

Mahmoud ElHefnawi

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64
papers

730
citations

17
h-index

24
g-index

69
ext. papers

1,040
ext. citations

5.1
avg, IF

4.22
L-index

#	Paper	IF	Citations
64	Derivation of "Egyptian varices prediction (EVP) index": A novel noninvasive index for diagnosing esophageal varices in HCV Patients.. <i>Journal of Advanced Research</i> , 2022 , 35, 87-97	13	
63	Drug repurposing through virtual screening and in vitro validation identifies tigecycline as a novel putative HCV polymerase inhibitor.. <i>Virology</i> , 2022 , 570, 9-17	3.6	
62	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
61	Identifying potential novel insights for COVID-19 pathogenesis and therapeutics using an integrated bioinformatics analysis of host transcriptome. <i>International Journal of Biological Macromolecules</i> , 2021 ,	7.9	2
60	In Silico and In Vivo Evaluation of SARS-CoV-2 Predicted Epitopes-Based Candidate Vaccine. <i>Molecules</i> , 2021 , 26,	4.8	9
59	Integrative assessment of CIP2A overexpression and mutational effects in human malignancies identifies possible deleterious variants. <i>Computers in Biology and Medicine</i> , 2021 , 139, 104986	7	0
58	Targeted delivery of miR-218 via decorated hyperbranched polyamidoamine for liver cancer regression. <i>International Journal of Pharmaceutics</i> , 2021 , 610, 121256	6.5	1
57	Complete genome sequence and bioinformatics analysis of nine Egyptian females with clinical information from different geographic regions in Egypt. <i>Gene</i> , 2021 , 769, 145237	3.8	1
56	Systematic auditing is essential to debiasing machine learning in biology. <i>Communications Biology</i> , 2021 , 4, 183	6.7	5
55	The oral microbiome of treated and untreated chronic HCV infection: A preliminary study. <i>Oral Diseases</i> , 2021 ,	3.5	1
54	Telaprevir is a potential drug for repurposing against SARS-CoV-2: computational and studies. <i>Heliyon</i> , 2021 , 7, e07962	3.6	29
53	Impact of type 2 diabetes mellitus on the immunoregulatory characteristics of adipose tissue-derived mesenchymal stem cells. <i>International Journal of Biochemistry and Cell Biology</i> , 2021 , 140, 106072	5.6	3
52	Clinical Implications of S100A12 and Resolvin D1 Serum Levels, and Related Genes in Children with Familial Mediterranean Fever. <i>Journal of Child Science</i> , 2021 , 11, e163-e169	0.2	
51	Expression profiling and analysis of some miRNAs in subcutaneous white adipose tissue during development of obesity. <i>Genes and Nutrition</i> , 2020 , 15, 8	4.3	3
50	Machine Learning Prediction Models for Diagnosing Hepatocellular Carcinoma with HCV-related Chronic Liver Disease. <i>Computer Methods and Programs in Biomedicine</i> , 2020 , 196, 105551	6.9	18
49	Immunomodulatory and Antioxidative potentials of adipose-derived Mesenchymal stem cells isolated from breast versus abdominal tissue: a comparative study. <i>Cell Regeneration</i> , 2020 , 9, 18	2.5	
48	Immunomodulatory and Antioxidative potentials of adipose-derived Mesenchymal stem cells isolated from breast versus abdominal tissue: a comparative study. <i>Cell Regeneration</i> , 2020 , 9, 18	2.5	2

47	Early diagnosis of esophageal varices using Boosted-Name Bayes Tree: A multicenter cross-sectional study on chronic hepatitis C patients. <i>Informatics in Medicine Unlocked</i> , 2020 , 20, 100421	5.3	2
46	Co-regulatory Network of Oncosuppressor miRNAs and Transcription Factors for Pathology of Human Hepatic Cancer Stem Cells (HCSC). <i>Scientific Reports</i> , 2019 , 9, 5564	4.9	10
45	Evaluation of computational techniques for predicting non-synonymous single nucleotide variants pathogenicity. <i>Genomics</i> , 2019 , 111, 869-882	4.3	18
44	Predicting Non-Synonymous Single Nucleotide Variants Pathogenic Effects in Human Diseases 2019 , 400-409		1
43	The Promise of miRNA Replacement Therapy for Hepatocellular Carcinoma. <i>Current Gene Therapy</i> , 2019 , 19, 290-304	4.3	5
42	Effect of Tumor Suppressor MiR-34a Loaded on ZSM-5 Nanozeolite in Hepatocellular Carcinoma: In Vitro and In Vivo Approach. <i>Current Gene Therapy</i> , 2019 , 19, 342-354	4.3	8
41	Performance of machine learning approaches on prediction of esophageal varices for Egyptian chronic hepatitis C patients. <i>Informatics in Medicine Unlocked</i> , 2019 , 17, 100267	5.3	18
40	A review study: Computational techniques for expecting the impact of non-synonymous single nucleotide variants in human diseases. <i>Gene</i> , 2019 , 680, 20-33	3.8	18
39	Altered expression of WFS1 and NOTCH2 genes associated with diabetic nephropathy in T2DM patients. <i>Diabetes Research and Clinical Practice</i> , 2018 , 140, 304-313	7.4	6
38	Down-regulation of circulating microRNA let-7a in Egyptian smokers. <i>Journal of Genetic Engineering and Biotechnology</i> , 2018 , 16, 53-56	3.1	5
37	Comparison of Machine Learning Approaches for Prediction of Advanced Liver Fibrosis in Chronic Hepatitis C Patients. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 861-868	3.8	50
36	MicroRNA-150 down Regulation in Acute Myeloid Leukaemia Patients and Its Prognostic Implication. <i>Open Access Macedonian Journal of Medical Sciences</i> , 2018 , 6, 1993-2000	1	2
35	Whole genome sequencing and bioinformatics analysis of two Egyptian genomes. <i>Gene</i> , 2018 , 668, 129-134	3.3	4
34	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. <i>Tumor Biology</i> , 2018 , 40, 1010428318773675	2.9	9
33	MicroTarget: MicroRNA target gene prediction approach with application to breast cancer. <i>Journal of Bioinformatics and Computational Biology</i> , 2017 , 15, 1750013	1	2
32	In silico identification of potential key regulatory factors in smoking-induced lung cancer. <i>BMC Medical Genomics</i> , 2017 , 10, 40	3.7	18
31	MicroRNA expression analysis in endometriotic serum treated mesenchymal stem cells. <i>EXCLI Journal</i> , 2017 , 16, 852-867	2.4	5
30	DeNovo: virus-host sequence-based protein-protein interaction prediction. <i>Bioinformatics</i> , 2016 , 32, 1144-50	4.5	46

29	In Silico Design and Experimental Validation of siRNAs Targeting Conserved Regions of Multiple Hepatitis C Virus Genotypes. <i>PLoS ONE</i> , 2016 , 11, e0159211	3.7	12
28	Computational Identification of Tissue-Specific Splicing Regulatory Elements in Human Genes from RNA-Seq Data. <i>PLoS ONE</i> , 2016 , 11, e0166978	3.7	14
27	Accurate Prediction of Advanced Liver Fibrosis Using the Decision Tree Learning Algorithm in Chronic Hepatitis C Egyptian Patients. <i>Gastroenterology Research and Practice</i> , 2016 , 2016, 2636390	2	17
26	DETECTING AND ANALYZING COPY NUMBER ALTERNATIONS IN ARRAY-BASED CGH DATA. <i>Biomedical Engineering - Applications, Basis and Communications</i> , 2016 , 28, 1650044	0.6	2
25	Modified gold nanoparticles for intracellular delivery of anti-liver cancer siRNA. <i>International Journal of Pharmaceutics</i> , 2016 , 504, 125-33	6.5	39
24	New benzimidazoles and their antitumor effects with Aurora A kinase and KSP inhibitory activities. <i>Archiv Der Pharmazie</i> , 2015 , 348, 475-86	4.3	11
23	Using Information Gain to Compare the Efficiency of Machine Learning Techniques When Classifying Influenza Based on Viral Hosts 2015 , 707-722		2
22	Hepatitis C virus genotype 1: how genetic variability of the core protein affects the response to pegylated-interferon and ribavirin therapy. <i>Journal of Medical Virology</i> , 2014 , 86, 224-34	19.7	4
21	Accurate classification and hemagglutinin amino acid signatures for influenza A virus host-origin association and subtyping. <i>Virology</i> , 2014 , 449, 328-38	3.6	9
20	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. <i>Journal of Translational Medicine</i> , 2014 , 12, 91	8.5	7
19	Hsa-miR-195 targets PCMT1 in hepatocellular carcinoma that increases tumor life span. <i>Tumor Biology</i> , 2014 , 35, 11301-9	2.9	30
18	Human microRNAs targeting hepatitis C virus 2014 ,		1
17	Ensemble-based classification approach for micro-RNA mining applied on diverse metagenomic sequences. <i>BMC Research Notes</i> , 2014 , 7, 286	2.3	2
16	Structure-based predictive model for some benzimidazole inhibitors of hepatitis C virus NS5B polymerase. <i>Medicinal Chemistry Research</i> , 2013 , 22, 1866-1883	2.2	4
15	An integrative meta-analysis of microRNAs in hepatocellular carcinoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2013 , 11, 354-67	6.5	30
14	MysiRNA: improving siRNA efficacy prediction using a machine-learning model combining multi-tools and whole stacking energy (G). <i>Journal of Biomedical Informatics</i> , 2012 , 45, 528-34	10.2	14
13	Synthesis, pharmacological activity evaluation and molecular modeling of new polynuclear heterocyclic compounds containing benzimidazole derivatives. <i>Archives of Pharmacal Research</i> , 2012 , 35, 2063-75	6.1	16
12	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. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 17, S5	3.6	25

11	Rational drug design for identifying novel multi-target inhibitors for hepatocellular carcinoma. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2012 , 12, 1088-97	2.2	9
10	Accurate Prediction of Response to Interferon-based Therapy in Egyptian Patients with Chronic Hepatitis C Using Machine-learning Approaches 2012 ,		5
9	The design of optimal therapeutic small interfering RNA molecules targeting diverse strains of influenza A virus. <i>Bioinformatics</i> , 2011 , 27, 3364-70	7.2	12
8	In-silico Approaches for RNAi Post-Transcriptional Gene Regulation: Optimizing siRNA Design and Selection 2011 ,		2
7	Identification of novel conserved functional motifs across most Influenza A viral strains. <i>Virology Journal</i> , 2011 , 8, 44	6.1	28
6	Part I: Synthesis, cancer chemopreventive activity and molecular docking study of novel quinoxaline derivatives. <i>European Journal of Medicinal Chemistry</i> , 2011 , 46, 327-40	6.8	50
5	MysiRNA-designer: a workflow for efficient siRNA design. <i>PLoS ONE</i> , 2011 , 6, e25642	3.7	25
4	Prediction of prognostic biomarkers for interferon-based therapy to hepatitis C virus patients: a meta-analysis of the NS5A protein in subtypes 1a, 1b, and 3a. <i>Virology Journal</i> , 2010 , 7, 130	6.1	14
3	An integrated methodology for mining promiscuous proteins: a case study of an integrative bioinformatics approach for hepatitis C virus non-structural 5A protein. <i>Advances in Experimental Medicine and Biology</i> , 2010 , 680, 299-305	3.6	2
2	Custommune: a web tool to design personalized and population-targeted vaccine epitopes		5
1	Deep feature selection for Identification of Essential Proteins of Learning and Memory in Mouse Model of Down Syndrome		2