

# Esmaeil Ebrahimie

## List of Publications by Citations

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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.

150  
papers

2,203  
citations

26  
h-index

37  
g-index

170  
ext. papers

3,332  
ext. citations

3.9  
avg, IF

5.27  
L-index

#	Paper	IF	Citations
150	Using the zebrafish model for Alzheimer's disease research. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 189	4.5	80
149	OR05-06 The Androgen Receptor Is a Tumour Suppressor in Estrogen Receptor Positive Breast Cancer. <i>Journal of the Endocrine Society</i> , <b>2020</b> , 4,	0.4	78
148	MicroRNA-194 Promotes Prostate Cancer Metastasis by Inhibiting SOCS2. <i>Cancer Research</i> , <b>2017</b> , 77, 1021-1034	10.1	74
147	Predicting academic performance by considering student heterogeneity. <i>Knowledge-Based Systems</i> , <b>2018</b> , 161, 134-146	7.3	69
146	DrugMiner: comparative analysis of machine learning algorithms for prediction of potential druggable proteins. <i>Drug Discovery Today</i> , <b>2016</b> , 21, 718-24	8.8	51
145	Comprehensive analysis of machine learning models for prediction of sub-clinical mastitis: Deep Learning and Gradient-Boosted Trees outperform other models. <i>Computers in Biology and Medicine</i> , <b>2019</b> , 114, 103456	7	48
144	Differential expression of seven conserved microRNAs in response to abiotic stress and their regulatory network in <i>Helianthus annuus</i> . <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 741	6.2	48
143	Neural network and SVM classifiers accurately predict lipid binding proteins, irrespective of sequence homology. <i>Journal of Theoretical Biology</i> , <b>2014</b> , 356, 213-22	2.3	46
142	Prediction of thermostability from amino acid attributes by combination of clustering with attribute weighting: a new vista in engineering enzymes. <i>PLoS ONE</i> , <b>2011</b> , 6, e23146	3.7	46
141	Underlying functional genomics of fat deposition in adipose tissue. <i>Gene</i> , <b>2013</b> , 521, 122-8	3.8	45
140	Comparative GO: a web application for comparative gene ontology and gene ontology-based gene selection in bacteria. <i>PLoS ONE</i> , <b>2013</b> , 8, e58759	3.7	45
139	Protein attributes contribute to halo-stability, bioinformatics approach. <i>Saline Systems</i> , <b>2011</b> , 7, 1		42
138	Integration of machine learning and meta-analysis identifies the transcriptomic bio-signature of mastitis disease in cattle. <i>PLoS ONE</i> , <b>2018</b> , 13, e0191227	3.7	42
137	De novo transcriptome assembly and comparative analysis of differentially expressed genes in <i>Prunus dulcis</i> Mill. in response to freezing stress. <i>PLoS ONE</i> , <b>2014</b> , 9, e104541	3.7	40
136	The androgen receptor is a tumor suppressor in estrogen receptor-positive breast cancer. <i>Nature Medicine</i> , <b>2021</b> , 27, 310-320	50.5	40
135	Determining the most important physiological and agronomic traits contributing to maize grain yield through machine learning algorithms: a new avenue in intelligent agriculture. <i>PLoS ONE</i> , <b>2014</b> , 9, e97288	3.7	37
134	The Magnitude of Androgen Receptor Positivity in Breast Cancer Is Critical for Reliable Prediction of Disease Outcome. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 2328-2341	12.9	32

133	Enhancement of anticancer activity by silibinin and paclitaxel combination on the ovarian cancer. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , <b>2018</b> , 46, 1483-1487	6.1	30
132	Hierarchical pattern recognition in milking parameters predicts mastitis prevalence. <i>Computers and Electronics in Agriculture</i> , <b>2018</b> , 147, 6-11	6.5	29
131	Genome-wide analysis of alternative splicing events in <i>Hordeum vulgare</i> : Highlighting retention of intron-based splicing and its possible function through network analysis. <i>FEBS Letters</i> , <b>2015</b> , 589, 3564-75	3.8	28
130	Quantitative expression analysis of TaSOS1 and TaSOS4 genes in cultivated and wild wheat plants under salt stress. <i>Molecular Biotechnology</i> , <b>2013</b> , 53, 189-97	3	28
129	Knowledge discovery and sequence-based prediction of pandemic influenza using an integrated classification and association rule mining (CBA) algorithm. <i>Journal of Biomedical Informatics</i> , <b>2015</b> , 57, 181-8	10.2	27
128	Genome-wide survey of Alternative Splicing in <i>Sorghum Bicolor</i> . <i>Physiology and Molecular Biology of Plants</i> , <b>2014</b> , 20, 323-9	2.8	27
127	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. <i>Gene</i> , <b>2013</b> , 531, 212-9	3.8	27
126	Efficient and simple production of insulin-producing cells from embryonal carcinoma stem cells using mouse neonate pancreas extract, as a natural inducer. <i>PLoS ONE</i> , <b>2014</b> , 9, e90885	3.7	27
125	Integrative meta-analysis of transcriptomic responses to abiotic stress in cotton. <i>Progress in Biophysics and Molecular Biology</i> , <b>2019</b> , 146, 112-122	4.7	26
124	The Inhibitory Effect of Ginger Extract on Ovarian Cancer Cell Line; Application of Systems Biology. <i>Advanced Pharmaceutical Bulletin</i> , <b>2017</b> , 7, 241-249	4.5	26
123	Genome-wide analysis of key salinity-tolerance transporter (HKT1;5) in wheat and wild wheat relatives (A and D genomes). <i>In Vitro Cellular and Developmental Biology - Plant</i> , <b>2013</b> , 49, 97-106	2.3	25
122	Amino Acid Features of P1B-ATPase Heavy Metal Transporters Enabling Small Numbers of Organisms to Cope with Heavy Metal Pollution. <i>Bioinformatics and Biology Insights</i> , <b>2011</b> , 5, 59-82	5.3	25
121	A rapid and efficient method for regeneration of plantlets from embryo explants of cumin ( <i>Cuminum cyminum</i> ). <i>Plant Cell, Tissue and Organ Culture</i> , <b>2003</b> , 75, 19-25	2.7	25
120	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. <i>Journal of Dairy Research</i> , <b>2018</b> , 85, 193-200	1.6	25
119	Alzheimer's disease-related peptide PS2V plays ancient, conserved roles in suppression of the unfolded protein response under hypoxia and stimulation of $\beta$ -secretase activity. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 3662-78	5.6	24
118	Recombinant M2e protein-based ELISA: a novel and inexpensive approach for differentiating avian influenza infected chickens from vaccinated ones. <i>PLoS ONE</i> , <b>2013</b> , 8, e56801	3.7	23
117	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. <i>SpringerPlus</i> , <b>2012</b> , 1, 30		22
116	Cross-Species Meta-Analysis of Transcriptomic Data in Combination With Supervised Machine Learning Models Identifies the Common Gene Signature of Lactation Process. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 235	4.5	21

115	Combined gene expression and proteomic analysis of EGF induced apoptosis in A431 cells suggests multiple pathways trigger apoptosis. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , <b>2013</b> , 18, 1291-1305	5.4	21
114	Prediction of potential cancer-risk regions based on transcriptome data: towards a comprehensive view. <i>PLoS ONE</i> , <b>2014</b> , 9, e96320	3.7	21
113	A genome-wide transcriptome map of pistachio ( <i>Pistacia vera</i> L.) provides novel insights into salinity-related genes and marker discovery. <i>BMC Genomics</i> , <b>2017</b> , 18, 627	4.5	20
112	Protein interaction network of <i>Arabidopsis thaliana</i> female gametophyte development identifies novel proteins and relations. <i>PLoS ONE</i> , <b>2012</b> , 7, e49931	3.7	20
111	Direct shoot regeneration from mature embryo as a rapid and genotype-independent pathway in tissue culture of heterogeneous diverse sets of cumin ( <i>Cuminum cyminum</i> L.) genotypes. <i>In Vitro Cellular and Developmental Biology - Plant</i> , <b>2006</b> , 42, 455-460	2.3	20
110	How the nucleus and mitochondria communicate in energy production during stress: nuclear MtATP6, an early-stress responsive gene, regulates the mitochondrial F <sub>1</sub> F <sub>0</sub> ATP synthase complex. <i>Molecular Biotechnology</i> , <b>2013</b> , 54, 756-69	3	19
109	Sequence-Based Prediction of Enzyme Thermostability Through Bioinformatics Algorithms. <i>Current Bioinformatics</i> , <b>2010</b> , 5, 195-203	4.7	19
108	Are there any differences between features of proteins expressed in malignant and benign breast cancers?. <i>Journal of Research in Medical Sciences</i> , <b>2010</b> , 15, 299-309	1.6	19
107	Mining expressed sequence tags of rapeseed ( <i>Brassica napus</i> L.) to predict the drought responsive regulatory network. <i>Physiology and Molecular Biology of Plants</i> , <b>2015</b> , 21, 329-40	2.8	18
106	Understanding the undelaying mechanism of HA-subtyping in the level of physic-chemical characteristics of protein. <i>PLoS ONE</i> , <b>2014</b> , 9, e96984	3.7	18
105	New Opportunities for Targeting the Androgen Receptor in Prostate Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2018</b> , 8,	5.4	17
104	Identification of water-deficit resistance genes in wild almond <i>Prunus scoparia</i> using cDNA-AFLP. <i>Scientia Horticulturae</i> , <b>2013</b> , 159, 19-28	4.1	17
103	New insights into the expression profile of MicroRNA-34c and P53 in infertile men spermatozoa and testicular tissue. <i>Cellular and Molecular Biology</i> , <b>2017</b> , 63, 77-83	1.1	17
102	A novel hypothesis-unbiased method for Gene Ontology enrichment based on transcriptome data. <i>PLoS ONE</i> , <b>2017</b> , 12, e0170486	3.7	16
101	Identification of the key regulating genes of diminished ovarian reserve (DOR) by network and gene ontology analysis. <i>Molecular Biology Reports</i> , <b>2016</b> , 43, 923-37	2.8	16
100	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. <i>Gene</i> , <b>2016</b> , 578, 194-204	3.8	16
99	Characterization of Pneumococcal Genes Involved in Bloodstream Invasion in a Mouse Model. <i>PLoS ONE</i> , <b>2015</b> , 10, e0141816	3.7	16
98	Identifying key factors of student academic performance by subgroup discovery. <i>International Journal of Data Science and Analytics</i> , <b>2019</b> , 7, 227-245	2	15

97	A functional genomics catalogue of activated transcription factors during pathogenesis of pneumococcal disease. <i>BMC Genomics</i> , <b>2014</b> , 15, 769	4.5	15
96	Genome annotation and comparative genomic analysis of <i>Bacillus subtilis</i> MJ01, a new bio-degradation strain isolated from oil-contaminated soil. <i>Functional and Integrative Genomics</i> , <b>2018</b> , 18, 533-543	3.8	14
95	Isolation and in silico functional analysis of MtATP6, a 6-kDa subunit of mitochondrial F <sub>1</sub> F <sub>0</sub> -ATP synthase, in response to abiotic stress. <i>Genetics and Molecular Research</i> , <b>2012</b> , 11, 3547-67	1.2	14
94	A transcription factor contributes to pathogenesis and virulence in <i>Streptococcus pneumoniae</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e70862	3.7	14
93	Petal: a reliable explant for direct bulblet regeneration of endangered wild populations of <i>Fritillaria imperialis</i> L.. <i>Acta Physiologiae Plantarum</i> , <b>2008</b> , 30, 395-399	2.6	14
92	The Zebrafish Equivalent of Alzheimer's Disease-Associated PRESENILIN Isoform PS2V Regulates Inflammatory and Other Responses to Hypoxic Stress. <i>Journal of Alzheimer's Disease</i> , <b>2016</b> , 52, 581-608	4.3	14
91	Novel approach for identification of influenza virus host range and zoonotic transmissible sequences by determination of host-related associative positions in viral genome segments. <i>BMC Genomics</i> , <b>2016</b> , 17, 925	4.5	14
90	Transcriptional regulatory network analysis of the over-expressed genes in adipose tissue. <i>Genes and Genomics</i> , <b>2014</b> , 36, 105-117	2.1	13
89	Multimeric recombinant M2e protein-based ELISA: a significant improvement in differentiating avian influenza infected chickens from vaccinated ones. <i>PLoS ONE</i> , <b>2014</b> , 9, e108420	3.7	13
88	Induction and comparison of different in vitro morphogenesis pathways using embryo of cumin ( <i>Cuminum cyminum</i> L.) as a model material. <i>Plant Cell, Tissue and Organ Culture</i> , <b>2007</b> , 90, 293-311	2.7	13
87	Application of functional genomic information to develop efficient EST-SSRs for the chicken ( <i>Gallus gallus</i> ). <i>Genetics and Molecular Research</i> , <b>2012</b> , 11, 1558-74	1.2	12
86	Field effectiveness of highly pathogenic avian influenza H5N1 vaccination in commercial layers in Indonesia. <i>PLoS ONE</i> , <b>2018</b> , 13, e0190947	3.7	12
85	Induction of pancreatic $\beta$ cell gene expression in mesenchymal stem cells. <i>Cell Biology International</i> , <b>2016</b> , 40, 486-500	4.5	12
84	Unified Transcriptomic Signature of Arbuscular Mycorrhiza Colonization in Roots of by Integration of Machine Learning, Promoter Analysis, and Direct Merging Meta-Analysis. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1550	6.2	12
83	Gene regulatory network in almond ( <i>Prunus dulcis</i> Mill.) in response to frost stress. <i>Tree Genetics and Genomes</i> , <b>2015</b> , 11, 1	2.1	11
82	Differentiation of P19 embryonal carcinoma stem cells into insulin-producing cells promoted by pancreas-conditioned medium. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , <b>2016</b> , 10, 600-12	4.4	11
81	Network analysis of inflammatory responses to sepsis by neutrophils and peripheral blood mononuclear cells. <i>PLoS ONE</i> , <b>2018</b> , 13, e0201674	3.7	11
80	New layers in understanding and predicting linolenic acid content in plants using amino acid characteristics of omega-3 fatty acid desaturase. <i>Computers in Biology and Medicine</i> , <b>2014</b> , 54, 14-23	7	11

79	Minimizing the cost of translocation failure with decision-tree models that predict species' behavioral response in translocation sites. <i>Conservation Biology</i> , <b>2015</b> , 29, 1208-16	6	11
78	In silico analysis of high affinity potassium transporter (HKT) isoforms in different plants. <i>Aquatic Biosystems</i> , <b>2014</b> , 10, 9		11
77	Discovery of EST-SSRs in lung cancer: tagged ESTs with SSRs lead to differential amino acid and protein expression patterns in cancerous tissues. <i>PLoS ONE</i> , <b>2011</b> , 6, e27118	3.7	11
76	Bidirectional and Opposite Effects of Na <sup>+</sup> Mesenchymal Stem Cells on Tumor Growth and Progression. <i>Advanced Pharmaceutical Bulletin</i> , <b>2019</b> , 9, 539-558	4.5	11
75	Unique ability of pandemic influenza to downregulate the genes involved in neuronal disorders. <i>Molecular Biology Reports</i> , <b>2015</b> , 42, 1377-90	2.8	10
74	Molecular characterization of Brassica napus stress related transcription factors, BnMYB44 and BnVIP1, selected based on comparative analysis of Arabidopsis thaliana and Eutrema salsugineum transcriptomes. <i>Molecular Biology Reports</i> , <b>2018</b> , 45, 1111-1124	2.8	10
73	A novel method based on combination of semi-in vitro and in vivo conditions in Agrobacterium rhizogenes-mediated hairy root transformation of Glycine species. <i>In Vitro Cellular and Developmental Biology - Plant</i> , <b>2014</b> , 50, 282-291	2.3	10
72	Computational Systems Biology Approach Predicts Regulators and Targets of microRNAs and Their Genomic Hotspots in Apoptosis Process. <i>Molecular Biotechnology</i> , <b>2016</b> , 58, 460-79	3	10
71	Differential expression of fatty acid desaturases in Mari and Shengeh olive cultivars during fruit development and ripening. <i>European Journal of Lipid Science and Technology</i> , <b>2015</b> , 117, 523-531	3	9
70	Computational systems biology analysis of biomarkers in lung cancer; unravelling genomic regions which frequently encode biomarkers, enriched pathways, and new candidates. <i>Gene</i> , <b>2018</b> , 659, 29-36	3.8	9
69	Machine Learning Based Classification of Microsatellite Variation: An Effective Approach for Phylogeographic Characterization of Olive Populations. <i>PLoS ONE</i> , <b>2015</b> , 10, e0143465	3.7	9
68	Comparative study of ammonium transporters in different organisms by study of a large number of structural protein features via data mining algorithms. <i>Genes and Genomics</i> , <b>2011</b> , 33, 565-575	2.1	9
67	A novel pairwise comparison method for in silico discovery of statistically significant cis-regulatory elements in eukaryotic promoter regions: application to Arabidopsis. <i>Journal of Theoretical Biology</i> , <b>2015</b> , 364, 364-76	2.3	8
66	Gene Ontology-Based Analysis of Zebrafish Omics Data Using the Web Tool Comparative Gene Ontology. <i>Zebrafish</i> , <b>2017</b> , 14, 492-494	2	8
65	Functional Analysis of a Pomegranate ( L.) MYB Transcription Factor Involved in the Regulation of Anthocyanin Biosynthesis. <i>Iranian Journal of Biotechnology</i> , <b>2015</b> , 13, 17-25	1	8
64	Transcriptome signature of the lactation process, identified by meta-analysis of microarray and RNA-Seq data. <i>Biotechnologia</i> , <b>2018</b> , 99, 153-163	1.7	8
63	Genomic analysis reveals variant association with high altitude adaptation in native chickens. <i>Scientific Reports</i> , <b>2019</b> , 9, 9224	4.9	7
62	Identifying mutation positions in all segments of influenza genome enables better differentiation between pandemic and seasonal strains. <i>Gene</i> , <b>2019</b> , 697, 78-85	3.8	7

61	Genomic analysis of fluoroquinolone-susceptible phylogenetic group B2 extraintestinal pathogenic <i>Escherichia coli</i> causing infections in cats. <i>Veterinary Microbiology</i> , <b>2020</b> , 245, 108685	3.3	7
60	Development of an improved <i>Streptococcus uberis</i> experimental mastitis challenge model using different doses and strains in lactating dairy cows. <i>Journal of Dairy Research</i> , <b>2015</b> , 82, 470-7	1.6	7
59	RNA-seq SSRs and small RNA-seq SSRs: new approaches in cancer biomarker discovery. <i>Gene</i> , <b>2015</b> , 560, 34-43	3.8	7
58	Prediction of key regulators and downstream targets of <i>E. coli</i> induced mastitis. <i>Journal of Applied Genetics</i> , <b>2019</b> , 60, 367-373	2.5	6
57	Interaction between Bovine leukemia virus (BLV) infection and age on telomerase misregulation. <i>Veterinary Research Communications</i> , <b>2015</b> , 39, 97-103	2.9	6
56	Comparative analysis of expressed sequence tags (ESTs) from <i>Triticum monococcum</i> shoot apical meristem at vegetative and reproductive stages. <i>Genes and Genomics</i> , <b>2013</b> , 35, 365-375	2.1	6
55	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. <i>Cells</i> , <b>2021</b> , 10,	7.9	6
54	Periodontal disease in free-ranging koalas ( <i>Phascolarctos cinereus</i> ) from the Mount Lofty Ranges, South Australia, and its association with koala retrovirus infection. <i>Australian Veterinary Journal</i> , <b>2020</b> , 98, 200-206	1.2	5
53	Application of Global Transcriptome Data in Gene Ontology Classification and Construction of a Gene Ontology Interaction Network		5
52	Anti-proliferative transcriptional effects of medroxyprogesterone acetate in estrogen receptor positive breast cancer cells are predominantly mediated by the progesterone receptor. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , <b>2020</b> , 199, 105548	5.1	5
51	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. <i>Molecular Carcinogenesis</i> , <b>2019</b> , 58, 862-874	5	5
50	Insights from the <i>Echinacea purpurea</i> (L.) Moench transcriptome: Global reprogramming of gene expression patterns towards activation of secondary metabolism pathways. <i>Industrial Crops and Products</i> , <b>2019</b> , 132, 365-376	5.9	4
49	Transcriptome signature of two lactation stages in Ghezel sheep identifies using RNA-Sequencing. <i>Animal Biotechnology</i> , <b>2020</b> , 1-11	1.4	4
48	Unraveling the transcriptional complexity of compactness in sistan grape cluster. <i>Plant Science</i> , <b>2018</b> , 270, 198-208	5.3	4
47	SpliceDetector: a software for detection of alternative splicing events in human and model organisms directly from transcript IDs. <i>Scientific Reports</i> , <b>2018</b> , 8, 5063	4.9	4
46	Root and shoot parts of strawberry: factories for production of functional human pro-insulin. <i>Molecular Biology Reports</i> , <b>2015</b> , 42, 1013-23	2.8	4
45	Epitope Mapping of Avian Influenza M2e Protein: Different Species Recognise Various Epitopes. <i>PLoS ONE</i> , <b>2016</b> , 11, e0156418	3.7	4
44	Fritillaria Species Are at Risk of Extinction in Iran: Study on Effective Factors and Necessity of International Attention. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , <b>2006</b> , 41, 1002B-1002	2.4	4

43	Tissue-specific transcriptional biomarkers in medicinal plants: Application of large-scale meta-analysis and computational systems biology. <i>Gene</i> , <b>2019</b> , 691, 114-124	3.8	4
42	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. <i>Genomics</i> , <b>2020</b> , 112, 820-830	4.3	4
41	Oxalate-degrading bacteria, including <i>Oxalobacter formigenes</i> , colonise the gastrointestinal tract of healthy koalas ( <i>Phascolarctos cinereus</i> ) and those with oxalate nephrosis. <i>Australian Veterinary Journal</i> , <b>2019</b> , 97, 166-170	1.2	3
40	The combined effects of three-dimensional cell culture and natural tissue extract on neural differentiation of P19 embryonal carcinoma stem cells. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , <b>2018</b> , 12, 1909-1924	4.4	3
39	The first report of the most important sequential differences between COVID-19 and MERS viruses by attribute weighting models, the importance of Nucleocapsid (N) protein		3
38	Indirect somatic embryogenesis from petal explant of endangered wild population of <i>Fritillaria imperialis</i> . <i>Pakistan Journal of Biological Sciences</i> , <b>2007</b> , 10, 1875-9	0.8	3
37	Rule Discovery in Milk Content towards Mastitis Diagnosis: Dealing with Farm Heterogeneity over Multiple Years through Classification Based on Associations. <i>Animals</i> , <b>2021</b> , 11,	3.1	3
36	A comparative system-level analysis of the neurodegenerative diseases. <i>Journal of Cellular Physiology</i> , <b>2019</b> , 234, 5215-5229	7	3
35	Identification of differential expressed transcripts of almond ( <i>Prunus dulcis</i> Desf.) in response to water-deficit stress by cDNA-AFLP. <i>Journal of Forest Research</i> , <b>2015</b> , 20, 403-410	1.4	2
34	Analysis of nicastrin gene phylogeny and expression in zebrafish. <i>Development Genes and Evolution</i> , <b>2015</b> , 225, 171-8	1.8	2
33	Comparison of hematopoietic cancer stem cells with normal stem cells leads to discovery of novel differentially expressed SSRs. <i>Gene</i> , <b>2014</b> , 550, 10-7	3.8	2
32	Differential expression of TLP, ERF1, and R2R3MYB in annual <i>Medicago</i> species under salinity conditions. <i>Genetics and Molecular Research</i> , <b>2015</b> , 14, 10152-64	1.2	2
31	Research paper Determining the structural amino acid attributes which are important in both protein thermostability and alkalophilicity: a case study on xylanase. <i>Biotechnologia</i> , <b>2014</b> , 2, 161-173	1.7	2
30	Combined direct regeneration protocols in tissue culture of different cumin genotypes based on pre-existing meristems. <i>Pakistan Journal of Biological Sciences</i> , <b>2007</b> , 10, 1360-70	0.8	2
29	Prepubertal exposure to high dose of cadmium induces hypothalamic injury through transcriptome profiling alteration and neuronal degeneration in female rats. <i>Chemico-Biological Interactions</i> , <b>2021</b> , 337, 109379	5	2
28	In vitro comparison of the dermal penetration of three different topical formulations containing lasalocid. <i>Veterinary Dermatology</i> , <b>2017</b> , 28, 342-e74	1.8	1
27	Expression analyses of salinity stress- associated ESTs in <i>Aeluropus littoralis</i> . <i>Gene Expression Patterns</i> , <b>2017</b> , 25-26, 76-84	1.5	1
26	Production of stable GFP-expressing neural cells from P19 embryonal carcinoma stem cells. <i>Molecular and Cellular Probes</i> , <b>2017</b> , 32, 46-54	3.3	1



25	Amino acid features: a missing compartment of prediction of protein function. <i>Nature Precedings</i> , <b>2011</b> ,		1
24	Comparative transcriptome analysis of two contrasting resistant and susceptible <i>Aegilops tauschii</i> accessions to wheat leaf rust ( <i>Puccinia triticina</i> ) using RNA-sequencing.. <i>Scientific Reports</i> , <b>2022</b> , 12, 821	4.9	1
23	Alternative RNA splicing in stem cells and cancer stem cells: Importance of transcript-based expression analysis. <i>World Journal of Stem Cells</i> , <b>2021</b> , 13, 1394-1416	5.6	1
22	Changes in Microsatellite Motifs in Response to Abiotic Stresses: a Case Study Using Wheat and Rice RNA-sequencing Data. <i>Asian Journal of Scientific Research</i> , <b>2017</b> , 11, 12-21	0.3	1
21	Molecular mechanisms of resistance to bovine mastitis. <i>Livestock Science</i> , <b>2020</b> , 239, 104068	1.7	1
20	Stallion Sperm Integrity After Centrifugation to Reduce Seminal Plasma Concentration and Cool Storage for 4 days. <i>Journal of Equine Veterinary Science</i> , <b>2020</b> , 85, 102819	1.2	1
19	AFExNet: An Adversarial Autoencoder for Differentiating Breast Cancer Sub-types and Extracting Biologically Relevant Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , PP,	3	1
18	Image processing unravels the evolutionary pattern of SARS-CoV-2 against SARS and MERS through position-based pattern recognition. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 134, 104471	7	1
17	<i>Porphyromonas</i> spp., <i>Fusobacterium</i> spp., and <i>Bacteroides</i> spp. dominate microbiota in the course of macropod progressive periodontal disease. <i>Scientific Reports</i> , <b>2021</b> , 11, 17775	4.9	1
16	Advances in understanding the specificity function of transporters by machine learning. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 138, 104893	7	1
15	Integration of meta-analysis and supervised machine learning for pattern recognition in breast cancer using epigenetic data. <i>Informatics in Medicine Unlocked</i> , <b>2021</b> , 24, 100629	5.3	1
14	Isolation of 2-phenylethanol biosynthesis related gene and developmental patterns of emission of scent compounds in Persian musk rose ( <i>Rosa moschata</i> Herrm.). <i>Biocatalysis and Agricultural Biotechnology</i> , <b>2019</b> , 19, 101176	4.2	0
13	Identification of Pathways and Candidate Genes Associated with Resistance to <i>Ascochyta</i> Blight in a Mutant Chickpea Variety using RNA-Seq Analysis. <i>Journal of Crop Breeding</i> , <b>2020</b> , 12, 69-75	0.1	0
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11	Machine learning models effectively distinguish attention-deficit/hyperactivity disorder using event-related potentials. <i>Cognitive Neurodynamics</i> , 1	4.2	0
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4	ABC Transporters are Hub Genes in Response of Resistant E. Coli ST131 to Ciprofloxacin. <i>Archives of Pharmacy Practice</i> , <b>2021</b> , 12, 82-88	0
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