characterization of the Phosphoinositide 3-Kinase-Dependent Transcriptome in Murine Embryonic Stem Cells: Identification of Novel Regulators of Pluripotency. <i>Stem Cells</i> , 2009, 27, 764-775.	1.4	66
66	Ranking Genes by Their Co-expression to Subsets of Pathway Members. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 1-13.	1.8	11
67	ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009, 93, 213-220.	1.3	87
68	Mining for coexpression across hundreds of datasets using novel rank aggregation and visualization methods. <i>Genome Biology</i> , 2009, 10, R139.	13.9	133
69	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. <i>PLoS ONE</i> , 2009, 4, e6804.	1.1	54
70	Fast approximate hierarchical clustering using similarity heuristics. <i>BioData Mining</i> , 2008, 1, 9.	2.2	14
71	GraphWeb: mining heterogeneous biological networks for gene modules with functional significance. <i>Nucleic Acids Research</i> , 2008, 36, W452-W459.	6.5	81
72	KEGGanim: pathway animations for high-throughput data. <i>Bioinformatics</i> , 2008, 24, 588-590.	1.8	31

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73	g:Profiler—a web-based toolset for functional profiling of gene lists from large-scale experiments. <i>Nucleic Acids Research</i> , 2007, 35, W193-W200.	6.5	1,203
74	Expression Profiler: next generation—an online platform for analysis of microarray data. <i>Nucleic Acids Research</i> , 2004, 32, W465-W470.	6.5	105
75	ArrayExpress: a public database of gene expression data at EBI. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1075-1078.	0.1	69
76	ArrayExpress—a public repository for microarray gene expression data at the EBI. <i>Nucleic Acids Research</i> , 2003, 31, 68-71.	6.5	727
77	Expression Profiler. <i>Statistics in the Health Sciences</i> , 2003, , 142-162.	0.2	5
78	Correlating gene promoters and expression in gene disruption experiments. <i>Bioinformatics</i> , 2002, 18, S172-S180.	1.8	16
79	From genomes to vaccines: <i>Leishmania</i> as a model. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 5-11.	1.8	49
80	Protein Interaction Verification and Functional Annotation by Integrated Analysis of Genome-Scale Data. <i>Molecular Cell</i> , 2002, 9, 1133-1143.	4.5	221
81	A first-generation linkage disequilibrium map of human chromosome 22. <i>Nature</i> , 2002, 418, 544-548.	13.7	376
82	Microarray Data Representation, Annotation and Storage. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2002, 77, 113-139.	0.6	21
83	Regulatory sequence analysis: application to the interpretation of gene expression. <i>European Neuropsychopharmacology</i> , 2001, 11, 399-411.	0.3	20
84	Gene expression data analysis#1Abridged version of article in <i>FEBS Lett.</i> 480 (2000) 17–24; with permission from Elsevier Science. PII of original article: S0014-5793(00)01772-5. <i>Microbes and Infection</i> , 2001, 3, 823-829.	1.0	56
85	Minimum information about a microarray experiment (MIAME)—toward standards for microarray data. <i>Nature Genetics</i> , 2001, 29, 365-371.	9.4	3,750
86	Prediction of the coupling specificity of G protein coupled receptors to their G proteins. <i>Bioinformatics</i> , 2001, 17, S174-S181.	1.8	73
87	Gene Expression Data Mining and Analysis. <i>Principles and Practice</i> , 2001, , 105-129.	0.3	3
88	Gene expression data analysis. <i>FEBS Letters</i> , 2000, 480, 17-24.	1.3	472
89	Predicting Gene Regulatory Elements in Silico on a Genomic Scale. <i>Genome Research</i> , 1998, 8, 1202-1215.	2.4	294
90	Pattern discovery in biosequences. <i>Lecture Notes in Computer Science</i> , 1998, , 257-270.	1.0	23

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91	Graphs in Bioinformatics and Social Networks. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 99, 3-4.	0.8	0