

Pierre R Bushel

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,139
citations

218677

26
h-index

161849

54
g-index

61
all docs

61
docs citations

61
times ranked

5492
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing Gene Significance from cDNA Microarray Expression Data via Mixed Models. <i>Journal of Computational Biology</i> , 2001, 8, 625-637.	1.6	987
2	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	17.5	420
3	Gene Expression Analysis Reveals Chemical-Specific Profiles. <i>Toxicological Sciences</i> , 2002, 67, 219-231.	3.1	385
4	Prediction of Compound Signature Using High Density Gene Expression Profiling. <i>Toxicological Sciences</i> , 2002, 67, 232-240.	3.1	251
5	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. <i>Toxicologic Pathology</i> , 2002, 30, 470-482.	1.8	135
6	The Evolution of Bioinformatics in Toxicology: Advancing Toxicogenomics. <i>Toxicological Sciences</i> , 2011, 120, S225-S237.	3.1	133
7	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	17.5	126
8	Database development in toxicogenomics: issues and efforts.. <i>Environmental Health Perspectives</i> , 2004, 112, 495-505.	6.0	112
9	A hybrid gene selection approach to create the S1500+ targeted gene sets for use in high-throughput transcriptomics. <i>PLoS ONE</i> , 2018, 13, e0191105.	2.5	110
10	Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. <i>Annual Review of Public Health</i> , 2017, 38, 279-294.	17.4	97
11	Mitochondrial nicotinamide adenine dinucleotide reduced (NADH) oxidation links the tricarboxylic acid (TCA) cycle with methionine metabolism and nuclear DNA methylation. <i>PLoS Biology</i> , 2018, 16, e2005707.	5.6	77
12	Revealing a human p53 universe. <i>Nucleic Acids Research</i> , 2018, 46, 8153-8167.	14.5	75
13	Technical guide for applications of gene expression profiling in human health risk assessment of environmental chemicals. <i>Regulatory Toxicology and Pharmacology</i> , 2015, 72, 292-309.	2.7	60
14	Extracting gene expression patterns and identifying co-expressed genes from microarray data reveals biologically responsive processes. <i>BMC Bioinformatics</i> , 2007, 8, 427.	2.6	58
15	Discovery in toxicology: Mediation by gene expression array technology. <i>Journal of Biochemical and Molecular Toxicology</i> , 2001, 15, 231-242.	3.0	57
16	Principal component analysis-based filtering improves detection for Affymetrix gene expression arrays. <i>Nucleic Acids Research</i> , 2011, 39, e86-e86.	14.5	57
17	Computational selection of distinct class- and subclass-specific gene expression signatures. <i>Journal of Biomedical Informatics</i> , 2002, 35, 160-170.	4.3	51
18	A Comparison of the TempO-Seq S1500+ Platform to RNA-Seq and Microarray Using Rat Liver Mode of Action Samples. <i>Frontiers in Genetics</i> , 2018, 9, 485.	2.3	51

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19	The Rat microRNA body atlas; Evaluation of the microRNA content of rat organs through deep sequencing and characterization of pancreas enriched miRNAs as biomarkers of pancreatic toxicity in the rat and dog. <i>BMC Genomics</i> , 2016, 17, 694.	2.8	50
20	Simultaneous clustering of gene expression data with clinical chemistry and pathological evaluations reveals phenotypic prototypes. <i>BMC Systems Biology</i> , 2007, 1, 15.	3.0	48
21	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. <i>Toxicologic Pathology</i> , 2002, 30, 470-482.	1.8	46
22	Gene expression response in target organ and whole blood varies as a function of target organ injury phenotype. <i>Genome Biology</i> , 2008, 9, R100.	9.6	45
23	Genes related to apoptosis predict necrosis of the liver as a phenotype observed in rats exposed to a compendium of hepatotoxicants. <i>BMC Genomics</i> , 2008, 9, 288.	2.8	41
24	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. <i>Scientific Reports</i> , 2018, 8, 10138.	3.3	38
25	LIN28A Modulates Splicing and Gene Expression Programs in Breast Cancer Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 3225-3243.	2.3	29
26	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	8.8	29
27	Decision tree-based method for integrating gene expression, demographic, and clinical data to determine disease endotypes. <i>BMC Systems Biology</i> , 2013, 7, 119.	3.0	25
28	Secondhand Smoke-Prevalent Polycyclic Aromatic Hydrocarbon Binary Mixture-Induced Specific Mitogenic and Pro-inflammatory Cell Signaling Events in Lung Epithelial Cells. <i>Toxicological Sciences</i> , 2017, 157, 156-171.	3.1	24
29	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	8.8	20
30	RATEmiRs: the rat atlas of tissue-specific and enriched miRNAs database. <i>BMC Genomics</i> , 2018, 19, 825.	2.8	19
31	Effects of mannose-binding lectin on pulmonary gene expression and innate immune inflammatory response to ozone. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2016, 311, L280-L291.	2.9	17
32	EPiG-Seq: extracting patterns and identifying co-expressed genes from RNA-Seq data. <i>BMC Genomics</i> , 2016, 17, 255.	2.8	16
33	Ancestry-dependent gene expression correlates with reprogramming to pluripotency and multiple dynamic biological processes. <i>Science Advances</i> , 2020, 6, .	10.3	16
34	Toxicogenomics profiling of bone marrow from rats treated with topotecan in combination with oxaliplatin: a mechanistic strategy to inform combination toxicity. <i>Frontiers in Genetics</i> , 2015, 6, 14.	2.3	13
35	Tunable regulation of CREB DNA binding activity couples genotoxic stress response and metabolism. <i>Nucleic Acids Research</i> , 2016, 44, gkw643.	14.5	13
36	Elucidation of Mechanisms of Topotecan-Induced Cell Death in Human Breast MCF-7 Cancer Cells by Gene Expression Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 775.	2.3	12

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37	Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. <i>BMC Systems Biology</i> , 2009, 3, 93.	3.0	10
38	goSTAG: gene ontology subtrees to tag and annotate genes within a set. <i>Source Code for Biology and Medicine</i> , 2017, 12, 6.	1.7	10
39	Crosstalk between Receptor and Non-receptor Mediated Chemical Modes of Action in Rat Livers Converges through a Dysregulated Gene Expression Network at Tumor Suppressor Tp53. <i>Frontiers in Genetics</i> , 2017, 8, 157.	2.3	9
40	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. <i>Journal of Biological Chemistry</i> , 2020, 295, 1271-1287.	3.4	9
41	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. <i>Journal of Biological Chemistry</i> , 2020, 295, 1271-1287.	3.4	9
42	Mitochondrial-nuclear epistasis underlying phenotypic variation in breast cancer pathology. <i>Scientific Reports</i> , 2022, 12, 1393.	3.3	9
43	Structure, Immunogenicity, and IgE Cross-Reactivity among Walnut and Peanut Vicilin-Buried Peptides. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 2389-2400.	5.2	9
44	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. <i>PLoS ONE</i> , 2012, 7, e34286.	2.5	8
45	Base-Resolution Analysis of DNA Methylation Patterns Downstream of <i>Dnmt3a</i> in Mouse Naïve B Cells. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 805-813.	1.8	8
46	Short-term tetrabromobisphenol A exposure promotes fibrosis of human uterine fibroid cells in a 3D culture system through TGF β signaling. <i>FASEB Journal</i> , 2022, 36, e22101.	0.5	8
47	CLUSTERING OF GENE EXPRESSION DATA AND END-POINT MEASUREMENTS BY SIMULATED ANNEALING. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 193-215.	0.8	6
48	RATemiRs: the rat atlas of tissue-specific and enriched miRNAs for discerning baseline expression exclusivity of candidate biomarkers. <i>RNA Biology</i> , 2020, 17, 630-636.	3.1	5
49	Structural Equation Modeling of In silico Perturbations. <i>Frontiers in Genetics</i> , 2021, 12, 727532.	2.3	5
50	Widespread Exonization of Transposable Elements in Human Coding Sequences is Associated with Epigenetic Regulation of Transcription. <i>Transcriptomics: Open Access</i> , 2013, 01, .	0.2	4
51	Editorial: Integrative Toxicogenomics: Analytical Strategies to Amalgamate Exposure Effects With Genomic Sciences. <i>Frontiers in Genetics</i> , 2018, 9, 563.	2.3	2
52	Databases for Toxicogenomics. , 2005, , 97-113.		0
53	Toxicogenomics. , 2006, , 5-23.		0
54	Transcriptomic profiles of tissues from rats treated with anticancer drug combinations. <i>Scientific Data</i> , 2019, 6, 180306.	5.3	0

#	ARTICLE	IF	CITATIONS
55	Toxicogenomics: A Primer for Toxicologic Pathologists. , 2022, , 491-543.		0