Mahmoud ElHefnawi

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9046635/publications.pdf

Version: 2024-02-01

331538 414303 1,297 63 21 citations h-index papers

g-index 69 69 69 2154 docs citations times ranked citing authors all docs

32

#	Article	IF	CITATIONS
1	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	6.0	144
2	Comparison of Machine Learning Approaches for Prediction of Advanced Liver Fibrosis in Chronic Hepatitis C Patients. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 861-868.	1.9	85
3	DeNovo: virus-host sequence-based protein–protein interaction prediction. Bioinformatics, 2016, 32, 1144-1150.	1.8	79
4	Telaprevir is a potential drug for repurposing against SARS-CoV-2: computational and in vitro studies. Heliyon, 2021, 7, e07962.	1.4	62
5	Part I: Synthesis, cancer chemopreventive activity and molecular docking study of novel quinoxaline derivatives. European Journal of Medicinal Chemistry, 2011, 46, 327-340.	2.6	61
6	Modified gold nanoparticles for intracellular delivery of anti-liver cancer siRNA. International Journal of Pharmaceutics, 2016, 504, 125-133.	2.6	50
7	A review study: Computational techniques for expecting the impact of non-synonymous single nucleotide variants in human diseases. Gene, 2019, 680, 20-33.	1.0	47
8	Machine Learning Prediction Models for Diagnosing Hepatocellular Carcinoma with HCV-related Chronic Liver Disease. Computer Methods and Programs in Biomedicine, 2020, 196, 105551.	2.6	41
9	Performance of machine learning approaches on prediction of esophageal varices for Egyptian chronic hepatitis C patients. Informatics in Medicine Unlocked, 2019, 17, 100267.	1.9	40
10	Hsa-miR-195 targets PCMT1 in hepatocellular carcinoma that increases tumor life span. Tumor Biology, 2014, 35, 11301-11309.	0.8	39
11	Identification of novel conserved functional motifs across most Influenza A viral strains. Virology Journal, 2011, 8, 44.	1.4	36
12	Evaluation of computational techniques for predicting non-synonymous single nucleotide variants pathogenicity. Genomics, 2019, 111, 869-882.	1.3	36
13	MysiRNA-Designer: A Workflow for Efficient siRNA Design. PLoS ONE, 2011, 6, e25642.	1.1	35
14	An Integrative Meta-analysis of MicroRNAs in Hepatocellular Carcinoma. Genomics, Proteomics and Bioinformatics, 2013, 11, 354-367.	3.0	33
15	Multiple virtual screening approaches for finding new Hepatitis c virus RNA-dependent RNA polymerase inhibitors: Structure-based screens and molecular dynamics for the pursue of new poly pharmacological inhibitors. BMC Bioinformatics, 2012, 13, S5.	1.2	30
16	In silico identification of potential key regulatory factors in smoking-induced lung cancer. BMC Medical Genomics, 2017, 10, 40.	0.7	27
17	Co-regulatory Network of Oncosuppressor miRNAs and Transcription Factors for Pathology of Human Hepatic Cancer Stem Cells (HCSC). Scientific Reports, 2019, 9, 5564.	1.6	27
18	In Silico Design and Experimental Validation of siRNAs Targeting Conserved Regions of Multiple Hepatitis C Virus Genotypes. PLoS ONE, 2016, 11, e0159211.	1.1	27

#	Article	IF	CITATIONS
19	Accurate Prediction of Advanced Liver Fibrosis Using the Decision Tree Learning Algorithm in Chronic Hepatitis C Egyptian Patients. Gastroenterology Research and Practice, 2016, 2016, 1-7.	0.7	26
20	MysiRNA: Improving siRNA efficacy prediction using a machine-learning model combining multi-tools and whole stacking energy (î"G). Journal of Biomedical Informatics, 2012, 45, 528-534.	2.5	23
21	In Silico and In Vivo Evaluation of SARS-CoV-2 Predicted Epitopes-Based Candidate Vaccine. Molecules, 2021, 26, 6182.	1.7	23
22	Prediction of prognostic biomarkers for Interferon-based therapy to Hepatitis C Virus patients: a metaanalysis of the NS5A protein in subtypes 1a, 1b, and 3a. Virology Journal, 2010, 7, 130.	1.4	22
23	Synthesis, pharmacological activity evaluation and molecular modeling of new polynuclear heterocyclic compounds containing benzimidazole derivatives. Archives of Pharmacal Research, 2012, 35, 2063-2075.	2.7	19
24	The design of optimal therapeutic small interfering RNA molecules targeting diverse strains of influenza A virus. Bioinformatics, 2011, 27, 3364-3370.	1.8	18
25	New Benzimidazoles and Their Antitumor Effects with Aurora A Kinase and KSP Inhibitory Activities. Archiv Der Pharmazie, 2015, 348, 475-486.	2.1	18
26	Computational Identification of Tissue-Specific Splicing Regulatory Elements in Human Genes from RNA-Seq Data. PLoS ONE, 2016, 11, e0166978.	1.1	17
27	Expression profiling and analysis of some miRNAs in subcutaneous white adipose tissue during development of obesity. Genes and Nutrition, 2020, 15, 8.	1.2	15
28	Systematic auditing is essential to debiasing machine learning in biology. Communications Biology, 2021, 4, 183.	2.0	14
29	Effect of Tumor Suppressor MiR-34a Loaded on ZSM-5 Nanozeolite in Hepatocellular Carcinoma: In Vitro and In Vivo Approach. Current Gene Therapy, 2019, 19, 342-354.	0.9	14
30	Impact of type 2 diabetes mellitus on the immunoregulatory characteristics of adipose tissue-derived mesenchymal stem cells. International Journal of Biochemistry and Cell Biology, 2021, 140, 106072.	1.2	13
31	Bioinformatics functional analysis of let-7a, miR-34a, and miR-199a/b reveals novel insights into immune system pathways and cancer hallmarks for hepatocellular carcinoma. Tumor Biology, 2018, 40, 101042831877367.	0.8	12
32	Accurate classification and hemagglutinin amino acid signatures for influenza A virus host-origin association and subtyping. Virology, 2014, 449, 328-338.	1.1	10
33	Altered expression of WFS1 and NOTCH2 genes associated with diabetic nephropathy in T2DM patients. Diabetes Research and Clinical Practice, 2018, 140, 304-313.	1.1	10
34	Targeted delivery of miR-218 via decorated hyperbranched polyamidoamine for liver cancer regression. International Journal of Pharmaceutics, 2021, 610, 121256.	2.6	10
35	Rational Drug Design for Identifying Novel Multi-target Inhibitors for Hepatocellular Carcinoma. Anti-Cancer Agents in Medicinal Chemistry, 2012, 12, 1088-1097.	0.9	9
36	Whole genome sequencing and bioinformatics analysis of two Egyptian genomes. Gene, 2018, 668, 129-134.	1.0	9

3

#	Article	IF	CITATIONS
37	Accurate Prediction of Response to Interferon-based Therapy in Egyptian Patients with Chronic Hepatitis C Using Machine-learning Approaches. , 2012, , .		8
38	Genetic variability of the core protein in hepatitis C virus genotype 4 in Saudi Arabian patients and its implication on pegylated interferon and ribavirin therapy. Journal of Translational Medicine, 2014, 12, 91.	1.8	8
39	Down-regulation of circulating microRNA let-7a in Egyptian smokers. Journal of Genetic Engineering and Biotechnology, 2018, 16, 53-56.	1.5	8
40	The Promise of miRNA Replacement Therapy for Hepatocellular Carcinoma. Current Gene Therapy, 2019, 19, 290-304.	0.9	8
41	Immunomodulatory and Antioxidative potentials of adipose-derived Mesenchymal stem cells isolated from breast versus abdominal tissue: a comparative study. Cell Regeneration, 2020, 9, 18.	1.1	7
42	MicroRNA expression analysis in endometriotic serum treated mesenchymal stem cells. EXCLI Journal, 2017, 16, 852-867.	0.5	6
43	MicroRNA-150 down Regulation in Acute Myeloid Leukaemia Patients and Its Prognostic Implication. Open Access Macedonian Journal of Medical Sciences, 2018, 6, 1993-2000.	0.1	6
44	Integrative assessment of CIP2A overexpression and mutational effects in human malignancies identifies possible deleterious variants. Computers in Biology and Medicine, 2021, 139, 104986.	3.9	6
45	Identifying potential novel insights for COVID-19 pathogenesis and therapeutics using an integrated bioinformatics analysis of host transcriptome. International Journal of Biological Macromolecules, 2022, 194, 770-780.	3.6	6
46	Hepatitis C virus genotype 1: How genetic variability of the core protein affects the response to pegylatedâ€∢scp>i⟨ scp>nterferon and ribavirin therapy. Journal of Medical Virology, 2014, 86, 224-234.	2.5	5
47	MicroTarget: MicroRNA target gene prediction approach with application to breast cancer. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750013.	0.3	5
48	Early diagnosis of esophageal varices using Boosted-NaÃ-ve Bayes Tree: A multicenter cross-sectional study on chronic hepatitis C patients. Informatics in Medicine Unlocked, 2020, 20, 100421.	1.9	5
49	Complete genome sequence and bioinformatics analysis of nine Egyptian females with clinical information from different geographic regions in Egypt. Gene, 2021, 769, 145237.	1.0	5
50	Structure-based predictive model for some benzimidazole inhibitors of hepatitis C virus NS5B polymerase. Medicinal Chemistry Research, 2013, 22, 1866-1883.	1.1	4
51	Ensemble-based classification approach for micro-RNA mining applied on diverse metagenomic sequences. BMC Research Notes, 2014, 7, 286.	0.6	4
52	An Integrated Methodology for Mining Promiscuous Proteins: A Case Study of an Integrative Bioinformatics Approach for Hepatitis C Virus Non-structural 5a Protein. Advances in Experimental Medicine and Biology, 2010, 680, 299-305.	0.8	3
53	In-silico Approaches for RNAi Post-Transcriptional Gene Regulation: Optimizing siRNA Design and Selection., 0,,.		2
54	DETECTING AND ANALYZING COPY NUMBER ALTERNATIONS IN ARRAY-BASED CGH DATA. Biomedical Engineering - Applications, Basis and Communications, 2016, 28, 1650044.	0.3	2

#	Article	IF	Citations
55	The oral microbiome of treated and untreated chronic HCV infection: A preliminary study. Oral Diseases, 2023, 29, 843-852.	1.5	2
56	Using Information Gain to Compare the Effeciency of Machine Learning Techniques When Classifying Influenza Based on Viral Hosts., 2015,, 707-722.		2
57	283 PREDICTION OF miRNA TARGET GENES INVOLVED IN LIVER CANCER PATHWAYS AND ITS VALIDATION. Journal of Hepatology, 2013, 58, S120.	1.8	1
58	Human microRNAs targeting hepatitis C virus. , 2014, , .		1
59	Predicting Non-Synonymous Single Nucleotide Variants Pathogenic Effects in Human Diseases. , 2019, , 400-409.		1
60	Derivation of "Egyptian varices prediction (EVP) index†A novel noninvasive index for diagnosing esophageal varices in HCV Patients. Journal of Advanced Research, 2022, 35, 87-97.	4.4	1
61	Immunomodulatory and Antioxidative potentials of adipose-derived Mesenchymal stem cells isolated from breast versus abdominal tissue: a comparative study. Cell Regeneration, 2020, 9, 18.	1.1	1
62	Drug repurposing through virtual screening and in vitro validation identifies tigecycline as a novel putative HCV polymerase inhibitor. Virology, 2022, 570, 9-17.	1.1	1
63	Clinical Implications of S100A12 and Resolvin D1 Serum Levels, and Related Genes in Children with Familial Mediterranean Fever. Journal of Child Science, 2021, 11, e163-e169.	0.1	0