Patrizio Arrigo

List of Publications by Year
in descending order

36 papers	**928** citations	567144 **15** h-index	642610 **23** g-index
37 all docs	**37** docs citations	**37** times ranked	**1616** citing authors

#	Article	IF	Citations
1	Downregulation of microRNA expression in the lungs of rats exposed to cigarette smoke. FASEB Journal, 2009, 23, 806-812.	0.2	399
2	Beta Caryophyllene and Caryophyllene Oxide, Isolated from Aegle Marmelos, as the Potent Anti-inflammatory Agents against Lymphoma and Neuroblastoma Cells. Anti-Inflammatory and Anti-Allergy Agents in Medicinal Chemistry, 2014, 13, 45-55.	1.1	56
3	The multidrug transporters belonging to major facilitator superfamily in Mycobacterium tuberculosis. Molecular Medicine, 2002, 8, 714-24.	1.9	56
4	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. Gene, 2002, 291, 233-239.	1.0	55
5	Reliability of hamilton-norwood classification. International Journal of Trichology, 2009, 1, 120.	0.1	43
6	Study of Bound Water of Poly-Adenine Using High Frequency Dielectric Measurements. Biophysical Journal, 1986, 49, 1003-1008.	0.2	38
7	Cloning a new human gene from chromosome 21q22.3 encoding a glutamic acid-rich protein expressed in heart and skeletal muscle. Human Genetics, 1997, 99, 387-392.	1.8	34
8	Mutagens interfere with microRNA maturation by inhibiting DICER. An in silico biology analysis. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2011, 717, 116-128.	0.4	31
9	Identification and characterization of a new human cDNA from chromosome 21q22.3 encoding a basic nuclear protein. Human Genetics, 1998, 102, 289-293.	1.8	29
10	Identification and Characterization of a New Human Gene Encoding a Small Protein with High Homology to the Proline-Rich Region of the SH3BGR Gene. Biochemical and Biophysical Research Communications, 1998, 247, 302-306.	1.0	29
11	Hamming-Clustering method for signals prediction in 5â€² and 3â€² regions of eukaryotic genes. Bioinformatics, 1996, 12, 399-404.	1.8	23
12	Noncoding RNAs: Possible Players in the Development of Fluorosis. BioMed Research International, 2015, 2015, 1-10.	0.9	19
13	Molecular mechanism of apoptosis induction in Jurkat E6-1 cells by Tribulus terrestris alkaloids extract. Journal of Traditional and Complementary Medicine, 2018, 8, 410-419.	1.5	19
14	A Novel Human Homologue of the SH3BGR Gene Encodes a Small Protein Similar to Glutaredoxin 1 of Escherichia coli. Biochemical and Biophysical Research Communications, 2001, 285, 540-545.	1.0	16
15	Lipoprotein lipase: A bioinformatics criterion for assessment of mutations as a risk factor for cardiovascular disease. Proteins: Structure, Function and Bioinformatics, 2008, 70, 855-862.	1.5	15
16	An integrated genomic and proteomic approach to identify signatures of endosulfan exposure in hepatocellular carcinoma cells. Pesticide Biochemistry and Physiology, 2015, 125, 8-16.	1.6	14
17	SUBCELLULAR LOCALIZATION CHARTS: A NEW VISUAL METHODOLOGY FOR THE SEMI-AUTOMATIC LOCALIZATION OF PROTEIN-RELATED DATA SETS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340005.	0.3	13
18	Visualization and analysis of a cardio vascular disease- and MUPP1-related biological network combining text mining and data warehouse approaches. Journal of Integrative Bioinformatics, 2010, 7, 148.	1.0	11

#	Article	IF	Citations
19	Visualization and Analysis of a Cardio Vascular Diseaseand MUPP1-related Biological Network combining Text Mining and Data Warehouse Approaches. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	10
20	Can functional regions of proteins be predicted from their coding sequences? The case study of G-protein coupled receptors. Gene, 1998, 221, GC65-GC110.	1.0	6
21	Different Mutations in Three Prime Repair Exonuclease 1 and Ribonuclease H2 Genes Affect Clinical Features in Aicardi-GoutiÃ¨res Syndrome. Journal of Child Neurology, 2012, 27, 51-60.	0.7	4
22	AgeWa: an integrated approach for antisense experiment design. IEEE Transactions on Nanobioscience, 2002, 1, 167-171.	2.2	3
23	Proteomic-based screening of miRNAs metabolic pathway targeting. International Journal of Computational Biology and Drug Design, 2010, 3, 164.	0.3	2
24	Integrated Bioinformatics analysis of structural differences in metabolic pathways. An application to Mycobacterium Leprae. , 2007, , .		1
25	In silicon evaluation of nanoparticle cell interaction via human TLR3. , 2010, , .		1
26	Software for Analysis of Gene Regulatory Sequences by Knowledge Discovery Methods. , 2006, , 491-498.		1
27	In silico screening of Rac1 ligand specificity. , 2008, 2008, 4098-101.		0
28	Backward proteomic approach for microrna's target recognition. , 2011, , .		0
29	Analysis of metabolic networks controlled by microRNAs in zebrafish. Journal of Biological Research (Italy), 2011, 84, .	0.0	0
30	Potential MiRNAs recognition site identification in 3' UTR regions by DSP methods. , 2012, 2012, 5558-61.		0
31	Toll-like receptor structural determinants: Variability analysis by digital signal processing methods. , 2013, , .		0
32	Prediction of potential barcoding sites on ITS1 by wavelet transform. Journal of Biomolecular Structure and Dynamics, 2016, 34, 814-823.	2.0	0
33	Prediction and 3D visualization of biological networks using cytological disease mapping. EMBnet Journal, 2012, 18, 116.	0.2	0
34	Optimize ncRNA Targeting: A Signal Analysis Based Approach. IFMBE Proceedings, 2014, , 662-665.	0.2	0
35	Computational Design of Nucleic Acid-Based Bioreceptor for Contaminants of Emerging Concern. Advanced Functional Materials and Sensors, 2020, , 213-231.	1.2	0
36	Topical Clustering of Biomedical Abstracts by Self-Organizing Maps. , 2006, , 481-490.		0