

Aristotelis A Chatziioannou

List of Publications by Year in descending order

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103
papers

2,035
citations

236612

25
h-index

276539

41
g-index

109
all docs

109
docs citations

109
times ranked

4236
citing authors

#	ARTICLE	IF	CITATIONS
1	Coactivation of GR and NFκB alters the repertoire of their binding sites and target genes. <i>Genome Research</i> , 2011, 21, 1404-1416.	2.4	184
2	Comparative Expression Profiling in Pulmonary Fibrosis Suggests a Role of Hypoxia-inducible Factor-1α in Disease Pathogenesis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2007, 176, 1108-1119.	2.5	178
3	Dual IRE1 and RNase functions dictate glioblastoma development. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	130
4	Low-Protein Diet Induces IRE1α-Dependent Anticancer Immunosurveillance. <i>Cell Metabolism</i> , 2018, 27, 828-842.e7.	7.2	99
5	CD90/Thy-1, a Cancer-Associated Cell Surface Signaling Molecule. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 66.	1.8	74
6	Role of the early secretory pathway in SARS-CoV-2 infection. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	63
7	Epigenetic memory in response to environmental stressors. <i>FASEB Journal</i> , 2017, 31, 2241-2251.	0.2	62
8	Discovery and Characterization of a Thermostable and Highly Halotolerant GH5 Cellulase from an Icelandic Hot Spring Isolate. <i>PLoS ONE</i> , 2016, 11, e0146454.	1.1	61
9	Radial Basis Function Neural Networks Classification for the Recognition of Idiopathic Pulmonary Fibrosis in Microscopic Images. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2008, 12, 42-54.	3.6	56
10	An in silico compartmentalized metabolic model of <i>Brassica napus</i> enables the systemic study of regulatory aspects of plant central metabolism. <i>Biotechnology and Bioengineering</i> , 2011, 108, 1673-1682.	1.7	53
11	Metagenomic mining for thermostable esterolytic enzymes uncovers a new family of bacterial esterases. <i>Scientific Reports</i> , 2016, 6, 38886.	1.6	53
12	Radiogenomic Analysis of F-18-Fluorodeoxyglucose Positron Emission Tomography and Gene Expression Data Elucidates the Epidemiological Complexity of Colorectal Cancer Landscape. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 177-185.	1.9	51
13	Control of anterior GRα dependent 2 (AGR2) dimerization links endoplasmic reticulum proteostasis to inflammation. <i>EMBO Molecular Medicine</i> , 2019, 11, .	3.3	48
14	Gene ARMADA: an integrated multi-analysis platform for microarray data implemented in MATLAB. <i>BMC Bioinformatics</i> , 2009, 10, 354.	1.2	40
15	Omics for prediction of environmental health effects: Blood leukocyte-based cross-omic profiling reliably predicts diseases associated with tobacco smoking. <i>Scientific Reports</i> , 2016, 6, 20544.	1.6	38
16	Epigenetics in Breast Cancer Therapy – New Strategies and Future Nanomedicine Perspectives. <i>Cancers</i> , 2020, 12, 3622.	1.7	36
17	KEGGconverter: a tool for the in-silico modelling of metabolic networks of the KEGG Pathways database. <i>BMC Bioinformatics</i> , 2009, 10, 324.	1.2	35
18	The KLK5 protease suppresses breast cancer by repressing the mevalonate pathway. <i>Oncotarget</i> , 2014, 5, 2390-2403.	0.8	34

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19	Computer-Supported Angiogenesis Quantification Using Image Analysis and Statistical Averaging. IEEE Transactions on Information Technology in Biomedicine, 2008, 12, 650-657.	3.6	33
20	Integrative workflows for metagenomic analysis. Frontiers in Cell and Developmental Biology, 2014, 2, 70.	1.8	32
21	Local intracerebral inhibition of IRE1 by MKC8866 sensitizes glioblastoma to irradiation/chemotherapy in vivo. Cancer Letters, 2020, 494, 73-83.	3.2	32
22	A transcriptomic computational analysis of mastic oil-treated Lewis lung carcinomas reveals molecular mechanisms targeting tumor cell growth and survival. BMC Medical Genomics, 2009, 2, 68.	0.7	30
23	Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: the StRAnGER web application. Frontiers in Neuroscience, 2011, 5, 8.	1.4	30
24	Metabolic flux analysis as a tool for the elucidation of the metabolism of neurotransmitter glutamate. Metabolic Engineering, 2003, 5, 201-210.	3.6	26
25	Novel pyrazolopyridine derivatives as potential angiogenesis inhibitors: Synthesis, biological evaluation and transcriptome-based mechanistic analysis. European Journal of Medicinal Chemistry, 2016, 121, 143-157.	2.6	25
26	GOrevenge: A Novel Generic Reverse Engineering Method for the Identification of Critical Molecular Players, Through the Use of Ontologies. IEEE Transactions on Biomedical Engineering, 2011, 58, 3522-3527.	2.5	24
27	Transcription of the NKG2D ligand MICA is suppressed by the IRE1/XBP1 pathway of the unfolded protein response through the regulation of E2F1. FASEB Journal, 2019, 33, 3481-3495.	0.2	23
28	Blood-based omic profiling supports female susceptibility to tobacco smoke-induced cardiovascular diseases. Scientific Reports, 2017, 7, 42870.	1.6	22
29	The Development of an Angiogenic Protein "Signature" in Ovarian Cancer Ascites as a Tool for Biologic and Prognostic Profiling. PLoS ONE, 2016, 11, e0156403.	1.1	22
30	ANASTASIA: An Automated Metagenomic Analysis Pipeline for Novel Enzyme Discovery Exploiting Next Generation Sequencing Data. Frontiers in Genetics, 2019, 10, 469.	1.1	21
31	Automated Angiogenesis Quantification through advanced Image Processing Techniques. , 2006, 2006, 2345-8.		18
32	Analyzing and Visualizing Genomic Complexity for the Derivation of the Emergent Molecular Networks. International Journal of Monitoring and Surveillance Technologies Research, 2016, 4, 30-49.	0.3	18
33	Dissecting the Mutational Landscape of Cutaneous Melanoma: An Omic Analysis Based on Patients from Greece. Cancers, 2018, 10, 96.	1.7	18
34	Non-apoptotic TRAIL function modulates NK cell activity during viral infection. EMBO Reports, 2020, 21, e48789.	2.0	18
35	Comparative Meta-Analysis of Transcriptomics Data during Cellular Senescence and <i>In Vivo</i> Tissue Ageing. Oxidative Medicine and Cellular Longevity, 2015, 2015, 1-17.	1.9	17
36	A Comparative Genomic Study in Schizophrenic and in Bipolar Disorder Patients, Based on Microarray Expression Profiling Meta-Analysis. Scientific World Journal, The, 2013, 2013, 1-14.	0.8	16

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37	Exploring Robust Diagnostic Signatures for Cutaneous Melanoma Utilizing Genetic and Imaging Data. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 190-198.	3.9	14
38	Abrogating GPT2 in triple-negative breast cancer inhibits tumor growth and promotes autophagy. International Journal of Cancer, 2021, 148, 1993-2009.	2.3	14
39	BRAF paradox breakers PLX8394, PLX7904 are more effective against BRAFV600E CRC cells compared with the BRAF inhibitor PLX4720 and shown by detailed pathway analysis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166061.	1.8	14
40	Decitabine potentiates efficacy of doxorubicin in a preclinical trastuzumab-resistant HER2-positive breast cancer models. Biomedicine and Pharmacotherapy, 2022, 147, 112662.	2.5	14
41	Evolving DNA methylation and gene expression markers of B-cell chronic lymphocytic leukemia are present in pre-diagnostic blood samples more than 10 years prior to diagnosis. BMC Genomics, 2017, 18, 728.	1.2	13
42	Pre-diagnostic blood immune markers, incidence and progression of B-cell lymphoma and multiple myeloma: Univariate and functionally informed multivariate analyses. International Journal of Cancer, 2018, 143, 1335-1347.	2.3	13
43	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. Mammalian Genome, 2019, 30, 260-275.	1.0	13
44	Splicing Genomics Events in Cervical Cancer: Insights for Phenotypic Stratification and Biomarker Potency. Genes, 2021, 12, 130.	1.0	13
45	Stromal NRG1 in luminal breast cancer defines pro-fibrotic and migratory cancer-associated fibroblasts. Oncogene, 2021, 40, 2651-2666.	2.6	13
46	KENeV : A web-application for the automated reconstruction and visualization of the enriched metabolic and signaling super-pathways deriving from genomic experiments. Computational and Structural Biotechnology Journal, 2015, 13, 248-255.	1.9	11
47	Operational criteria for selecting a cDNA microarray data normalization algorithm. Oncology Reports, 2006, 15, 983-996.	1.2	9
48	Escherichia coli genome-wide promoter analysis: Identification of additional AtoC binding target elements. BMC Genomics, 2011, 12, 238.	1.2	9
49	Evaluating the effect of various background correction methods regarding noise reduction, in two-channel microarray data. Computers in Biology and Medicine, 2012, 42, 19-29.	3.9	9
50	Elucidating the identity of resistance mechanisms to prednisolone exposure in acute lymphoblastic leukemia cells through transcriptomic analysis: A computational approach. Journal of Clinical Bioinformatics, 2011, 1, 36.	1.2	8
51	Genetic mapping of novel modifiers for ApcMin induced intestinal polyps development using the genetic architecture power of the collaborative cross mice. BMC Genomics, 2021, 22, 566.	1.2	8
52	Immunosuppressive Signaling Pathways as Targeted Cancer Therapies. Biomedicines, 2022, 10, 682.	1.4	8
53	An open data mining framework for the analysis of medical images: Application on Obstructive Nephropathy microscopy images. , 2010, 2010, 4108-11.		7
54	Integration of High-Volume Molecular and Imaging Data for Composite Biomarker Discovery in the Study of Melanoma. BioMed Research International, 2014, 2014, 1-14.	0.9	7

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55	The Expression of Myeloproliferative Neoplasm-Associated Calreticulin Variants Depends on the Functionality of ER-Associated Degradation. <i>Cancers</i> , 2019, 11, 1921.	1.7	7
56	Cancer Biomarkers from Genome-Scale DNA Methylation: Comparison of Evolutionary and Semantic Analysis Methods. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 647-670.	1.4	6
57	A Computational Pipeline for the Extraction of Actionable Biological Information From NGS-Phage Display Experiments. <i>Frontiers in Physiology</i> , 2019, 10, 1160.	1.3	6
58	Application of an Integrative Computational Framework in Transcriptomic Data of Atherosclerotic Mice Suggests Numerous Molecular Players. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-9.	5.7	5
59	Prioritized functional analysis of biological experiments using resampling and noise control methodologies. , 2013, , .		5
60	Identifying gender independent biomarkers responsible for human muscle aging using microarray data. , 2013, , .		5
61	A Composite Framework for the Statistical Analysis of Epidemiological DNA Methylation Data with the Infinium Human Methylation 450K BeadChip. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2014, 18, 817-823.	3.9	5
62	Integrative Bioinformatic Analysis of Transcriptomic Data Identifies Conserved Molecular Pathways Underlying Ionizing Radiation-Induced Bystander Effects (RIBE). <i>Cancers</i> , 2017, 9, 160.	1.7	5
63	Designing a QTL Mapping Study for Implementation in the Realized Collaborative Cross Genetic Reference Population. <i>Current Protocols in Mouse Biology</i> , 2019, 9, e66.	1.2	5
64	Integration of Raman spectra with transcriptome data in glioblastoma multiforme defines tumour subtypes and predicts patient outcome. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 10846-10856.	1.6	5
65	Dual IRE1 RNase functions dictate glioblastoma development. <i>EMBO Molecular Medicine</i> , 2022, 14, e15622.	3.3	5
66	Delineation and interpretation of gene networks towards their effect in cellular physiology- A reverse engineering approach for the identification of critical molecular players, through the use of ontologies. , 2010, 2010, 6709-12.		4
67	An Integrated Platform for Skin Cancer Heterogenous and Multilayered Data Management. <i>Journal of Medical Systems</i> , 2021, 45, 10.	2.2	4
68	Prognostic Alternative Splicing Signatures in Esophageal Carcinoma. <i>Cancer Management and Research</i> , 2021, Volume 13, 4509-4527.	0.9	4
69	Feature Selection Study on Separate Multi-modal Datasets: Application on Cutaneous Melanoma. <i>International Federation for Information Processing</i> , 2012, , 36-45.	0.4	4
70	HECTOR: Enabling Microarray Experiments over the Hellenic Grid Infrastructure. <i>Journal of Grid Computing</i> , 2009, 7, 395-416.	2.5	3
71	GRISSOM Platform: Enabling Distributed Processing and Management of Biological Data Through Fusion of Grid and Web Technologies. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2011, 15, 83-92.	3.6	3
72	A Galaxy Workflow for the Functional Annotation of Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2012, , 247-253.	1.0	3

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73	HuR-Regulated mRNAs Associated with Nuclear hnRNP A1-RNP Complexes. International Journal of Molecular Sciences, 2013, 14, 20256-20281.	1.8	3
74	GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments. , 2009, , .		2
75	Unifying the integration, analysis and interpretation of multi-omic datasets: Exploration of the disease networks of Obstructive Nephropathy in children. , 2011, 2011, 3716-9.		2
76	Heterogeneous data fusion and selection in high-volume molecular and imaging datasets. , 2012, , .		2
77	Inference of a robust diagnostic signature in the case of Melanoma: Gene selection by information gain and Gene Ontology tree exploration. , 2013, , .		2
78	Intelligent identification of biomarkers for the study of obstructive nephropathy. Intelligent Decision Technologies, 2013, 7, 11-22.	0.6	2
79	Redesigning EHRs and Clinical Decision Support Systems for the Precision Medicine Era. , 2015, , .		2
80	Making sense of the biological complexity through the platform-driven unification of the analytical and visualization tasks. , 2015, , .		2
81	“An RNA-seq analysis from non-small cell lung cancer biopsies suggests an important role for aberrant alternative splicing in its pathophysiology” Health and Technology, 2017, 7, 133-140.	2.1	2
82	Modulation of Pathways Underlying Distinct Cell Death Mechanisms in Two Human Lung Cancer Cell Lines in Response to SN1 Methylating Agents Treatment. PLoS ONE, 2016, 11, e0160248.	1.1	2
83	Development and validation of a skin fibroblast biomarker profile for schizophrenic patients. AIMS Bioengineering, 2016, 3, 552-565.	0.6	2
84	ANDROMEDA: A MATLAB Automated cDNA Microarray Data Analysis Platform. International Federation for Information Processing, 2007, , 127-136.	0.4	2
85	An in-silico model of the biosynthesis of neurotransmitter glutamate, elucidates the complex regulatory role of glucocorticoids in neurotransmitter glutamate release. Computers in Biology and Medicine, 2009, 39, 501-511.	3.9	1
86	Studying the nonlinearities of T-cell leukemia growth and the underlying metabolism upon glucocorticoid treatment through the application of dynamic mathematical methodologies. , 2010, , .		1
87	Analysis of DNA methylation epidemiological data through a generic composite statistical framework. , 2012, , .		1
88	Prediction of enzymatic activity of proteins based on structural and functional domains. , 2013, , .		1
89	Exploring the Molecular Determinants of Tumor-Stroma Interaction in Non-small Cell Lung Cancer Through the Utilization of RNA-seq Data from Lung Biopsies. IFMBE Proceedings, 2016, , 495-499.	0.2	1
90	Integrative Bioinformatic Analysis of a Greek Epidemiological Cohort Provides Insight into the Pathogenesis of Primary Cutaneous Melanoma. IFIP Advances in Information and Communication Technology, 2016, , 39-52.	0.5	1

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91	Derivation of Cancer Related Biomarkers from DNA Methylation Data from an Epidemiological Cohort. Communications in Computer and Information Science, 2013, , 249-256.	0.4	1
92	Comparative computational methods for identification of inherent or acquired mechanisms of resistance to prednisolone in Acute Lymphoblastic Leukemia cells. , 2009, , .		0
93	An Epidemiological population study reveals a sex-related differential effect of PAH exposure and gene polymorphisms on bulky DNA adducts formation. , 2010, , .		0
94	Analysis of pediatric obstructive nephropathy using protein antibody arrays and computational techniques. , 2010, , .		0
95	Advanced characterization of microscopic Kidney biopsies utilizing image analysis techniques. , 2012, 2012, 4414-7.		0
96	Integrative transcriptomic analysis of two cell lines elucidates the architecture of endoplasmic reticulum stress signaling in glioblastoma. , 2013, , .		0
97	An Entropy-based Statistical Workflow Provides Noise-Minimizing Biological Annotation for. , 2014, , .		0
98	Long-Term Functional Outcome and Quality of Life After Restorative Proctocolectomy With Mucosectomy and Hand Suture IPAA: 20 Years' Experience in 326 Patients. International Surgery, 2016, 101, 202-211.	0.0	0
99	Combining Pathway Analysis and Supervised Machine Learning for the Functional Classification of Single-Cell Transcriptomic Data. , 2019, , .		0
100	Entropic Ranks: A Methodology for Enhanced, Threshold-Free, Information-Rich Data Partition and Interpretation. Applied Sciences (Switzerland), 2020, 10, 7077.	1.3	0
101	Bioinformatic framework for analysis of transcription factor changes as the molecular link between replicative cellular senescence signaling pathways and carcinogenesis. Biogerontology, 2020, 21, 357-366.	2.0	0
102	Network analysis in aged C. elegans reveals candidate regulatory genes of ageing. Biogerontology, 2021, 22, 345-367.	2.0	0
103	A Novel Image Analysis Methodology for the Evaluation of Angiogenesis in Matrigel Assays and Screening of Angiogenesis-Modulating Compounds. IFIP Advances in Information and Communication Technology, 2015, , 61-71.	0.5	0