

Eleftherios Pilalis

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

383
citations

932766

10
h-index

839053

18
g-index

30
all docs

30
docs citations

30
times ranked

1133
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Control of anterior <i>GR</i> adjacent 2 (<i>AGR</i> 2) dimerization links endoplasmic reticulum proteostasis to inflammation. <i>EMBO Molecular Medicine</i> , 2019, 11, .	3.3	48
4	Epigenetics in Breast Cancer Therapy—New Strategies and Future Nanomedicine Perspectives. <i>Cancers</i> , 2020, 12, 3622.	1.7	36
5	Regulated IRE1 \pm -dependent decay (RIDD)-mediated reprogramming of lipid metabolism in cancer. <i>Nature Communications</i> , 2022, 13, 2493.	5.8	28
6	RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	25
7	The Development of an Angiogenic Protein “Signature” in Ovarian Cancer Ascites as a Tool for Biologic and Prognostic Profiling. <i>PLoS ONE</i> , 2016, 11, e0156403.	1.1	22
8	ANASTASIA: An Automated Metagenomic Analysis Pipeline for Novel Enzyme Discovery Exploiting Next Generation Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 469.	1.1	21
9	Analyzing and Visualizing Genomic Complexity for the Derivation of the Emergent Molecular Networks. <i>International Journal of Monitoring and Surveillance Technologies Research</i> , 2016, 4, 30-49.	0.3	18
10	Decitabine potentiates efficacy of doxorubicin in a preclinical trastuzumab-resistant HER2-positive breast cancer models. <i>Biomedicine and Pharmacotherapy</i> , 2022, 147, 112662.	2.5	14
11	KENeV : A web-application for the automated reconstruction and visualization of the enriched metabolic and signaling super-pathways deriving from genomic experiments. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 248-255.	1.9	11
12	<i>Escherichia coli</i> genome-wide promoter analysis: Identification of additional AtoC binding target elements. <i>BMC Genomics</i> , 2011, 12, 238.	1.2	9
13	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. <i>BMC Genomics</i> , 2020, 21, 761.	1.2	7
14	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
15	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
16	Prioritized functional analysis of biological experiments using resampling and noise control methodologies. , 2013, , .		5
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	A Galaxy Workflow for the Functional Annotation of Metagenomic Samples. Lecture Notes in Computer Science, 2012, , 247-253.	1.0	3
20	GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments. , 2009, , .		2
21	ANASTASIA a versatile web platform for metagenomic analysis. New Biotechnology, 2014, 31, S170.	2.4	2
22	Making sense of the biological complexity through the platform-driven unification of the analytical and visualization tasks. , 2015, , .		2
23	Development and validation of a skin fibroblast biomarker profile for schizophrenic patients. AIMS Bioengineering, 2016, 3, 552-565.	0.6	2
24	Prediction of enzymatic activity of proteins based on structural and functional domains. , 2013, , .		1
25	An Entropy-based Statistical Workflow Provides Noise-Minimizing Biological Annotation for. , 2014, , .		0
26	Combining Pathway Analysis and Supervised Machine Learning for the Functional Classification of Single-Cell Transcriptomic Data. , 2019, , .		0
27	Study of a protein based angiogenic profile in endometrial tissue of women undergoing assisted reproductive techniques - A pilot study. Clinical Practice (London, England), 0, , .	0.1	0