Esmaeil Ebrahimie

List of Publications by Year
in descending order

160 papers	3,739 citations	117453 34 h-index	182168 51 g-index
170 all docs	170 docs citations	170 times ranked	3855 citing authors

#	Article	IF	Citations
1	The androgen receptor is a tumor suppressor in estrogen receptor–positive breast cancer. Nature Medicine, 2021, 27, 310-320.	15.2	122
2	Predicting academic performance by considering student heterogeneity. Knowledge-Based Systems, 2018, 161, 134-146.	4.0	115
3	Integration of machine learning and meta-analysis identifies the transcriptomic bio-signature of mastitis disease in cattle. PLoS ONE, 2018, 13, e0191227.	1.1	115
4	Using the zebrafish model for Alzheimerââ¬â¢s disease research. Frontiers in Genetics, 2014, 5, 189.	1.1	110
5	DrugMiner: comparative analysis of machine learning algorithms for prediction of potential druggable proteins. Drug Discovery Today, 2016, 21, 718-724.	3.2	99
6	Comparative GO: A Web Application for Comparative Gene Ontology and Gene Ontology-Based Gene Selection in Bacteria. PLoS ONE, 2013, 8, e58759.	1.1	97
7	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. Cancer Research, 2017, 77, 1021-1034.	0.4	94
8	Comprehensive analysis of machine learning models for prediction of sub-clinical mastitis: Deep Learning and Gradient-Boosted Trees outperform other models. Computers in Biology and Medicine, 2019, 114, 103456.	3.9	91
9	Determining the Most Important Physiological and Agronomic Traits Contributing to Maize Grain Yield through Machine Learning Algorithms: A New Avenue in Intelligent Agriculture. PLoS ONE, 2014, 9, e97288.	1.1	89
10	Prediction of Thermostability from Amino Acid Attributes by Combination of Clustering with Attribute Weighting: A New Vista in Engineering Enzymes. PLoS ONE, 2011, 6, e23146.	1.1	77
11	Hierarchical pattern recognition in milking parameters predicts mastitis prevalence. Computers and Electronics in Agriculture, 2018, 147, 6-11.	3.7	65
12	Underlying functional genomics of fat deposition in adipose tissue. Gene, 2013, 521, 122-128.	1.0	64
13	Differential expression of seven conserved microRNAs in response to abiotic stress and their regulatory network in Helianthus annuus. Frontiers in Plant Science, 2015, 6, 741.	1.7	64
14	The Magnitude of Androgen Receptor Positivity in Breast Cancer Is Critical for Reliable Prediction of Disease Outcome. Clinical Cancer Research, 2018, 24, 2328-2341.	3.2	63
15	Protein attributes contribute to halo-stability, bioinformatics approach. Saline Systems, 2011, 7, 1.	2.0	62
16	Neural network and SVM classifiers accurately predict lipid binding proteins, irrespective of sequence homology. Journal of Theoretical Biology, 2014, 356, 213-222.	0.8	61
17	A large-scale study of indicators of sub-clinical mastitis in dairy cattle by attribute weighting analysis of milk composition features: highlighting the predictive power of lactose and electrical conductivity. Journal of Dairy Research, 2018, 85, 193-200.	0.7	59
18	De Novo Transcriptome Assembly and Comparative Analysis of Differentially Expressed Genes in Prunus dulcis Mill. in Response to Freezing Stress. PLoS ONE, 2014, 9, e104541.	1.1	55

#	Article	IF	Citations
19	Integrative meta-analysis of transcriptomic responses to abiotic stress in cotton. Progress in Biophysics and Molecular Biology, 2019, 146, 112-122.	1.4	53
20	The Inhibitory Effect of Ginger Extract on Ovarian Cancer Cell Line; Application of Systems Biology. Advanced Pharmaceutical Bulletin, 2017, 7, 241-249.	0.6	51
21	A novel hypothesis-unbiased method for Gene Ontology enrichment based on transcriptome data. PLoS ONE, 2017, 12, e0170486.	1.1	48
22	Enhancement of anticancer activity by silibinin and paclitaxel combination on the ovarian cancer. Artificial Cells, Nanomedicine and Biotechnology, 2018, 46, 1483-1487.	1.9	44
23	Amino Acid Features of PIB-ATPase Heavy Metal Transporters Enabling small Numbers of Organisms to Cope with Heavy Metal Pollution. Bioinformatics and Biology Insights, 2011, 5, BBI.S6206.	1.0	42
24	Knowledge discovery and sequence-based prediction of pandemic influenza using an integrated classification and association rule mining (CBA) algorithm. Journal of Biomedical Informatics, 2015, 57, 181-188.	2.5	40
25	Unravelling evolution of Nanog, the key transcription factor involved in self-renewal of undifferentiated embryonic stem cells, by pattern recognition in nucleotide and tandem repeats characteristics. Gene, 2016, 578, 194-204.	1.0	40
26	Cross-Species Meta-Analysis of Transcriptomic Data in Combination With Supervised Machine Learning Models Identifies the Common Gene Signature of Lactation Process. Frontiers in Genetics, 2018, 9, 235.	1.1	40
27	Sequence-Based Prediction of Enzyme Thermostability Through Bioinformatics Algorithms. Current Bioinformatics, 2010, 5, 195-203.	0.7	38
28	Predicting distinct organization of transcription factor binding sites on the promoter regions: a new genome-based approach to expand human embryonic stem cell regulatory network. Gene, 2013, 531, 212-219.	1.0	38
29	Understanding the Underlying Mechanism of HA-Subtyping in the Level of Physic-Chemical Characteristics of Protein. PLoS ONE, 2014, 9, e96984.	1.1	37
30	Minimizing the cost of translocation failure with decision‐tree models that predict species' behavioral response in translocation sites. Conservation Biology, 2015, 29, 1208-1216.	2.4	37
31	Protein Interaction Network of Arabidopsis thaliana Female Gametophyte Development Identifies Novel Proteins and Relations. PLoS ONE, 2012, 7, e49931.	1.1	36
32	Quantitative Expression Analysis of TaSOS1 and TaSOS4 Genes in Cultivated and Wild Wheat Plants Under Salt Stress. Molecular Biotechnology, 2013, 53, 189-197.	1.3	36
33	Genome-wide survey of Alternative Splicing in Sorghum Bicolor. Physiology and Molecular Biology of Plants, 2014, 20, 323-329.	1.4	35
34	Computational Systems Biology Approach Predicts Regulators and Targets of microRNAs and Their Genomic Hotspots in Apoptosis Process. Molecular Biotechnology, 2016, 58, 460-479.	1.3	35
35	Transcriptome signature of the lactation process, identified by meta-analysis of microarray and RNA-Seq data. Biotechnologia, 2018, 99, 153-163.	0.3	35
36	Efficient and Simple Production of Insulin-Producing Cells from Embryonal Carcinoma Stem Cells Using Mouse Neonate Pancreas Extract, As a Natural Inducer. PLoS ONE, 2014, 9, e90885.	1.1	34

#	Article	IF	Citations
37	Genome‐wide analysis of alternative splicing events in *Hordeum vulgare*: Highlighting retention of intron‐based splicing and its possible function through network analysis. FEBS Letters, 2015, 589, 3564-3575.	1.3	34
38	Identification of the key regulating genes of diminished ovarian reserve (DOR) by network and gene ontology analysis. Molecular Biology Reports, 2016, 43, 923-937.	1.0	34
39	Title is missing!. Plant Cell, Tissue and Organ Culture, 2003, 75, 19-25.	1.2	33
40	Genome-wide analysis of key salinity-tolerance transporter (HKT1;5) in wheat and wild wheat relatives (A and D genomes). In Vitro Cellular and Developmental Biology - Plant, 2013, 49, 97-106.	0.9	33
41	Alzheimer's disease-related peptide PS2V plays ancient, conserved roles in suppression of the unfolded protein response under hypoxia and stimulation of Î³-secretase activity. Human Molecular Genetics, 2015, 24, 3662-3678.	1.4	33
42	A genome-wide transcriptome map of pistachio (Pistacia vera L.) provides novel insights into salinity-related genes and marker discovery. BMC Genomics, 2017, 18, 627.	1.2	33
43	Finding the undiscovered roles of genes: an approach using mutual ranking of coexpressed genes and promoter architecture-case study: dual roles of thaumatin like proteins in biotic and abiotic stresses. SpringerPlus, 2012, 1, 30.	1.2	32
44	Transcriptional regulatory network analysis of the over-expressed genes in adipose tissue. Genes and Genomics, 2014, 36, 105-117.	0.5	31
45	Novel approach for identification of influenza virus host range and zoonotic transmissible sequences by determination of host-related associative positions in viral genome segments. BMC Genomics, 2016, 17, 925.	1.2	29
46	Identifying key factors of student academic performance by subgroup discovery. International Journal of Data Science and Analytics, 2019, 7, 227-245.	2.4	29
47	Direct shoot regeneration from mature embryo as a rapid and genotype-independent pathway in tissue culture of heterogeneous diverse sets of cumin (Cuminum cyminum L.) genotypes. In Vitro Cellular and Developmental Biology - Plant, 2006, 42, 455-460.	0.9	28
48	Prediction of key regulators and downstream targets of E. coli induced mastitis. Journal of Applied Genetics, 2019, 60, 367-373.	1.0	28
49	Unique ability of pandemic influenza to downregulate the genes involved in neuronal disorders. Molecular Biology Reports, 2015, 42, 1377-1390.	1.0	27
50	Recombinant M2e Protein-Based ELISA: A Novel and Inexpensive Approach for Differentiating Avian Influenza Infected Chickens from Vaccinated Ones. PLoS ONE, 2013, 8, e56801.	1.1	27
51	How the Nucleus and Mitochondria Communicate in Energy Production During Stress: Nuclear MtATP6, an Early-Stress Responsive Gene, Regulates the Mitochondrial F1F0-ATP Synthase Complex. Molecular Biotechnology, 2013, 54, 756-769.	1.3	26
52	Gene Ontology-Based Analysis of Zebrafish Omics Data Using the Web Tool Comparative Gene Ontology. Zebrafish, 2017, 14, 492-494.	0.5	26
53	A Transcription Factor Contributes to Pathogenesis and Virulence in Streptococcus pneumoniae. PLoS ONE, 2013, 8, e70862.	1.1	25
54	A functional genomics catalogue of activated transcription factors during pathogenesis of pneumococcal disease. BMC Genomics, 2014, 15, 769.	1.2	25

#	Article	IF	Citations
55	New layers in understanding and predicting α-linolenic acid content in plants using amino acid characteristics of omega-3 fatty acid desaturase. Computers in Biology and Medicine, 2014, 54, 14-23.	3.9	25
56	The Zebrafish Equivalent of Alzheimer's Disease-Associated PRESENILIN Isoform PS2V Regulates Inflammatory and Other Responses to Hypoxic Stress. Journal of Alzheimer's Disease, 2016, 52, 581-608.	1.2	25
57	In silico analysis of high affinity potassium transporter (HKT) isoforms in different plants. Aquatic Biosystems, 2014, 10, 9.	1.8	24
58	Combined gene expression and proteomic analysis of EGF induced apoptosis in A431 cells suggests multiple pathways trigger apoptosis. Apoptosis: an International Journal on Programmed Cell Death, 2013, 18, 1291-1305.	2.2	23
59	Computational systems biology analysis of biomarkers in lung cancer; unravelling genomic regions which frequently encode biomarkers, enriched pathways, and new candidates. Gene, 2018, 659, 29-36.	1.0	23
60	Identification of water-deficit resistance genes in wild almond Prunus scoparia using cDNA-AFLP. Scientia Horticulturae, 2013, 159, 19-28.	1.7	22
61	Genome annotation and comparative genomic analysis of Bacillus subtilis MJ01, a new bio-degradation strain isolated from oil-contaminated soil. Functional and Integrative Genomics, 2018, 18, 533-543.	1.4	22
62	Network analysis of inflammatory responses to sepsis by neutrophils and peripheral blood mononuclear cells. PLoS ONE, 2018, 13, e0201674.	1.1	22
63	Prediction of Potential Cancer-Risk Regions Based on Transcriptome Data: Towards a Comprehensive View. PLoS ONE, 2014, 9, e96320.	1.1	21
64	Mining expressed sequence tags of rapeseed (Brassica napus L.) to predict the drought responsive regulatory network. Physiology and Molecular Biology of Plants, 2015, 21, 329-340.	1.4	21
65	Molecular characterization of Brassica napus stress related transcription factors, BnMYB44 and BnVIP1, selected based on comparative analysis of Arabidopsis thaliana and Eutrema salsugineum transcriptomes. Molecular Biology Reports, 2018, 45, 1111-1124.	1.0	21
66	New insights into the expression profile of MicroRNA-34c and P53 in infertile men spermatozoa and testicular tissue. Cellular and Molecular Biology, 2017, 63, 77-83.	0.3	21
67	Gene regulatory network in almond (Prunus dulcis Mill.) in response to frost stress. Tree Genetics and Genomes, 2015, 11, 1.	0.6	20
68	Unified Transcriptomic Signature of Arbuscular Mycorrhiza Colonization in Roots of Medicago truncatula by Integration of Machine Learning, Promoter Analysis, and Direct Merging Meta-Analysis. Frontiers in Plant Science, 2018, 9, 1550.	1.7	20
69	A Transcription Regulatory Sequence in the 5′ Untranslated Region of SARS-CoV-2 Is Vital for Virus Replication with an Altered Evolutionary Pattern against Human Inhibitory MicroRNAs. Cells, 2021, 10, 319.	1.8	20
70	New Opportunities for Targeting the Androgen Receptor in Prostate Cancer. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a030478.	2.9	19
71	Characterization of Pneumococcal Genes Involved in Bloodstream Invasion in a Mouse Model. PLoS ONE, 2015, 10, e0141816.	1.1	19
72	Are there any differences between features of proteins expressed in malignant and benign breast cancers?. Journal of Research in Medical Sciences, 2010, 15, 299-309.	0.4	19

#	Article	IF	Citations
73	Petal: a reliable explant for direct bulblet regeneration of endangered wild populations of Fritillaria imperialis L.. Acta Physiologiae Plantarum, 2008, 30, 395-399.	1.0	18
74	Isolation and in silico functional analysis of MtATP6, a 6-kDa subunit of mitochondrial F1F0-ATP synthase, in response to abiotic stress. Genetics and Molecular Research, 2012, 11, 3547-3567.	0.3	18
75	Differential expression of fatty acid desaturases in Mari and Shengeh olive cultivars during fruit development and ripening. European Journal of Lipid Science and Technology, 2015, 117, 523-531.	1.0	17
76	A novel pairwise comparison method for in silico discovery of statistically significant cis-regulatory elements in eukaryotic promoter regions: Application to Arabidopsis. Journal of Theoretical Biology, 2015, 364, 364-376.	0.8	17
77	Field effectiveness of highly pathogenic avian influenza H5N1 vaccination in commercial layers in Indonesia. PLoS ONE, 2018, 13, e0190947.	1.1	17
78	Induction and comparison of different inÂvitro morphogenesis pathways using embryo of cumin (Cuminum cyminum L.) as a model material. Plant Cell, Tissue and Organ Culture, 2007, 90, 293-311.	1.2	16
79	Multimeric Recombinant M2e Protein-Based ELISA: A Significant Improvement in Differentiating Avian Influenza Infected Chickens from Vaccinated Ones. PLoS ONE, 2014, 9, e108420.	1.1	16
80	Machine Learning Based Classification of Microsatellite Variation: An Effective Approach for Phylogeographic Characterization of Olive Populations. PLoS ONE, 2015, 10, e0143465.	1.1	16
81	Bidirectional and Opposite Effects of NaÃ¯ve Mesenchymal Stem Cells Ontumor Growth and Progression. Advanced Pharmaceutical Bulletin, 2019, 9, 539-558.	0.6	16
82	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. Genomics, 2020, 112, 820-830.	1.3	15
83	Induction of pancreatic Î² cell gene expression in mesenchymal stem cells. Cell Biology International, 2016, 40, 486-500.	1.4	14
84	Differentiation of P19 embryonal carcinoma stem cells into insulin-producing cells promoted by pancreas-conditioned medium. Journal of Tissue Engineering and Regenerative Medicine, 2016, 10, 600-612.	1.3	14
85	Tissue-specific transcriptional biomarkers in medicinal plants: Application of large-scale meta-analysis and computational systems biology. Gene, 2019, 691, 114-124.	1.0	14
86	Application of functional genomic information to develop efficient EST-SSRs for the chicken (Gallus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.3	13
87	Anti-proliferative transcriptional effects of medroxyprogesterone acetate in estrogen receptor positive breast cancer cells are predominantly mediated by the progesterone receptor. Journal of Steroid Biochemistry and Molecular Biology, 2020, 199, 105548.	1.2	12
88	Genomic analysis of fluoroquinolone-susceptible phylogenetic group B2 extraintestinal pathogenic Escherichia coli causing infections in cats. Veterinary Microbiology, 2020, 245, 108685.	0.8	12
89	Comparative transcriptome analysis of two contrasting resistant and susceptible Aegilops tauschii accessions to wheat leaf rust (Puccinia triticina) using RNA-sequencing. Scientific Reports, 2022, 12, 821.	1.6	12
90	Discovery of EST-SSRs in Lung Cancer: Tagged ESTs with SSRs Lead to Differential Amino Acid and Protein Expression Patterns in Cancerous Tissues. PLoS ONE, 2011, 6, e27118.	1.1	11

#	Article	IF	Citations
91	A novel method based on combination of semi-in vitro and in vivo conditions in Agrobacterium rhizogenes-mediated hairy root transformation of Glycine species. In Vitro Cellular and Developmental Biology - Plant, 2014, 50, 282-291.	0.9	11
92	Genomic analysis reveals variant association with high altitude adaptation in native chickens. Scientific Reports, 2019, 9, 9224.	1.6	11
93	Functional Analysis of a Pomegranate (Punica granatum L.) MYB Transcription Factor Involved in the Regulation of Anthocyanin Biosynthesis. Iranian Journal of Biotechnology, 2015, 13, 17-25.	0.3	11
94	Comparative study of ammonium transporters in different organisms by study of a large number of structural protein features via data mining algorithms. Genes and Genomics, 2011, 33, 565-575.	0.5	10
95	Unraveling the transcriptional complexity of compactness in sistan grape cluster. Plant Science, 2018, 270, 198-208.	1.7	10
96	Transcriptome signature of two lactation stages in Ghezel sheep identifies using RNA-Sequencing. Animal Biotechnology, 2022, 33, 223-233.	0.7	10
97	Porphyromonas spp., Fusobacterium spp., and Bacteroides spp. dominate microbiota in the course of macropod progressive periodontal disease. Scientific Reports, 2021, 11, 17775.	1.6	10
98	RNA-Seq SSRs and small RNA-Seq SSRs: New approaches in cancer biomarker discovery. Gene, 2015, 560, 34-43.	1.0	9
99	Interaction between Bovine leukemia virus (BLV) infection and age on telomerase misregulation. Veterinary Research Communications, 2015, 39, 97-103.	0.6	9
100	Insights from the Echinacea purpurea (L.) Moench transcriptome: Global reprogramming of gene expression patterns towards activation of secondary metabolism pathways. Industrial Crops and Products, 2019, 132, 365-376.	2.5	9
101	Development of an improved *Streptococcus uberis* experimental mastitis challenge model using different doses and strains in lactating dairy cows. Journal of Dairy Research, 2015, 82, 470-477.	0.7	8
102	Identifying mutation positions in all segments of influenza genome enables better differentiation between pandemic and seasonal strains. Gene, 2019, 697, 78-85.	1.0	8
103	Periodontal disease in free‑ranging koalas (Phascolarctos cinereus) from the Mount Lofty Ranges, South Australia, and its association with koala retrovirus infection. Australian Veterinary Journal, 2020, 98, 200-206.	0.5	8
104	Epitope Mapping of Avian Influenza M2e Protein: Different Species Recognise Various Epitopes. PLoS ONE, 2016, 11, e0156418.	1.1	8
105	Comparative analysis of expressed sequence tags (ESTs) from Triticum monococcum shoot apical meristem at vegetative and reproductive stages. Genes and Genomics, 2013, 35, 365-375.	0.5	7
106	SpliceDetector: a software for detection of alternative splicing events in human and model organisms directly from transcript IDs. Scientific Reports, 2018, 8, 5063.	1.6	7
107	The combined effects of three-dimensional cell culture and natural tissue extract on neural differentiation of P19 embryonal carcinoma stem cells. Journal of Tissue Engineering and Regenerative Medicine, 2018, 12, 1909-1924.	1.3	7
108	Molecular mechanisms of fat deposition: <i>IL-6</i> is a hub gene in fat lipolysis, comparing thin-tailed with fat-tailed sheep breeds. Archives Animal Breeding, 2021, 64, 53-68.	0.5	7

#	Article	IF	Citations
109	Prepubertal exposure to high dose of cadmium induces hypothalamic injury through transcriptome profiling alteration and neuronal degeneration in female rats. Chemico-Biological Interactions, 2021, 337, 109379.	1.7	7
110	Rule Discovery in Milk Content towards Mastitis Diagnosis: Dealing with Farm Heterogeneity over Multiple Years through Classification Based on Associations. Animals, 2021, 11, 1638.	1.0	7
111	Advances in understanding the specificity function of transporters by machine learning. Computers in Biology and Medicine, 2021, 138, 104893.	3.9	7
112	Machine learning models effectively distinguish attention-deficit/hyperactivity disorder using event-related potentials. Cognitive Neurodynamics, 2022, 16, 1335-1349.	2.3	7
113	Differential expression of TLP, ERF1, and R2R3MYB in annual Medicago species under salinity conditions. Genetics and Molecular Research, 2015, 14, 10152-10164.	0.3	6
114	A comparative system–level analysis of the neurodegenerative diseases. Journal of Cellular Physiology, 2019, 234, 5215-5229.	2.0	6
115	Non–coding and coding genomic variants distinguish prostate cancer, castration–resistant prostate cancer, familial prostate cancer, and metastatic castration–resistant prostate cancer from each other. Molecular Carcinogenesis, 2019, 58, 862-874.	1.3	6
116	AFExNet: An Adversarial Autoencoder for Differentiating Breast Cancer Sub-Types and Extracting Biologically Relevant Genes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2060-2070.	1.9	6
117	Indirect Somatic Embryogenesis from Petal Explant of Endangered Wild Population of Fritillaria imperialis. Pakistan Journal of Biological Sciences, 2007, 10, 1875-1879.	0.2	6
118	New insights into the evolution of SPX gene family from algae to legumes; a focus on soybean. BMC Genomics, 2021, 22, 915.	1.2	6
119	Oxalate–degrading bacteria, including <i>Oxalobacter formigenes,</i> colonise the gastrointestinal tract of healthy koalas (<scp><i>Phascolarctos cinereus</i></scp>) and those with oxalate nephrosis. Australian Veterinary Journal, 2019, 97, 166-170.	0.5	5
120	Integration of meta-analysis and supervised machine learning for pattern recognition in breast cancer using epigenetic data. Informatics in Medicine Unlocked, 2021, 24, 100629.	1.9	5
121	Fritillaria Species Are at Risk of Extinction in Iran: Study on Effective Factors and Necessity of International Attention. Hortscience: A Publication of the American Society for Hortcultural Science, 2006, 41, 1002B-1002.	0.5	5
122	Root and shoot parts of strawberry: factories for production of functional human pro-insulin. Molecular Biology Reports, 2015, 42, 1013-1023.	1.0	4
123	Analysis of nicastrin gene phylogeny and expression in zebrafish. Development Genes and Evolution, 2015, 225, 171-178.	0.4	4
124	Stallion Sperm Integrity After Centrifugation to Reduce Seminal Plasma Concentration and Cool Storage for 4 days. Journal of Equine Veterinary Science, 2020, 85, 102819.	0.4	4
125	Whole-Genome Resequencing Reveals Adaptation Prior to the Divergence of Buffalo Subspecies. Genome Biology and Evolution, 2021, 13, .	1.1	4
126	The Restorative Effect of Human Amniotic Fluid Stem Cells on Spinal Cord Injury. Cells, 2021, 10, 2565.	1.8	4

#	Article	IF	Citations
127	Alternative RNA splicing in stem cells and cancer stem cells: Importance of transcript-based expression analysis. World Journal of Stem Cells, 2021, 13, 1394-1416.	1.3	4
128	Molecular mechanisms of resistance to bovine mastitis. Livestock Science, 2020, 239, 104068.	0.6	4
129	Evaluation of the Effectiveness of Herbal Components Based on Their Regulatory Signature on Carcinogenic Cancer Cells. Cells, 2021, 10, 3139.	1.8	4
130	Systems Biology–Derived Genetic Signatures of Mastitis in Dairy Cattle: A New Avenue for Drug Repurposing. Animals, 2022, 12, 29.	1.0	3
131	Further insights into the association of the protein phosphatase gene ABI1 with drought and salinity stress responses in Brassica species. Journal of Plant Biochemistry and Biotechnology, 2023, 32, 106-120.	0.9	3
132	Comparison of hematopoietic cancer stem cells with normal stem cells leads to discovery of novel differentially expressed SSRs. Gene, 2014, 550, 10-17.	1.0	2
133	Identification of differential expressed transcripts of almond (*Prunus dulcis* â€˜Sefiedâ€™) in response to water-deficit stress by cDNA-AFLP. Journal of Forest Research, 2015, 20, 403-410.	0.7	2
134	Expression analyses of salinity stress- associated ESTs in Aeluropus littoralis. Gene Expression Patterns, 2017, 25-26, 76-84.	0.3	2
135	Isolation of 2-phenylethanol biosynthesis related gene and developmental patterns of emission of scent compounds in Persian musk rose (Rosa moschata Herrm.). Biocatalysis and Agricultural Biotechnology, 2019, 19, 101176.	1.5	2
136	Gene network analysis to determine the effect of hypoxia-associated genes on brain damages and tumorigenesis using an avian model. Journal of Genetic Engineering and Biotechnology, 2021, 19, 100.	1.5	2
137	Image processing unravels the evolutionary pattern of SARS-CoV-2 against SARS and MERS through position-based pattern recognition. Computers in Biology and Medicine, 2021, 134, 104471.	3.9	2
138	Research paper Determining the structural amino acid attributes which are important in both protein thermostability and alkalophilicity: a case study on xylanase. Biotechnologia, 2014, 2, 161-173.	0.3	2
139	Combined Direct Regeneration Protocols in Tissue Culture of Different Cumin Genotypes Based on Pre-existing Meristems. Pakistan Journal of Biological Sciences, 2007, 10, 1360-1370.	0.2	2
140	Fast school closures correspond with a lower rate of COVID-19 incidence and deaths in most countries. Informatics in Medicine Unlocked, 2021, 27, 100805.	1.9	2
141	Splice-disrupt genomic variants in prostate cancer. Molecular Biology Reports, 2022, , 1.	1.0	2
142	Transcriptome Analysis of Breast Muscle Reveals Pathways Related to Protein Deposition in High Feed Efficiency of Native Turkeys. Animals, 2022, 12, 1240.	1.0	2
143	Amino acid features: a missing compartment of prediction of protein function. Nature Precedings, 2011, , .	0.1	1
144	*In vitro* comparison of the dermal penetration of three different topical formulations containing lasalocid. Veterinary Dermatology, 2017, 28, 342.	0.4	1

#	Article	IF	Citations
145	Production of stable GFP -expressing neural cells from P19 embryonal carcinoma stem cells. Molecular and Cellular Probes, 2017, 32, 46-54.	0.9	1
146	Changes in Microsatellite Motifs in Response to Abiotic Stresses: a Case Study Using Wheat and Rice RNA-sequencing Data. Asian Journal of Scientific Research, 2017, 11, 12-21.	0.3	1
147	Identification of Pathways and Candidate Genes Associated with Resistance to Ascochyta Blight in a Mutant Chickpea Variety using RNA-Seq Analysis. Journal of Crop Breeding, 2020, 12, 69-75.	0.4	1
148	ABC Transporters are Hub Genes in Response of Resistant E. Coli ST131 to Ciprofloxacin. Archives of Pharmacy Practice, 2021, 12, 82-88.	0.2	1
149	Pharmacokinetic profile and effect on the faecal microbiome of a single dose of pradofloxacin oral suspension in the rabbit <i>(Oryctolagus cuniculus)</i>. Journal of Veterinary Pharmacology and Therapeutics, 2022, 45, 203-212.	0.6	1
150	Apoptotic effects of human amniotic fluid mesenchymal stem cells conditioned medium on human MCF-7 breast cancer cell line. BioImpacts, 2022, , .	0.7	1
151	Application of neural networks methods to define the most important features contributing to xylanase enzyme thermostability. , 2009, , .		0
152	Application of bioinformatics algorithms to define the most important protein features contribute to GABA receptors diversity GABA receptors' diversity, bioinformatic applications. , 2010, , .		0
153	OR05-06 The Androgen Receptor Is a Tumour Suppressor in Estrogen Receptor Positive Breast Cancer. Journal of the Endocrine Society, 2020, 4, .	0.1	0
154	Experimental direct-contact transmission of influenza A/H9N2 virus in the guinea pig model in Iran. Future Virology, 2020, 15, 277-292.	0.9	0
155	Molecular characterization of low pathogenic avian influenza H9N2 virus during co-circulation with newly-emerged highly pathogenic avian influenza H5N8 virus in Iran. Acta Virologica, 2021, 65, 200-211.	0.3	0
156	Different Developmental Stages of Mother Plants Induct Different Morphogenesis Pathways in In Vitro Culture of Fritillaria imperialis and Fritillaria persica. Hortscience: A Publication of the American Society for Hortcultural Science, 2006, 41, 984D-985.	0.5	0
157	Nuclear ErbB-2 activity modulates the interferon signaling pathway in breast cancer cells resistant to anti-ErbB-2 therapies. Oncology Abstracts, 0, , .	0.0	0
158	Abstract GS2-03: The androgen receptor is a tumour suppressor in estrogen receptor positive breast cancer. , 2020, , .		0
159	An Integrative Analysis of The Micro-RNAs Contributing in Stemness, Metastasis and B-Raf Pathways in Malignant Melanoma and Melanoma Stem Cell. Cell Journal, 2021, 23, 261-272.	0.2	0
160	Biocompatibility study of P (N-isopropylacrylamide)-based nanocomposite and its cytotoxic effect on HeLa cells as a drug delivery system for Cisplatin. Journal of Drug Delivery Science and Technology, 2022, , 103254.	1.4	0