Richard S Paules

List of Publications by Year
in descending order

119 papers	12,701 citations	38742 50 h-index	24258 110 g-index
129 all docs	129 docs citations	129 times ranked	15076 citing authors

#	Article	IF	Citations
1	The Tox21 10K Compound Library: Collaborative Chemistry Advancing Toxicology. Chemical Research in Toxicology, 2021, 34, 189-216.	3.3	145
2	DNA damage responses in murine Pre-B cells with genetic deficiencies in damage response genes. Cell Cycle, 2020, 19, 67-83.	2.6	6
3	Utility of Extrapolating Human S1500+ Genes to the Whole Transcriptome: Tunicamycin Case Study. Bioinformatics and Biology Insights, 2020, 14, 117793222095274.	2.0	5
4	Evaluation of 5-day In Vivo Rat Liver and Kidney With High-throughput Transcriptomics for Estimating Benchmark Doses of Apical Outcomes. Toxicological Sciences, 2020, 176, 343-354.	3.1	45
5	Comparison of Normalization Methods for Analysis of TempO-Seq Targeted RNA Sequencing Data. Frontiers in Genetics, 2020, 11, 594.	2.3	13
6	KRAS-retroviral fusion transcripts and gene amplification in arsenic-transformed, human prostate CAsE-PE cancer cells. Toxicology and Applied Pharmacology, 2020, 397, 115017.	2.8	6
7	Development of a Zebrafish S1500+ Sentinel Gene Set for High-Throughput Transcriptomics. Zebrafish, 2019, 16, 331-347.	1.1	5
8	Arsenite malignantly transforms human prostate epithelial cells in vitro by gene amplification of mutated KRAS. PLoS ONE, 2019, 14, e0215504.	2.5	16
9	The Power of Resolution: Contextualized Understanding of Biological Responses to Liver Injury Chemicals Using High-throughput Transcriptomics and Benchmark Concentration Modeling. Toxicological Sciences, 2019, 169, 553-566.	3.1	54
10	BMDExpress 2: enhanced transcriptomic dose-response analysis workflow. Bioinformatics, 2019, 35, 1780-1782.	4.1	123
11	Detection and Prioritization of Developmentally Neurotoxic and/or Neurotoxic Compounds Using Zebrafish. Toxicological Sciences, 2019, 168, 225-240.	3.1	30
12	Screening for Developmental Neurotoxicity at the National Toxicology Program: The Future Is Here. Toxicological Sciences, 2019, 167, 6-14.	3.1	36
13	Genomic dose response: Successes, challenges, and next steps. Current Opinion in Toxicology, 2018, 11-12, 84-92.	5.0	5
14	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
15	Comprehensive Analyses and Prioritization of Tox21 10K Chemicals Affecting Mitochondrial Function by in-Depth Mechanistic Studies. Environmental Health Perspectives, 2018, 126, 077010.	6.0	60
16	Toxicity profiling of flame retardants in zebrafish embryos using a battery of assays for developmental toxicity, neurotoxicity, cardiotoxicity and hepatotoxicity toward human relevance. Neurotoxicology and Teratology, 2018, 70, 40-50.	2.4	104
17	A hybrid gene selection approach to create the S1500+ targeted gene sets for use in high-throughput transcriptomics. PLoS ONE, 2018, 13, e0191105.	2.5	110
18	The US Federal Tox21 Program: A strategic and operational plan for continued leadership. ALTEX: Alternatives To Animal Experimentation, 2018, 35, 163-168.	1.5	134

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19	Blood gene expression profiling of an early acetaminophen response. Pharmacogenomics Journal, 2017, 17, 230-236.	2.0	10
20	Identifying environmental chemicals as agonists of the androgen receptor by using a quantitative high-throughput screening platform. Toxicology, 2017, 385, 48-58.	4.2	24
21	From the Cover: Three-Dimensional (3D) HepaRG Spheroid Model With Physiologically Relevant Xenobiotic Metabolism Competence and Hepatocyte Functionality for Liver Toxicity Screening. Toxicological Sciences, 2017, 159, 124-136.	3.1	85
22	Molecular effects of 1-naphthyl-methylcarbamate and solar radiation exposures on human melanocytes. Toxicology in Vitro, 2017, 38, 67-76.	2.4	3
23	Real-time cell toxicity profiling of Tox21 10K compounds reveals cytotoxicity dependent toxicity pathway linkage. PLoS ONE, 2017, 12, e0177902.	2.5	40
24	Comment on â€œOn the Utility of ToxCastâ„¢ and ToxPi as Methods for Identifying New Obesogensâ€•. Environmental Health Perspectives, 2017, 125, A8-A11.	6.0	6
25	A type I IFN-dependent DNA damage response regulates the genetic program and inflammasome activation in macrophages. ELife, 2017, 6, .	6.0	40
26	Blood transcript immune signatures distinguish a subset of people with elevated serum ALT from others given acetaminophen. Clinical Pharmacology and Therapeutics, 2016, 99, 432-441.	4.7	13
27	Changing the Paradigm of Toxicity Testing From Observational to Predictive: An Update on Two Global In Vitro Screening Initiatives. Applied in Vitro Toxicology, 2015, 1, 91-98.	1.1	0
28	Intersection of toxicogenomics and high throughput screening in the Tox21 program: an NIEHS perspective. International Journal of Biotechnology, 2015, 14, 7.	1.2	39
29	Depletion of ATR selectively sensitizes ATM-deficient human mammary epithelial cells to ionizing radiation and DNA-damaging agents. Cell Cycle, 2014, 13, 3541-3550.	2.6	22
30	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
31	Application of In Vivo Genomics to the Prediction of Chemical-Induced (hepato)Carcinogenesis. , 2014, , 15-33.		0
32	DNA damage activates a complex transcriptional response in murine lymphocytes that includes both physiological and cancer-predisposition programs. BMC Genomics, 2013, 14, 163.	2.8	13
33	Dissecting cellular responses to irradiation via targeted disruptions of the ATM-CHK1-PP2A circuit. Cell Cycle, 2013, 12, 1105-1118.	2.6	15
34	A prognostic signature of Gâ‚‚ checkpoint function in melanoma cell lines. Cell Cycle, 2013, 12, 1071-1082.	2.6	13
35	Gene expression signatures but not cell cycle checkpoint functions distinguish AT carriers from normal individuals. Physiological Genomics, 2013, 45, 907-916.	2.3	1
36	Genome-Wide Small RNA Sequencing and Gene Expression Analysis Reveals a microRNA Profile of Cancer Susceptibility in ATM-Deficient Human Mammary Epithelial Cells. PLoS ONE, 2013, 8, e64779.	2.5	8

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37	Abstract B22: Combined disruption of ATM and CHK1 functionalities reveals redundancies in the DNA damage response pathways and results in synthetic growth inhibition following Î³-irradiation. , 2013, , .		0
38	Perturbation of microRNAs in Rat Heart during Chronic Doxorubicin Treatment. PLoS ONE, 2012, 7, e40395.	2.5	86
39	Abstract LB-461: Genome-wide small RNA sequencing and gene expression analysis reveals a microRNA profile reflective of cancer-susceptibility in ATM deficient human mammary epithelial cells. , 2012, , .		0
40	Environmental Toxicogenomics: How Genomic Technologies are Impacting the Science of Toxicology. Qscience Proceedings, 2012, 2012, 29.	0.0	0
41	Gene expression profiles from discordant monozygotic twins suggest that molecular pathways are shared among multiple systemic autoimmune diseases. Arthritis Research and Therapy, 2011, 13, R69.	3.5	37
42	Genomic-Derived Markers for Early Detection of Calcineurin Inhibitor Immunosuppressantâ€“Mediated Nephrotoxicity. Toxicological Sciences, 2011, 124, 23-34.	3.1	18
43	Moving Forward in Human Cancer Risk Assessment. Environmental Health Perspectives, 2011, 119, 739-743.	6.0	24
44	Acetaminophen dosing of humans results in blood transcriptome and metabolome changes consistent with impaired oxidative phosphorylation. Hepatology, 2010, 51, 227-236.	7.3	81
45	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
46	Consistency of predictive signature genes and classifiers generated using different microarray platforms. Pharmacogenomics Journal, 2010, 10, 247-257.	2.0	53
47	Human AlkB Homolog ABH8 Is a tRNA Methyltransferase Required for Wobble Uridine Modification and DNA Damage Survival. Molecular and Cellular Biology, 2010, 30, 2449-2459.	2.3	182
48	Use of transcriptomics in understanding mechanisms of drug-induced toxicity. Pharmacogenomics, 2010, 11, 573-585.	1.3	99
49	Genomic indicators in the blood predict drug-induced liver injury. Pharmacogenomics Journal, 2010, 10, 267-277.	2.0	54
50	Revised genetic requirements for the decatenation G2 checkpoint: The role of ATM. Cell Cycle, 2010, 9, 1617-1628.	2.6	25
51	Parallelogram Approach Using Rat-Human In Vitro and Rat In Vivo Toxicogenomics Predicts Acetaminophen-induced Hepatotoxicity in Humans. Toxicological Sciences, 2009, 107, 544-552.	3.1	53
52	DNA double-strand breaks activate a multi-functional genetic program in developing lymphocytes. Nature, 2008, 456, 819-823.	27.8	137
53	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
54	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

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55	DNA Protein Kinaseâ€“Dependent G2 Checkpoint Revealed following Knockdown of Ataxia-Telangiectasia Mutated in Human Mammary Epithelial Cells. Cancer Research, 2008, 68, 89-97.	0.9	31
56	Cdc7-Dbf4 and the Human S Checkpoint Response to UVC. Journal of Biological Chemistry, 2007, 282, 9458-9468.	3.4	66
57	Gene Expression Analysis Offers Unique Advantages to Histopathology in Liver Biopsy Evaluations. Toxicologic Pathology, 2007, 35, 276-283.	1.8	25
58	Blood gene expression signatures predict exposure levels. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18211-18216.	7.1	115
59	Identification of Primary Transcriptional Regulation of Cell Cycle-Regulated Genes upon DNA Damage. Cell Cycle, 2007, 6, 972-981.	2.6	23
60	CEBS Chemical Effects in Biological Systems: a public data repository integrating study design and toxicity data with microarray and proteomics data. Nucleic Acids Research, 2007, 36, D892-D900.	14.5	119
61	Ataxia Telangiectasia-Mutatedâ€“Dependent DNA Damage Checkpoint Functions Regulate Gene Expression in Human Fibroblasts. Molecular Cancer Research, 2007, 5, 813-822.	3.4	14
62	Multicenter Study of Acetaminophen Hepatotoxicity Reveals the Importance of Biological Endpoints in Genomic Analyses. Toxicological Sciences, 2007, 99, 326-337.	3.1	79
63	Heat map visualization of high-density clinical chemistry data. Physiological Genomics, 2007, 31, 352-356.	2.3	17
64	Identification of Genes Implicated in Methapyrilene-Induced Hepatotoxicity by Comparing Differential Gene Expression in Target and Nontarget Tissue. Environmental Health Perspectives, 2007, 115, 572-578.	6.0	20
65	Folate deficiency in normal human fibroblasts leads to altered expression of genes primarily linked to cell signaling, the cytoskeleton and extracellular matrix. Journal of Nutritional Biochemistry, 2007, 18, 541-552.	4.2	24
66	Extracting gene expression patterns and identifying co-expressed genes from microarray data reveals biologically responsive processes. BMC Bioinformatics, 2007, 8, 427.	2.6	58
67	Major carcinogenic pathways identified by gene expression analysis of peritoneal mesotheliomas following chemical treatment in F344 rats. Toxicology and Applied Pharmacology, 2006, 214, 144-151.	2.8	36
68	Profiles of Global Gene Expression in Ionizing-Radiationâ€“Damaged Human Diploid Fibroblasts Reveal Synchronization behind the G 1 Checkpoint in a G 0 -like State of Quiescence. Environmental Health Perspectives, 2006, 114, 553-559.	6.0	55
69	Global Gene Expression Associated with Hepatocarcinogenesis in Adult Male Mice Induced by in Utero Arsenic Exposure. Environmental Health Perspectives, 2006, 114, 404-411.	6.0	72
70	Phenotypic Anchoring of Acetaminophen-Induced Oxidative Stress with Gene Expression Profiles in Rat Liver. Toxicological Sciences, 2006, 93, 213-222.	3.1	78
71	ATM Requirement in Gene Expression Responses to Ionizing Radiation in Human Lymphoblasts and Fibroblasts. Molecular Cancer Research, 2006, 4, 197-207.	3.4	17
72	Toxicogenomics. , 2006, , 5-23.		0

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73	Toxicogenomics and environmental diseases: the search for biomarkers predictive of adverse effects. Medicina Del Lavoro, 2006, 97, 322-3.	0.4	2
74	Standardizing global gene expression analysis between laboratories and across platforms. Nature Methods, 2005, 2, 351-356.	19.0	416
75	Differential gene expression profiling in whole blood during acute systemic inflammation in lipopolysaccharide-treated rats. Physiological Genomics, 2005, 21, 92-104.	2.3	43
76	Differential renal gene expression in prehypertensive and hypertensive spontaneously hypertensive rats. American Journal of Physiology - Renal Physiology, 2005, 289, F552-F561.	2.7	35
77	SYSTEMATIC VARIATION NORMALIZATION IN MICROARRAY DATA TO GET GENE EXPRESSION COMPARISON UNBIASED. Journal of Bioinformatics and Computational Biology, 2005, 03, 225-241.	0.8	22
78	Chemical Effects in Biological Systemsâ€"Data Dictionary (CEBS-DD): A Compendium of Terms for the Capture and Integration of Biological Study Design Description, Conventional Phenotypes, and â€˜Omics Data. Toxicological Sciences, 2005, 88, 585-601.	3.1	43
79	Microarray Data Analysis of Mouse Neoplasia. Toxicologic Pathology, 2005, 33, 127-135.	1.8	9
80	Use of a mixed tissue RNA design for performance assessments on multiple microarray formats. Nucleic Acids Research, 2005, 33, e187-e187.	14.5	30
81	Cellular and Molecular Targets of ProteinS-Glutathiolation. Antioxidants and Redox Signaling, 2005, 7, 940-950.	5.4	48
82	Cross-site comparison of gene expression data reveals high similarity.. Environmental Health Perspectives, 2004, 112, 449-455.	6.0	47
83	Application of Toxicogenomics to Toxicology: Basic Concepts in the Analysis of Microarray Data. Toxicologic Pathology, 2004, 32, 72-83.	1.8	78
84	Analysis of ATP-Binding Cassette Transporter Expression in Drug-Selected Cell Lines by a Microarray Dedicated to Multidrug Resistance. Molecular Pharmacology, 2004, 66, 1397-1405.	2.3	79
85	Gene Expression Profiling of Rat Livers Reveals Indicators of Potential Adverse Effects. Toxicological Sciences, 2004, 80, 193-202.	3.1	199
86	Cell survival and changes in gene expression in cells unable to synthesize glutathione. BioFactors, 2003, 17, 13-19.	5.4	5
87	Identification of distinct and common gene expression changes after oxidative stress and gamma and ultraviolet radiation. Molecular Carcinogenesis, 2003, 37, 65-82.	2.7	53
88	An Integrated Stress Response Regulates Amino Acid Metabolism and Resistance to Oxidative Stress. Molecular Cell, 2003, 11, 619-633.	9.7	2,791
89	ATM-Dependent and -Independent Gene Expression Changes in Response to Oxidative Stress, Gamma Irradiation, and UV Irradiation. Radiation Research, 2003, 160, 273-290.	1.5	52
90	Changes in global gene and protein expression during early mouse liver carcinogenesis induced by non-genotoxic model carcinogens oxazepam and Wyeth-14,643. Carcinogenesis, 2003, 24, 757-770.	2.8	82

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91	Phenotypic anchoring: linking cause and effect.. Environmental Health Perspectives, 2003, 111, A338-9.	6.0	110
92	Systems toxicology and the Chemical Effects in Biological Systems (CEBS) knowledge base. EHP Toxicogenomics: Journal of the National Institute of Environmental Health Sciences, 2003, 111, 15-28.	0.9	16
93	An ATR- and Chk1-Dependent S Checkpoint Inhibits Replicon Initiation following UVC-Induced DNA Damage. Molecular and Cellular Biology, 2002, 22, 8552-8561.	2.3	228
94	ATR Enforces the Topoisomerase II-dependent G2 Checkpoint through Inhibition of Plk1 Kinase. Journal of Biological Chemistry, 2002, 277, 36832-36838.	3.4	52
95	Gene Expression Analysis Reveals Chemical-Specific Profiles. Toxicological Sciences, 2002, 67, 219-231.	3.1	385
96	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. Toxicologic Pathology, 2002, 30, 470-482.	1.8	135
97	Prediction of Compound Signature Using High Density Gene Expression Profiling. Toxicological Sciences, 2002, 67, 232-240.	3.1	251
98	<title>Gene expression pattern recognition algorithm inferences to classify samples exposed to chemical agents</title>. , 2002, , .		0
99	Computational selection of distinct class- and subclass-specific gene expression signatures. Journal of Biomedical Informatics, 2002, 35, 160-170.	4.3	51
100	Genomic interrogation of mechanism(s) underlying cellular responses to toxicants. Toxicology, 2002, 181-182, 555-563.	4.2	68
101	Methapyrilene Toxicity: Anchorage of Pathologic Observations to Gene Expression Alterations. Toxicologic Pathology, 2002, 30, 470-482.	1.8	46
102	An overview of toxicogenomics. Current Issues in Molecular Biology, 2002, 4, 45-56.	2.4	96
103	Discovery in toxicology: Mediation by gene expression array technology. Journal of Biochemical and Molecular Toxicology, 2001, 15, 231-242.	3.0	57
104	Analysis of Genetic and Epigenetic Mechanisms of Toxicity: Potential Roles of Toxicogenomics and Proteomics in Toxicology. Toxicological Sciences, 2001, 59, 193-195.	3.1	45
105	The Ataxia telangiectasia Gene Product Is Required for Oxidative Stress-induced G1 and G2Checkpoint Function in Human Fibroblasts. Journal of Biological Chemistry, 2001, 276, 21951-21959.	3.4	107
106	The human decatenation checkpoint. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 12044-12049.	7.1	183
107	Assessing Gene Significance from cDNA Microarray Expression Data via Mixed Models. Journal of Computational Biology, 2001, 8, 625-637.	1.6	987
108	Oxidative stress and cell cycle checkpoint function11Both Drs. Paules and Kaufmann received their doctoral degrees in Experimental Pathology from the University of North Carolina at Chapel Hill School of Medicine (in 1984 and 1979, respectively).. Free Radical Biology and Medicine, 2000, 28, 1387-1404.	2.9	468

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109	Deregulation of specific E2F complexes by the v-mos oncogene. Oncogene, 1997, 14, 3029-3038.	5.9	7
110	Serum starved v-mos-transformed cells are unable to appropriately downregulate cyclins and CDKs. Oncogene, 1997, 14, 3017-3027.	5.9	10
111	DNA damage and cell cycle checkpoints. FASEB Journal, 1996, 10, 238-247.	0.5	258
112	v-mos-Transformed Cells Fail to Enter Quiescence but Growth Arrest in G1 Following Serum Withdrawal. Experimental Cell Research, 1994, 213, 210-217.	2.6	8
113	Ability of the c-mos product to associate with and phosphorylate tubulin. Science, 1991, 251, 671-675.	12.6	145
114	A characterization of cytostatic factor activity from Xenopus eggs and c-mos-transformed cells.. Journal of Cell Biology, 1991, 114, 329-335.	5.2	83
115	The ras oncoprotein and M-phase activity. Science, 1991, 253, 74-76.	12.6	74
116	Mouse Mos protooncogene product is present and functions during oogenesis.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 5395-5399.	7.1	175
117	Benzo[alpha]pyrene diol epoxide I binds to DNA at replication forks.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 2176-2180.	7.1	36
118	Quantitation by electron microscopy of the binding of highly specific antibodies to benzo[a]pyrene-DNA adducts. Carcinogenesis, 1985, 6, 193-198.	2.8	13
119	Systems Toxicology and the Chemical Effects in Biological Systems (CEBS) Knowledge Base. Environmental Health Perspectives, 0, , .	6.0	6