

Patrizio Arrigo

List of Publications by Year in descending order

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36
papers

928
citations

567144

15
h-index

642610

23
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all docs

37
docs citations

37
times ranked

1616
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational Design of Nucleic Acid-Based Bioreceptor for Contaminants of Emerging Concern. <i>Advanced Functional Materials and Sensors</i> , 2020, , 213-231.	1.2	0
2	Molecular mechanism of apoptosis induction in Jurkat E6-1 cells by <i>Tribulus terrestris</i> alkaloids extract. <i>Journal of Traditional and Complementary Medicine</i> , 2018, 8, 410-419.	1.5	19
3	Prediction of potential barcoding sites on ITS1 by wavelet transform. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 814-823.	2.0	0
4	Noncoding RNAs: Possible Players in the Development of Fluorosis. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	19
5	An integrated genomic and proteomic approach to identify signatures of endosulfan exposure in hepatocellular carcinoma cells. <i>Pesticide Biochemistry and Physiology</i> , 2015, 125, 8-16.	1.6	14
6	Beta Caryophyllene and Caryophyllene Oxide, Isolated from <i>Aegle Marmelos</i> , as the Potent Anti-inflammatory Agents against Lymphoma and Neuroblastoma Cells. <i>Anti-Inflammatory and Anti-Allergy Agents in Medicinal Chemistry</i> , 2014, 13, 45-55.	1.1	56
7	Optimize ncRNA Targeting: A Signal Analysis Based Approach. <i>IFMBE Proceedings</i> , 2014, , 662-665.	0.2	0
8	SUBCELLULAR LOCALIZATION CHARTS: A NEW VISUAL METHODOLOGY FOR THE SEMI-AUTOMATIC LOCALIZATION OF PROTEIN-RELATED DATA SETS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340005.	0.3	13
9	Toll-like receptor structural determinants: Variability analysis by digital signal processing methods. , 2013, , .		0
10	Potential MiRNAs recognition site identification in 3' UTR regions by DSP methods. , 2012, 2012, 5558-61.		0
11	Different Mutations in Three Prime Repair Exonuclease 1 and Ribonuclease H2 Genes Affect Clinical Features in Aicardi-GoutiÃres Syndrome. <i>Journal of Child Neurology</i> , 2012, 27, 51-60.	0.7	4
12	Prediction and 3D visualization of biological networks using cytological disease mapping. <i>EMBnet Journal</i> , 2012, 18, 116.	0.2	0
13	Backward proteomic approach for microrna's target recognition. , 2011, , .		0
14	Analysis of metabolic networks controlled by microRNAs in zebrafish. <i>Journal of Biological Research (Italy)</i> , 2011, 84, .	0.0	0
15	Mutagens interfere with microRNA maturation by inhibiting DICER. An in silico biology analysis. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2011, 717, 116-128.	0.4	31
16	Proteomic-based screening of miRNAs metabolic pathway targeting. <i>International Journal of Computational Biology and Drug Design</i> , 2010, 3, 164.	0.3	2
17	Visualization and Analysis of a Cardio Vascular Diseaseand MUPP1-related Biological Network combining Text Mining and Data Warehouse Approaches. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	10
18	In silicon evaluation of nanoparticle cell interaction via human TLR3. , 2010, , .		1

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19	Visualization and analysis of a cardio vascular disease- and MUPP1-related biological network combining text mining and data warehouse approaches. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, 148.	1.0	11
20	Reliability of hamilton-norwood classification. <i>International Journal of Trichology</i> , 2009, 1, 120.	0.1	43
21	Downregulation of microRNA expression in the lungs of rats exposed to cigarette smoke. <i>FASEB Journal</i> , 2009, 23, 806-812.	0.2	399
22	Lipoprotein lipase: A bioinformatics criterion for assessment of mutations as a risk factor for cardiovascular disease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 855-862.	1.5	15
23	In silico screening of Rac1 ligand specificity. , 2008, 2008, 4098-101.		0
24	Integrated Bioinformatics analysis of structural differences in metabolic pathways. An application to <i>Mycobacterium Leprae</i> . , 2007, , .		1
25	Topical Clustering of Biomedical Abstracts by Self-Organizing Maps. , 2006, , 481-490.		0
26	Software for Analysis of Gene Regulatory Sequences by Knowledge Discovery Methods. , 2006, , 491-498.		1
27	AgeWa: an integrated approach for antisense experiment design. <i>IEEE Transactions on Nanobioscience</i> , 2002, 1, 167-171.	2.2	3
28	The identification of a novel human homologue of the SH3 binding glutamic acid-rich (SH3BGR) gene establishes a new family of highly conserved small proteins related to Thioredoxin Superfamily. <i>Gene</i> , 2002, 291, 233-239.	1.0	55
29	The multidrug transporters belonging to major facilitator superfamily in <i>Mycobacterium tuberculosis</i> . <i>Molecular Medicine</i> , 2002, 8, 714-24.	1.9	56
30	A Novel Human Homologue of the SH3BGR Gene Encodes a Small Protein Similar to Glutaredoxin 1 of <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2001, 285, 540-545.	1.0	16
31	Identification and characterization of a new human cDNA from chromosome 21q22.3 encoding a basic nuclear protein. <i>Human Genetics</i> , 1998, 102, 289-293.	1.8	29
32	Can functional regions of proteins be predicted from their coding sequences? The case study of G-protein coupled receptors. <i>Gene</i> , 1998, 221, GC65-GC110.	1.0	6
33	Identification and Characterization of a New Human Gene Encoding a Small Protein with High Homology to the Proline-Rich Region of the SH3BGR Gene. <i>Biochemical and Biophysical Research Communications</i> , 1998, 247, 302-306.	1.0	29
34	Cloning a new human gene from chromosome 21q22.3 encoding a glutamic acid-rich protein expressed in heart and skeletal muscle. <i>Human Genetics</i> , 1997, 99, 387-392.	1.8	34
35	Hamming-Clustering method for signals prediction in 5' and 3' regions of eukaryotic genes. <i>Bioinformatics</i> , 1996, 12, 399-404.	1.8	23
36	Study of Bound Water of Poly-Adenine Using High Frequency Dielectric Measurements. <i>Biophysical Journal</i> , 1986, 49, 1003-1008.	0.2	38