Mario Medvedovic

List of Publications by Year
in descending order

123 papers	6,529 citations	66343 42 h-index	76900 74 g-index
132 all docs	132 docs citations	132 times ranked	10858 citing authors

#	Article	IF	Citations
1	Proximity of Chromosomal Loci That Participate in Radiation-Induced Rearrangements in Human Cells. Science, 2000, 290, 138-141.	12.6	450
2	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
3	MicroRNA-494 Targeting Both Proapoptotic and Antiapoptotic Proteins Protects Against Ischemia/Reperfusion-Induced Cardiac Injury. Circulation, 2010, 122, 1308-1318.	1.6	296
4	The N ⁶ -Methyladenosine mRNA Methylase METTL3 Controls Cardiac Homeostasis and Hypertrophy. Circulation, 2019, 139, 533-545.	1.6	279
5	Bayesian infinite mixture model based clustering of gene expression profiles. Bioinformatics, 2002, 18, 1194-1206.	4.1	248
6	The transcriptional signature of dioxin in human hepatoma HepG2 cells. Biochemical Pharmacology, 2000, 60, 1129-1142.	4.4	212
7	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. Bioinformatics, 2009, 25, 211-217.	4.1	163
8	Control of Nutrient Stress-Induced Metabolic Reprogramming by PKCÎ¶ in Tumorigenesis. Cell, 2013, 152, 599-611.	28.9	160
9	The genetic fingerprint of susceptibility for transplant-associated thrombotic microangiopathy. Blood, 2016, 127, 989-996.	1.4	152
10	Data Portal for the Library of Integrated Network-based Cellular Signatures (LINCS) program: integrated access to diverse large-scale cellular perturbation response data. Nucleic Acids Research, 2018, 46, D558-D566.	14.5	143
11	Conditional Activation of RET/PTC3 and BRAFV600E in Thyroid Cells Is Associated with Gene Expression Profiles that Predict a Preferential Role of BRAF in Extracellular Matrix Remodeling. Cancer Research, 2006, 66, 6521-6529.	0.9	129
12	GREIN: An Interactive Web Platform for Re-analyzing GEO RNA-seq Data. Scientific Reports, 2019, 9, 7580.	3.3	126
13	Loss of the miR-144/451 cluster impairs ischaemic preconditioning-mediated cardioprotection by targeting Rac-1. Cardiovascular Research, 2012, 94, 379-390.	3.8	124
14	Loss of microRNA-128 promotes cardiomyocyte proliferation and heart regeneration. Nature Communications, 2018, 9, 700.	12.8	124
15	LINCS Data Portal 2.0: next generation access point for perturbation-response signatures. Nucleic Acids Research, 2020, 48, D431-D439.	14.5	112
16	An Organoid-Based Preclinical Model of Human Gastric Cancer. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 161-184.	4.5	97
17	Expression of genes in the TGF-Î² signaling pathway is significantly deregulated in smooth muscle cells from aorta of aryl hydrocarbon receptor knockout mice. Toxicology and Applied Pharmacology, 2004, 194, 79-89.	2.8	93
18	Genomewide Analysis of Aryl Hydrocarbon Receptor Binding Targets Reveals an Extensive Array of Gene Clusters that Control Morphogenetic and Developmental Programs. Environmental Health Perspectives, 2009, 117, 1139-1146.	6.0	90

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19	Comprehensive microRNA-sequencing of exosomes derived from head and neck carcinoma cellsin vitroreveals common secretion profiles and potential utility as salivary biomarkers. Oncotarget, 2017, 8, 82459-82474.	1.8	80
20	The Development of Spasmolytic Polypeptide/TFF2-Expressing Metaplasia (SPEM) During Gastric Repair Is Absent in the Aged Stomach. Cellular and Molecular Gastroenterology and Hepatology, 2016, 2, 605-624.	4.5	79
21	Microarray results improve significantly as hybridization approaches equilibrium. BioTechniques, 2004, 36, 790-796.	1.8	76
22	SPDEF Inhibits Prostate Carcinogenesis by Disrupting a Positive Feedback Loop in Regulation of the Foxm1 Oncogene. PLoS Genetics, 2014, 10, e1004656.	3.5	75
23	Gene Expression Changes during the Development of Acute Lung Injury Role of Transforming Growth Factor Î². American Journal of Respiratory and Critical Care Medicine, 2005, 172, 1399-1411.	5.6	71
24	Reprogramming of the Epigenome by MLL1 Links Early-Life Environmental Exposures to Prostate Cancer Risk. Molecular Endocrinology, 2016, 30, 856-871.	3.7	68
25	CLEAN: CLustering Enrichment ANalysis. BMC Bioinformatics, 2009, 10, 234.	2.6	65
26	GRcalculator: an online tool for calculating and mining doseâ€“response data. BMC Cancer, 2017, 17, 698.	2.6	64
27	Identification of sex-specific DNA methylation changes driven by specific chemicals in cord blood in a Faroese birth cohort. Epigenetics, 2018, 13, 290-300.	2.7	62
28	4-Aminobiphenyl-Induced Liver and Urinary Bladder DNA Adduct Formation in Cyp1a2(-/-) and Cyp1a2(+/+) Mice. Journal of the National Cancer Institute, 2003, 95, 1227-1237.	6.3	61
29	SERPINB3/B4 Contributes to Early Inflammation and Barrier Dysfunction in an Experimental Murine Model of Atopic Dermatitis. Journal of Investigative Dermatology, 2015, 135, 160-169.	0.7	61
30	Genomic Profile of Matrix and Vasculature Remodeling in TGF-Î±â€“Induced Pulmonary Fibrosis. American Journal of Respiratory Cell and Molecular Biology, 2007, 37, 309-321.	2.9	60
31	DNA methylome changes by estradiol benzoate and bisphenol A links early-life environmental exposures to prostate cancer risk. Epigenetics, 2016, 11, 674-689.	2.7	59
32	IL-31-Driven Skin Remodeling Involves Epidermal Cell Proliferation and Thickening That Lead to Impaired Skin-Barrier Function. PLoS ONE, 2016, 11, e0161877.	2.5	59
33	Ah Receptor Activation by Dioxin Disrupts Activin, BMP, and WNT Signals During the Early Differentiation of Mouse Embryonic Stem Cells and Inhibits Cardiomyocyte Functions. Toxicological Sciences, 2016, 149, 346-357.	3.1	54
34	Identification of SecretaglobinScgb2a1as a target for developmental reprogramming by BPA in the rat prostate. Epigenetics, 2015, 10, 127-134.	2.7	53
35	Sex- and tissue-specific methylome changes in brains of mice perinatally exposed to lead. NeuroToxicology, 2015, 46, 92-100.	3.0	52
36	Balancing yield, purity and practicality: a modified differential ultracentrifugation protocol for efficient isolation of small extracellular vesicles from human serum. RNA Biology, 2019, 16, 5-12.	3.1	52

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37	Different Global Gene Expression Profiles in Benzo[<I>a</I>]Pyrene- and Dioxin-Treated Vascular Smooth Muscle Cells of AHR-Knockout and Wild-Type Mice. Cardiovascular Toxicology, 2004, 4, 47-74.	2.7	49
38	c-Myc phosphorylation by PKCÎ¶ represses prostate tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6418-6423.	7.1	49
39	Transcriptome Analyses in Normal Prostate Epithelial Cells Exposed to Low-Dose Cadmium: Oncogenic and Immunomodulations Involving the Action of Tumor Necrosis Factor. Environmental Health Perspectives, 2008, 116, 769-776.	6.0	48
40	Epigenetic Changes with Dietary Soy in Cynomolgus Monkeys. PLoS ONE, 2011, 6, e26791.	2.5	48
41	The Role of Metallothionein in the Pathogenesis of Acute Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2006, 34, 73-82.	2.9	46
42	Candidate genes controlling pulmonary function in mice: transcript profiling and predicted protein structure. Physiological Genomics, 2007, 31, 410-421.	2.3	45
43	Disruption of Aryl Hydrocarbon Receptor Homeostatic Levels during Embryonic Stem Cell Differentiation Alters Expression of Homeobox Transcription Factors that Control Cardiomyogenesis. Environmental Health Perspectives, 2013, 121, 1334-1343.	6.0	45
44	Targeting GPR30 with G-1: a new therapeutic target for castration-resistant prostate cancer. Endocrine-Related Cancer, 2014, 21, 903-914.	3.1	45
45	Exposure of Human Prostaspheres to Bisphenol A Epigenetically Regulates SNORD Family Noncoding RNAs via Histone Modification. Endocrinology, 2015, 156, 3984-3995.	2.8	45
46	Stratified randomization controls better for batch effects in 450K methylation analysis: a cautionary tale. Frontiers in Genetics, 2014, 5, 354.	2.3	43
47	Critical regulation of genes for tumor cell migration by AP-1. Clinical and Experimental Metastasis, 2004, 21, 293-304.	3.3	42
48	Disruption of Ah Receptor Signaling during Mouse Development Leads to Abnormal Cardiac Structure and Function in the Adult. PLoS ONE, 2015, 10, e0142440.	2.5	42
49	NF-Î°B driven cardioprotective gene programs; Hsp70.3 and cardioprotection after late ischemic preconditioning. Journal of Molecular and Cellular Cardiology, 2010, 49, 664-672.	1.9	41
50	CD44 variant isoform 9 emerges in response to injury and contributes to the regeneration of the gastric epithelium. Journal of Pathology, 2017, 242, 463-475.	4.5	41
51	Interferon-complement loop in transplant-associated thrombotic microangiopathy. Blood Advances, 2020, 4, 1166-1177.	5.2	41
52	Regeneration of the adult thymus is preceded by the expansion of K5+K8+ epithelial cell progenitors and by increased expression of Trp63, cMyc and Tcf3 transcription factors in the thymic stroma. International Immunology, 2007, 19, 1249-1260.	4.0	38
53	Haplotype Association Mapping of Acute Lung Injury in Mice Implicates Activin A Receptor, Type 1. American Journal of Respiratory and Critical Care Medicine, 2011, 183, 1499-1509.	5.6	38
54	Ah Receptor Signaling Controls the Expression of Cardiac Development and Homeostasis Genes. Toxicological Sciences, 2015, 147, 425-435.	3.1	38

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55	Phase II Clinical Trial of Neoadjuvant and Adjuvant Pembrolizumab in Resectable Localâ€“Regionally Advanced Head and Neck Squamous Cell Carcinoma. Clinical Cancer Research, 2022, 28, 1345-1352.	7.0	38
56	Isozyme-Specific Abnormalities of PKC in Thyroid Cancer: Evidence for Post-Transcriptional Changes in PKC Epsilon. Journal of Clinical Endocrinology and Metabolism, 2002, 87, 2150-2159.	3.6	37
57	A new method to remove hybridization bias for interspecies comparison of global gene expression profiles uncovers an association between mRNA sequence divergence and differential gene expression in Xenopus. Nucleic Acids Research, 2006, 34, 185-200.	14.5	37
58	Mass spectrometry proteomics reveals a function for mammalian CALCOCO1 in MTOR-regulated selective autophagy. Autophagy, 2020, 16, 2219-2237.	9.1	37
59	A semi-parametric Bayesian model for unsupervised differential co-expression analysis. BMC Bioinformatics, 2010, 11, 234.	2.6	35
60	Identification of a NF-Î¹B cardioprotective gene program: NF-Î¹B regulation of Hsp70.1 contributes to cardioprotection after permanent coronary occlusion. Journal of Molecular and Cellular Cardiology, 2011, 51, 82-89.	1.9	32
61	Gene expression and discovery during lens regeneration in mouse: regulation of epithelial to mesenchymal transition and lens differentiation. Molecular Vision, 2006, 12, 422-40.	1.1	32
62	Long-term exposure to low-concentrations of Cr(VI) induce DNA damage and disrupt the transcriptional response to benzo[a]pyrene. Toxicology, 2014, 316, 14-24.	4.2	31
63	Monocyte and bone marrow macrophage transcriptional phenotypes in systemic juvenile idiopathic arthritis reveal TRIM8 as a mediator of IFN-Î³ hyper-responsiveness and risk for macrophage activation syndrome. Annals of the Rheumatic Diseases, 2021, 80, 617-625.	0.9	31
64	Deletion Hotspots in AMACR Promoter CpG Island Are cis-Regulatory Elements Controlling the Gene Expression in the Colon. PLoS Genetics, 2009, 5, e1000334.	3.5	30
65	Genome-Wide Signatures of Transcription Factor Activity: Connecting Transcription Factors, Disease, and Small Molecules. PLoS Computational Biology, 2013, 9, e1003198.	3.2	30
66	Context-specific infinite mixtures for clustering gene expression profiles across diverse microarray dataset. Bioinformatics, 2006, 22, 1737-1744.	4.1	29
67	Expressomal approach for comprehensive analysis and visualization of ligand sensitivities of xenoestrogen responsive genes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16508-16513.	7.1	29
68	Fibrocytes Regulate Wilms Tumor 1â€“Positive Cell Accumulation in Severe Fibrotic Lung Disease. Journal of Immunology, 2015, 195, 3978-3991.	0.8	29
69	Gene position within chromosome territories correlates with their involvement in distinct rearrangement types in thyroid cancer cells. Genes Chromosomes and Cancer, 2009, 48, 222-228.	2.8	28
70	Integrative Assessment of Chlorine-Induced Acute Lung Injury in Mice. American Journal of Respiratory Cell and Molecular Biology, 2012, 47, 234-244.	2.9	28
71	Differential expression and prognostic value of long nonâ€coding RNA in HPVâ€negative head and neck squamous cell carcinoma. Head and Neck, 2018, 40, 1555-1564.	2.0	28
72	Mutational specificity in a shuttle vector replicating in chromium(VI)-treated mammalian cells. , 1999, 33, 313-319.		26

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73	In utero exposure of rats to high-fat diets perturbs gene expression profiles and cancer susceptibility of prepubertal mammary glands. Journal of Nutritional Biochemistry, 2016, 29, 73-82.	4.2	26
74	SigCom LINCS: data and metadata search engine for a million gene expression signatures. Nucleic Acids Research, 2022, 50, W697-W709.	14.5	26
75	Dual Targeting of MEK and PI3K Pathways Attenuates Established and Progressive Pulmonary Fibrosis. PLoS ONE, 2014, 9, e86536.	2.5	24
76	Longitudinal Estimates of Pulmonary Function in Refractory Ceramic Fiber Manufacturing Workers. American Journal of Respiratory and Critical Care Medicine, 1998, 157, 1226-1233.	5.6	23
77	Folliculin Contributes to VHL Tumor Suppressing Activity in Renal Cancer through Regulation of Autophagy. PLoS ONE, 2013, 8, e70030.	2.5	23
78	Bisphenol A Disrupts HNF4Î±-Regulated Gene Networks Linking to Prostate Preneoplasia and Immune Disruption in Noble Rats. Endocrinology, 2016, 157, 207-219.	2.8	22
79	Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. Scientific Data, 2018, 5, 180117.	5.3	22
80	Gene Expression Profiles of Mouse Aorta and Cultured Vascular Smooth Muscle Cells Differ Widely, Yet Show Common Responses to Dioxin Exposure. Cardiovascular Toxicology, 2004, 4, 385-404.	2.7	21
81	Rhinovirus infection results in stronger and more persistent genomic dysregulation: Evidence for altered innate immune response in asthmatics at baseline, early in infection, and during convalescence. PLoS ONE, 2017, 12, e0178096.	2.5	21
82	Chromium disrupts chromatin organization and CTCF access to its cognate sites in promoters of differentially expressed genes. Epigenetics, 2018, 13, 363-375.	2.7	21
83	Overexpression of Dimethylarginine Dimethylaminohydrolase 1 Attenuates Airway Inflammation in a Mouse Model of Asthma. PLoS ONE, 2014, 9, e85148.	2.5	21
84	Surfactant-Associated Protein B Is Critical to Survival in Nickel-Induced Injury in Mice. American Journal of Respiratory Cell and Molecular Biology, 2009, 41, 226-236.	2.9	20
85	Rapid and Weight-Independent Improvement of Glucose Tolerance Induced by a Peptide Designed to Elicit Apoptosis in Adipose Tissue Endothelium. Diabetes, 2012, 61, 2299-2310.	0.6	20
86	Expression of ATM in ataxia telangiectasia fibroblasts rescues defects in DNA double-strand break repair in nuclear extracts. Environmental and Molecular Mutagenesis, 2001, 37, 128-140.	2.2	19
87	MicroRNA networks associated with active systemic juvenile idiopathic arthritis regulate CD163 expression and anti-inflammatory functions in macrophages through two distinct mechanisms. Journal of Leukocyte Biology, 2018, 103, 71-85.	3.3	19
88	Generalized random set framework for functional enrichment analysis using primary genomics datasets. Bioinformatics, 2011, 27, 70-77.	4.1	18
89	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic Acids Research, 2020, 48, W85-W93.	14.5	18
90	Melanoma Cell Intrinsic GABAA Receptor Enhancement Potentiates Radiation and Immune Checkpoint Inhibitor Response by Promoting Direct and T Cell-Mediated Antitumor Activity. International Journal of Radiation Oncology Biology Physics, 2021, 109, 1040-1053.	0.8	18

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91	Neural system-enriched gene expression: relationship to biological pathways and neurological diseases. Physiological Genomics, 2004, 18, 167-183.	2.3	15
92	Genomewide Association Analysis of Respiratory Syncytial Virus Infection in Mice. Journal of Virology, 2010, 84, 2257-2269.	3.4	15
93	Low-Dose Bisphenol A in a Rat Model of Endometrial Cancer: A CLARITY-BPA Study. Environmental Health Perspectives, 2020, 128, 127005.	6.0	15
94	NBCe1 Na⁺-HCO3⁻ cotransporter ablation causes reduced apoptosis following cardiac ischemia-reperfusion injury in vivo. World Journal of Cardiology, 2018, 10, 97-109.	1.5	15
95	Research Resource: Estrogen-Driven Prolactin-Mediated Gene-Expression Networks in Hormone-Induced Prostatic Intraepithelial Neoplasia. Molecular Endocrinology, 2010, 24, 2207-2217.	3.7	14
96	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. Journal of Clinical Investigation, 2021, 131, .	8.2	14
97	Gene Expression Profiling Identifies Lobe-Specific and Common Disruptions of Multiple Gene Networks in Testosterone-Supported, 17Î²-Estradiol- or Diethylstilbestrol-Induced Prostate Dysplasia in Noble Rats. Neoplasia, 2008, 10, 20-IN18.	5.3	13
98	Genomics Portals: integrative web-platform for mining genomics data. BMC Genomics, 2010, 11, 27.	2.8	13
99	Deciphering gene expression program of MAP3K1 in mouse eyelid morphogenesis. Developmental Biology, 2013, 374, 96-107.	2.0	13
100	Model reduction and parameter estimation of nonâ€linear dynamical biochemical reaction networks. IET Systems Biology, 2016, 10, 10-16.	1.5	12
101	Nonredundant Functions of Î±Î² and Î³Î´ T Cells in Acrolein-Induced Pulmonary Pathology. Toxicological Sciences, 2008, 105, 188-199.	3.1	11
102	Comparability of the small RNA secretome across human biofluids concomitantly collected from healthy adults. PLoS ONE, 2020, 15, e0229976.	2.5	11
103	Modeling variation in tumors in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2408-2413.	7.1	10
104	Loss of IÎºB kinase Î² promotes myofibroblast transformation and senescence through activation of the ROS-TGFÎ² autocrine loop. Protein and Cell, 2016, 7, 338-350.	11.0	10
105	Formaldehyde-Assisted Isolation of Regulatory Elements (FAIRE) Analysis Uncovers Broad Changes in Chromatin Structure Resulting from Hexavalent Chromium Exposure. PLoS ONE, 2014, 9, e97849.	2.5	9
106	ChIAPoP: a new tool for ChIA-PET data analysis. Nucleic Acids Research, 2019, 47, e37-e37.	14.5	9
107	Genetic susceptibility to toxicologic lung responses among inbred mouse strains following exposure to carbon nanotubes and profiling of underlying gene networks. Toxicology and Applied Pharmacology, 2017, 327, 59-70.	2.8	8
108	Connectivity Map Analysis of a Single-Cell RNA-Sequencing -Derived Transcriptional Signature of mTOR Signaling. International Journal of Molecular Sciences, 2021, 22, 4371.	4.1	8

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109	Interleukin-22 levels are increased in gastrointestinal graft-versus-host disease in children. Haematologica, 2018, 103, e480-e482.	3.5	7
110	Dioxin Disrupts Dynamic DNA Methylation Patterns in Genes That Govern Cardiomyocyte Maturation. Toxicological Sciences, 2020, 178, 325-337.	3.1	7
111	WebGimm: An integrated web-based platform for cluster analysis, functional analysis, and interactive visualization of results. Source Code for Biology and Medicine, 2011, 6, 3.	1.7	6
112	Predicting mechanism of action of cellular perturbations with pathway activity signatures. Bioinformatics, 2020, 36, 4781-4788.	4.1	6
113	XPA protein alters the specificity of ultraviolet light-induced mutagenesis in vitro. Environmental and Molecular Mutagenesis, 2001, 37, 329-339.	2.2	5
114	Clustering mutational spectra via classification likelihood and markov chain monte carlo algorithms. Journal of Agricultural, Biological, and Environmental Statistics, 2001, 6, 19-37.	1.4	5
115	Expression of Signaling Components in Embryonic Eyelid Epithelium. PLoS ONE, 2014, 9, e87038.	2.5	5
116	RNA SEQ Analysis Indicates that the AE3 Clâ^'/HCO3 â^' Exchanger Contributes to Active Transport-Mediated CO2 Disposal in Heart. Scientific Reports, 2017, 7, 7264.	3.3	5
117	What Is the Potential Measurement Error in Occupational Exposure Studies?. Journal of the Air and Waste Management Association, 2000, 50, 941-947.	1.9	3
118	Identification of maternally regulated fetal gene networks in the placenta with a novel embryo transfer system in mice. Physiological Genomics, 2011, 43, 317-324.	2.3	3
119	Comprehensive mapping of the methylation landscape of 16 CpG-dense regions in oral and pharyngeal squamous cell carcinoma. Epigenomics, 2019, 11, 987-1002.	2.1	3
120	Hexavalent chromium promotes differential binding of CTCF to its cognate sites in Euchromatin. Epigenetics, 2021, 16, 1-16.	2.7	3
121	Gene expression profiling of blood to predict the onset of leukemia. Blood Cells, Molecules, and Diseases, 2009, 42, 64-70.	1.4	2
122	Ultra-Deep Genomic Sequencing of HCV NS5A Resistance-Associated Substitutions in HCV/HIV Coinfected Patients. Digestive Diseases and Sciences, 2018, 63, 645-652.	2.3	1
123	ALOHA: Aggregated local extrema splines for high-throughput doseâ€“response analysis. Computational Toxicology, 2022, 21, 100196.	3.3	0