

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	Toxicogenomics: A Primer for Toxicologic Pathologists. , 2022, , 491-543.		0
2	Short-term tetrabromobisphenol A exposure promotes fibrosis of human uterine fibroid cells in a 3D culture system through TGF- β signaling. FASEB Journal, 2022, 36, e22101.	0.5	8
3	Mitochondrial-nuclear epistasis underlying phenotypic variation in breast cancer pathology. Scientific Reports, 2022, 12, 1393.	3.3	9
4	Structure, Immunogenicity, and IgE Cross-Reactivity among Walnut and Peanut Vicilin-Buried Peptides. Journal of Agricultural and Food Chemistry, 2022, 70, 2389-2400.	5.2	9
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
6	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
7	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	8.8	29
8	Structural Equation Modeling of In silico Perturbations. Frontiers in Genetics, 2021, 12, 727532.	2.3	5
9	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. Journal of Biological Chemistry, 2020, 295, 1271-1287.	3.4	9
10	Ancestry-dependent gene expression correlates with reprogramming to pluripotency and multiple dynamic biological processes. Science Advances, 2020, 6, .	10.3	16
11	Elucidation of Mechanisms of Topotecan-Induced Cell Death in Human Breast MCF-7 Cancer Cells by Gene Expression Analysis. Frontiers in Genetics, 2020, 11, 775.	2.3	12
12	RATEmiRs: the rat atlas of tissue-specific and enriched miRNAs for discerning baseline expression exclusivity of candidate biomarkers. RNA Biology, 2020, 17, 630-636.	3.1	5
13	Proteasome inhibition creates a chromatin landscape favorable to RNA Pol II processivity. Journal of Biological Chemistry, 2020, 295, 1271-1287.	3.4	9
14	Transcriptomic profiles of tissues from rats treated with anticancer drug combinations. Scientific Data, 2019, 6, 180306.	5.3	0
15	Base-Resolution Analysis of DNA Methylation Patterns Downstream of <i>Dnmt3a</i> in Mouse Na ⁺ ve B Cells. G3: Genes, Genomes, Genetics, 2018, 8, 805-813.	1.8	8
16	Editorial: Integrative Toxicogenomics: Analytical Strategies to Amalgamate Exposure Effects With Genomic Sciences. Frontiers in Genetics, 2018, 9, 563.	2.3	2
17	RATEmiRs: the rat atlas of tissue-specific and enriched miRNAs database. BMC Genomics, 2018, 19, 825.	2.8	19
18	A Comparison of the TempO-Seq S1500+ Platform to RNA-Seq and Microarray Using Rat Liver Mode of Action Samples. Frontiers in Genetics, 2018, 9, 485.	2.3	51

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19	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. <i>Scientific Reports</i> , 2018, 8, 10138.	3.3	38
20	Revealing a human p53 universe. <i>Nucleic Acids Research</i> , 2018, 46, 8153-8167.	14.5	75
21	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
22	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
23	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
24	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
25	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
26	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
27	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
28	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
29	Tunable regulation of CREB DNA binding activity couples genotoxic stress response and metabolism. <i>Nucleic Acids Research</i> , 2016, 44, gkw643.	14.5	13
30	EPIG-Seq: extracting patterns and identifying co-expressed genes from RNA-Seq data. <i>BMC Genomics</i> , 2016, 17, 255.	2.8	16
31	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
32	LIN28A Modulates Splicing and Gene Expression Programs in Breast Cancer Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 3225-3243.	2.3	29
33	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
34	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
35	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
36	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

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37	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. PLoS ONE, 2012, 7, e34286.	2.5	8
38	Principal component analysis-based filtering improves detection for Affymetrix gene expression arrays. Nucleic Acids Research, 2011, 39, e86-e86.	14.5	57
39	The Evolution of Bioinformatics in Toxicology: Advancing Toxicogenomics. Toxicological Sciences, 2011, 120, S225-S237.	3.1	133
40	CLUSTERING OF GENE EXPRESSION DATA AND END-POINT MEASUREMENTS BY SIMULATED ANNEALING. Journal of Bioinformatics and Computational Biology, 2009, 07, 193-215.	0.8	6
41	Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. BMC Systems Biology, 2009, 3, 93.	3.0	10
42	Genes related to apoptosis predict necrosis of the liver as a phenotype observed in rats exposed to a compendium of hepatotoxicants. BMC Genomics, 2008, 9, 288.	2.8	41
43	Gene expression response in target organ and whole blood varies as a function of target organ injury phenotype. Genome Biology, 2008, 9, R100.	9.6	45
44	Simultaneous clustering of gene expression data with clinical chemistry and pathological evaluations reveals phenotypic prototypes. BMC Systems Biology, 2007, 1, 15.	3.0	48
45	Extracting gene expression patterns and identifying co-expressed genes from microarray data reveals biologically responsive processes. BMC Bioinformatics, 2007, 8, 427.	2.6	58
46	Toxicogenomics. , 2006, , 5-23.		0
47	Databases for Toxicogenomics. , 2005, , 97-113.		0
48	Database development in toxicogenomics: issues and efforts.. Environmental Health Perspectives, 2004, 112, 495-505.	6.0	112
49	Gene Expression Analysis Reveals Chemical-Specific Profiles. Toxicological Sciences, 2002, 67, 219-231.	3.1	385
50	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. Toxicologic Pathology, 2002, 30, 470-482.	1.8	135
51	Prediction of Compound Signature Using High Density Gene Expression Profiling. Toxicological Sciences, 2002, 67, 232-240.	3.1	251
52	Computational selection of distinct class- and subclass-specific gene expression signatures. Journal of Biomedical Informatics, 2002, 35, 160-170.	4.3	51
53	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. Toxicologic Pathology, 2002, 30, 470-482.	1.8	46
54	Discovery in toxicology: Mediation by gene expression array technology. Journal of Biochemical and Molecular Toxicology, 2001, 15, 231-242.	3.0	57

#	ARTICLE	IF	CITATIONS
55	Assessing Gene Significance from cDNA Microarray Expression Data via Mixed Models. Journal of Computational Biology, 2001, 8, 625-637.	1.6	987