

Jörg Rahnert

List of Publications by Year in descending order

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121
papers

8,094
citations

61857

43
h-index

56606

83
g-index

137
all docs

137
docs citations

137
times ranked

13384
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved scoring of functional groups from gene expression data by decorrelating GO graph structure. <i>Bioinformatics</i> , 2006, 22, 1600-1607.	1.8	1,927
2	Benchmark for filter methods for feature selection in high-dimensional classification data. <i>Computational Statistics and Data Analysis</i> , 2020, 143, 106839.	0.7	356
3	Arabidopsis Female Gametophyte Gene Expression Map Reveals Similarities between Plant and Animal Gametes. <i>Current Biology</i> , 2010, 20, 506-512.	1.8	302
4	Biomarker Discovery in Non-Small Cell Lung Cancer: Integrating Gene Expression Profiling, Meta-analysis, and Tissue Microarray Validation. <i>Clinical Cancer Research</i> , 2013, 19, 194-204.	3.2	293
5	A Comprehensive Analysis of Human Gene Expression Profiles Identifies Stromal Immunoglobulin κ C as a Compatible Prognostic Marker in Human Solid Tumors. <i>Clinical Cancer Research</i> , 2012, 18, 2695-2703.	3.2	237
6	Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions. <i>Journal of Clinical Investigation</i> , 2009, 119, 1727-1740.	3.9	230
7	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
8	Loss of circadian clock gene expression is associated with tumor progression in breast cancer. <i>Cell Cycle</i> , 2014, 13, 3282-3291.	1.3	193
9	Role of thioredoxin reductase 1 and thioredoxin interacting protein in prognosis of breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R44.	2.2	180
10	The prognostic relevance of tumour-infiltrating plasma cells and immunoglobulin kappa C indicates an important role of the humoral immune response in non-small cell lung cancer. <i>Cancer Letters</i> , 2013, 333, 222-228.	3.2	162
11	Toxicogenomics directory of chemically exposed human hepatocytes. <i>Archives of Toxicology</i> , 2014, 88, 2261-2287.	1.9	143
12	Going from where to why—interpretable prediction of protein subcellular localization. <i>Bioinformatics</i> , 2010, 26, 1232-1238.	1.8	133
13	ERBB2 and TOP2A in Breast Cancer: A Comprehensive Analysis of Gene Amplification, RNA Levels, and Protein Expression and Their Influence on Prognosis and Prediction. <i>Clinical Cancer Research</i> , 2010, 16, 2391-2401.	3.2	113
14	Learning Multiple Evolutionary Pathways from Cross-Sectional Data. <i>Journal of Computational Biology</i> , 2005, 12, 584-598.	0.8	105
15	Design Principles of Concentration-Dependent Transcriptome Deviations in Drug-Exposed Differentiating Stem Cells. <i>Chemical Research in Toxicology</i> , 2014, 27, 408-420.	1.7	103
16	Interferon-inducible guanylate binding protein (GBP2) is associated with better prognosis in breast cancer and indicates an efficient T cell response. <i>Breast Cancer</i> , 2014, 21, 491-499.	1.3	91
17	Altered Stress-Induced Regulation of Genes in Monocytes in Adults with a History of Childhood Adversity. <i>Neuropsychopharmacology</i> , 2016, 41, 2530-2540.	2.8	90
18	Prediction of human drug-induced liver injury (DILI) in relation to oral doses and blood concentrations. <i>Archives of Toxicology</i> , 2019, 93, 1609-1637.	1.9	86

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19	A transcriptome-based classifier to identify developmental toxicants by stem cell testing: design, validation and optimization for histone deacetylase inhibitors. Archives of Toxicology, 2015, 89, 1599-1618.	1.9	82
20	Profiling cancer testis antigens in non-“small-cell lung cancer. JCI Insight, 2016, 1, e86837.	2.3	82
21	Retention time alignment algorithms for LC/MS data must consider non-linear shifts. Bioinformatics, 2009, 25, 758-764.	1.8	78
22	Estimating HIV Evolutionary Pathways and the Genetic Barrier to Drug Resistance. Journal of Infectious Diseases, 2005, 191, 1953-1960.	1.9	76
23	Retinal properties and potential of the adult mammalian ciliary epithelium stem cells. Vision Research, 2005, 45, 1653-1666.	0.7	71
24	CORRESPONDENCE OF TUMOR LOCALIZATION WITH TUMOR RECURRENCE AND CYTOGENETIC PROGRESSION IN MENINGIOMAS. Neurosurgery, 2008, 62, 61-70.	0.6	71
25	Stem Cell-Derived Immature Human Dorsal Root Ganglia Neurons to Identify Peripheral Neurotoxicants. Stem Cells Translational Medicine, 2016, 5, 476-487.	1.6	69
26	Mtreemix: a software package for learning and using mixture models of mutagenetic trees. Bioinformatics, 2005, 21, 2106-2107.	1.8	68
27	Identification of c-Kit receptor as a regulator of adult neural stem cells in the mammalian eye: interactions with Notch signaling. Developmental Biology, 2004, 273, 87-105.	0.9	67
28	From transient transcriptome responses to disturbed neurodevelopment: role of histone acetylation and methylation as epigenetic switch between reversible and irreversible drug effects. Archives of Toxicology, 2014, 88, 1451-1468.	1.9	67
29	Expression of aurora kinase A is associated with metastasis-free survival in node-negative breast cancer patients. BMC Cancer, 2012, 12, 562.	1.1	62
30	Molecular Biological Determinations of Meningioma Progression and Recurrence. PLoS ONE, 2014, 9, e94987.	1.1	58
31	Glycerol-3-phosphate Acyltransferase 1 Promotes Tumor Cell Migration and Poor Survival in Ovarian Carcinoma. Cancer Research, 2017, 77, 4589-4601.	0.4	58
32	TiMEx: a waiting time model for mutually exclusive cancer alterations. Bioinformatics, 2016, 32, 968-975.	1.8	57
33	Benchmark of filter methods for feature selection in high-dimensional gene expression survival data. Briefings in Bioinformatics, 2022, 23, .	3.2	57
34	Cellular and molecular characterization of early and late retinal stem cells/progenitors: Differential regulation of proliferation and context dependent role of Notch signaling. Journal of Neurobiology, 2004, 61, 359-376.	3.7	56
35	Patients with High-Grade Gliomas Harboring Deletions of Chromosomes 9p and 10q Benefit from Temozolomide Treatment. Neoplasia, 2005, 7, 883-893.	2.3	55
36	The lung-“specific proteome defined by integration of transcriptomics and antibody-“based profiling. FASEB Journal, 2014, 28, 5184-5196.	0.2	54

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37	Prognostic Impact of Tumor Cell Programmed Death Ligand 1 Expression and Immune Cell Infiltration in NSCLC. <i>Journal of Thoracic Oncology</i> , 2019, 14, 628-640.	0.5	54
38	Definition of transcriptome-based indices for quantitative characterization of chemically disturbed stem cell development: introduction of the STOP-Toxukn and STOP-Toxukk tests. <i>Archives of Toxicology</i> , 2017, 91, 839-864.	1.9	53
39	Integrative analysis of genome-wide gene copy number changes and gene expression in non-small cell lung cancer. <i>PLoS ONE</i> , 2017, 12, e0187246.	1.1	51
40	TEAD-YAP Interaction Inhibitors and MDM2 Binders from DNA-Encoded Indole-Focused Ugi Peptidomimetics. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 20338-20342.	7.2	50
41	Glycerophospholipid profile in oncogene-induced senescence. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2012, 1821, 1256-1268.	1.2	49
42	Estimating cancer survival and clinical outcome based on genetic tumor progression scores. <i>Bioinformatics</i> , 2005, 21, 2438-2446.	1.8	46
43	ERBB2 Induces an Antiapoptotic Expression Pattern of Bcl-2 Family Members in Node-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2010, 16, 451-460.	3.2	46
44	<sc>D</sc>-score: A search engine independent <sc>MD</sc>-score. <i>Proteomics</i> , 2013, 13, 1036-1041.	1.3	46
45	Identification of sample annotation errors in gene expression datasets. <i>Archives of Toxicology</i> , 2015, 89, 2265-2272.	1.9	46
46	Toxicogenomics directory of rat hepatotoxicants in vivo and in cultivated hepatocytes. <i>Archives of Toxicology</i> , 2018, 92, 3517-3533.	1.9	46
47	Probabilistic Consensus Scoring Improves Tandem Mass Spectrometry Peptide Identification. <i>Journal of Proteome Research</i> , 2011, 10, 3332-3343.	1.8	45
48	Application of oncogenetic trees mixtures as a biostatistical model of the clonal cytogenetic evolution of meningiomas. <i>International Journal of Cancer</i> , 2007, 121, 1473-1480.	2.3	44
49	Epsin Family Member 3 and Ribosome-Related Genes Are Associated with Late Metastasis in Estrogen Receptor-Positive Breast Cancer and Long-Term Survival in Non-Small Cell Lung Cancer Using a Genome-Wide Identification and Validation Strategy. <i>PLoS ONE</i> , 2016, 11, e0167585.	1.1	44
50	Identification of transcriptome signatures and biomarkers specific for potential developmental toxicants inhibiting human neural crest cell migration. <i>Archives of Toxicology</i> , 2016, 90, 159-180.	1.9	43
51	Long-term prognostic significance of HER2-low and HER2-zero in node-negative breast cancer. <i>European Journal of Cancer</i> , 2022, 173, 10-19.	1.3	42
52	Peek a peak: a glance at statistics for quantitative label-free proteomics. <i>Expert Review of Proteomics</i> , 2010, 7, 249-261.	1.3	41
53	Relevance of the incubation period in cytotoxicity testing with primary human hepatocytes. <i>Archives of Toxicology</i> , 2018, 92, 3505-3515.	1.9	41
54	LIPG-promoted lipid storage mediates adaptation to oxidative stress in breast cancer. <i>International Journal of Cancer</i> , 2019, 145, 901-915.	2.3	41

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55	Prognostic Influence of Pre-Operative C-Reactive Protein in Node-Negative Breast Cancer Patients. PLoS ONE, 2014, 9, e111306.	1.1	40
56	Human Pluripotent Stem Cell Based Developmental Toxicity Assays for Chemical Safety Screening and Systems Biology Data Generation. Journal of Visualized Experiments, 2015, , e52333.	0.2	39
57	Stem Cell Transcriptome Responses and Corresponding Biomarkers That Indicate the Transition from Adaptive Responses to Cytotoxicity. Chemical Research in Toxicology, 2017, 30, 905-922.	1.7	37
58	Reef calcifiers are adapted to episodic heat stress but vulnerable to sustained warming. PLoS ONE, 2017, 12, e0179753.	1.1	37
59	The G Protein-Coupled Bile Acid Receptor TGR5 (Gpbar1) Modulates Endothelin-1 Signaling in Liver. Cells, 2019, 8, 1467.	1.8	35
60	EDI3 links choline metabolism to integrin expression, cell adhesion and spreading. Cell Adhesion and Migration, 2014, 8, 499-508.	1.1	34
61	Comparison of a teratogenic transcriptome-based predictive test based on human embryonic versus inducible pluripotent stem cells. Stem Cell Research and Therapy, 2016, 7, 190.	2.4	34
62	Development of a neural rosette formation assay (RoFA) to identify neurodevelopmental toxicants and to characterize their transcriptome disturbances. Archives of Toxicology, 2020, 94, 151-171.	1.9	32
63	Hepatotoxicity of piperazine designer drugs: up-regulation of key enzymes of cholesterol and lipid biosynthesis. Archives of Toxicology, 2016, 90, 3045-3060.	1.9	31
64	Interruption of bile acid uptake by hepatocytes after acetaminophen overdose ameliorates hepatotoxicity. Journal of Hepatology, 2022, 77, 71-83.	1.8	31
65	Ep-CAM RNA expression predicts metastasis-free survival in three cohorts of untreated node-negative breast cancer. Breast Cancer Research and Treatment, 2011, 125, 637-646.	1.1	30
66	Test systems of developmental toxicity: state-of-the art and future perspectives. Archives of Toxicology, 2013, 87, 2037-2042.	1.9	29
67	Gelsolin Is Associated with Longer Metastasis-free Survival and Reduced Cell Migration in Estrogen Receptor-positive Breast Cancer. Anticancer Research, 2015, 35, 5277-85.	0.5	29
68	Prognostic impact of COX-2 in non-small cell lung cancer: A comprehensive compartment-specific evaluation of tumor and stromal cell expression. Cancer Letters, 2015, 356, 837-845.	3.2	28
69	Protein phosphatase and TRAIL receptor genes as new candidate tumor genes on chromosome 8p in prostate cancer. Cancer Genomics and Proteomics, 2008, 5, 123-36.	1.0	27
70	Metabolic profiling of ob/ob mouse fatty liver using HR-MAS 1H-NMR combined with gene expression analysis reveals alterations in betaine metabolism and the transsulfuration pathway. Analytical and Bioanalytical Chemistry, 2017, 409, 1591-1606.	1.9	26
71	Assessment of stem cell differentiation based on genome-wide expression profiles. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170221.	1.8	26
72	Variable thermal stress tolerance of the reef-associated symbiont-bearing foraminifera Amphistegina linked to differences in symbiont type. Coral Reefs, 2018, 37, 811-824.	0.9	26

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73	Impact of intratumoral heterogeneity of breast cancer tissue on quantitative metabolomics using high-resolution magic angle spinning ¹ H NMR spectroscopy. <i>NMR in Biomedicine</i> , 2018, 31, e3862.	1.6	25
74	Introduction to statistical simulations in health research. <i>BMJ Open</i> , 2020, 10, e039921.	0.8	24
75	Spatio-Temporal Multiscale Analysis of Western Diet-Fed Mice Reveals a Translationally Relevant Sequence of Events during NAFLD Progression. <i>Cells</i> , 2021, 10, 2516.	1.8	24
76	Analysis of Compound Synergy in High-Throughput Cellular Screens by Population-Based Lifetime Modeling. <i>PLoS ONE</i> , 2010, 5, e8919.	1.1	24
77	Hyperdiploidy defines a distinct cytogenetic entity of meningiomas. <i>Journal of Neuro-Oncology</i> , 2007, 83, 213-221.	1.4	23
78	Cumulative disease progression models for cross-sectional data: A review and comparison. <i>Biometrical Journal</i> , 2012, 54, 617-640.	0.6	20
79	The hepatocyte export carrier inhibition assay improves the separation of hepatotoxic from non-hepatotoxic compounds. <i>Chemico-Biological Interactions</i> , 2022, 351, 109728.	1.7	18
80	Polymorphisms in the IGF1 signalling pathway including the myostatin gene are associated with left ventricular mass in male athletes. <i>British Journal of Sports Medicine</i> , 2011, 45, 36-41.	3.1	17
81	Reaching the limits of prognostication in non-small cell lung cancer: an optimized biomarker panel fails to outperform clinical parameters. <i>Modern Pathology</i> , 2017, 30, 964-977.	2.9	17
82	No Longer Confidential: Estimating the Confidence of Individual Regression Predictions. <i>PLoS ONE</i> , 2012, 7, e48723.	1.1	16
83	Cost-Constrained feature selection in binary classification: adaptations for greedy forward selection and genetic algorithms. <i>BMC Bioinformatics</i> , 2020, 21, 26.	1.2	16
84	Classification with High-Dimensional Genetic Data: Assigning Patients and Genetic Features to Known Classes. <i>Biometrical Journal</i> , 2008, 50, 911-926.	0.6	15
85	Clonal cytogenetic progression within intratumorally heterogeneous meningiomas predicts tumor recurrence. <i>International Journal of Oncology</i> , 2011, 39, 1601-8.	1.4	15
86	DISMS2: A flexible algorithm for direct proteome-wide distance calculation of LC-MS/MS runs. <i>BMC Bioinformatics</i> , 2017, 18, 148.	1.2	15
87	Normalization of data for viability and relative cell function curves. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2018, 35, 268-271.	0.9	15
88	Clinical Outcome of Patients with Lymph Node-Positive Prostate Cancer following Radical Prostatectomy and Extended Sentinel Lymph Node Dissection. <i>Urologia Internationalis</i> , 2015, 94, 296-306.	0.6	14
89	A Multicriteria Approach to Find Predictive and Sparse Models with Stable Feature Selection for High-Dimensional Data. <i>Computational and Mathematical Methods in Medicine</i> , 2017, 2017, 1-18.	0.7	13
90	Kinetic modeling of stem cell transcriptome dynamics to identify regulatory modules of normal and disturbed neuroectodermal differentiation. <i>Nucleic Acids Research</i> , 2020, 48, 12577-12592.	6.5	13

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91	Rtreemix: an R package for estimating evolutionary pathways and genetic progression scores. <i>Bioinformatics</i> , 2008, 24, 2391-2392.	1.8	12
92	Runtime and memory consumption analyses for machine learning R programs. <i>Journal of Statistical Computation and Simulation</i> , 2015, 85, 14-29.	0.7	12
93	Impairment of human neural crest cell migration by prolonged exposure to interferon-beta. <i>Archives of Toxicology</i> , 2017, 91, 3385-3402.	1.9	12
94	Gene Expressionâ€‘Based Prediction of Neoadjuvant Chemotherapy Response in Early Breast Cancer: Results of the Prospective Multicenter EXPRESSION Trial. <i>Clinical Cancer Research</i> , 2021, 27, 2148-2158.	3.2	12
95	Determination of benchmark concentrations and their statistical uncertainty for cytotoxicity test data and functional in vitro assays. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2020, 37, 155-163.	0.9	12
96	Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2017, 16, 4035-4044.	1.8	10
97	Modelling non-stationary dynamic gene regulatory processes with the BGM model. <i>Computational Statistics</i> , 2011, 26, 199-218.	0.8	9
98	From smoking guns to footprints: mining for critical events of toxicity pathways in transcriptome data. <i>Archives of Toxicology</i> , 2015, 89, 813-817.	1.9	9
99	Handling deviating control values in concentration-response curves. <i>Archives of Toxicology</i> , 2020, 94, 3787-3798.	1.9	9
100	Prognostic Impact of Immunoglobulin Kappa C (IGKC) in Early Breast Cancer. <i>Cancers</i> , 2021, 13, 3626.	1.7	9
101	Optimal Strategies for Sequential Validation of Significant Features from High-Dimensional Genomic Data. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2012, 75, 447-460.	1.1	8
102	Adjusted Measures for Feature Selection Stability for Data Sets with Similar Features. <i>Lecture Notes in Computer Science</i> , 2020, , 203-214.	1.0	8
103	Stability analysis of mixtures of mutagenetic trees. <i>BMC Bioinformatics</i> , 2008, 9, 165.	1.2	7
104	A detailed comparison of analysis processes for MCC-IMS data in disease classificationâ€‘Automated methods can replace manual peak annotations. <i>PLoS ONE</i> , 2017, 12, e0184321.	1.1	7
105	Mechanical strain mimicking breathing amplifies alterations in gene expression induced by SiO ₂ NPs in lung epithelial cells. <i>Nanotoxicology</i> , 2019, 13, 1227-1243.	1.6	7
106	Comparison of observation-based and model-based identification of alert concentrations from concentrationâ€‘expression data. <i>Bioinformatics</i> , 2021, 37, 1990-1996.	1.8	7
107	Improving Latent Dirichlet Allocation: On Reliability of the Novel Method LDAPrototype. <i>Lecture Notes in Computer Science</i> , 2020, , 118-125.	1.0	7
108	Detection of Patient Subgroups with Differential Expression in Omics Data: A Comprehensive Comparison of Univariate Measures. <i>PLoS ONE</i> , 2013, 8, e79380.	1.1	6

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109	Robust Selection of Cancer Survival Signatures from High-Throughput Genomic Data Using Two-Fold Subsampling. PLoS ONE, 2014, 9, e108818.	1.1	6
110	MODES: model-based optimization on distributed embedded systems. Machine Learning, 2021, 110, 1527-1547.	3.4	5
111	Model-based optimization of subgroup weights for survival analysis. Bioinformatics, 2019, 35, i484-i491.	1.8	4
112	Model selection characteristics when using MCPâ€Mod for doseâ€response gene expression data. Biometrical Journal, 2022, 64, 883-897.	0.6	4
113	Classification of Developmental Toxicants in a Human iPSC Transcriptomics-Based Test. Chemical Research in Toxicology, 2022, , .	1.7	4
114	Variable selection for disease progression models: methods for oncogenetic trees and application to cancer and HIV. BMC Bioinformatics, 2017, 18, 358.	1.2	3
115	Combining heterogeneous subgroups with graph-structured variable selection priors for Cox regression. BMC Bioinformatics, 2021, 22, 586.	1.2	3
116	Cost-effective Screening for Differentially Expressed Genes in Microarray Experiments Based on Normal Mixtures. Austrian Journal of Statistics, 2016, 32, 225-238.	0.2	1
117	Weighted Cox regression for the prediction of heterogeneous patient subgroups. BMC Medical Informatics and Decision Making, 2021, 21, 342.	1.5	1
118	Influence of bile acids on the cytotoxicity of chemicals in cultivated human hepatocytes. Toxicology in Vitro, 2022, 81, 105344.	1.1	1
119	Implications on Feature Detection When Using the Benefitâ€Cost Ratio. SN Computer Science, 2021, 2, 1.	2.3	0
120	Assessing the Uncertainty of the Text Generating Process Using Topic Models. Communications in Computer and Information Science, 2020, , 385-396.	0.4	0
121	td2pLL: An intuitive time-dose-response model for cytotoxicity data with varying exposure durations. Computational Toxicology, 2022, 23, 100234.	1.8	0