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Citation Report

#	ARTICLE	IF	CITATIONS
1	Bacillus anthracis Thioredoxin Systems, Characterization and Role as Electron Donors for Ribonucleotide Reductase. <i>Journal of Biological Chemistry</i> , 2012, 287, 39686-39697.	1.6	33
2	Post-collection processing of Schirmer strip-collected human tear fluid impacts protein content. <i>Analyst</i> , 2012, 137, 5088.	1.7	44
3	BRENDA in 2013: integrated reactions, kinetic data, enzyme function data, improved disease classification: new options and contents in BRENDA. <i>Nucleic Acids Research</i> , 2012, 41, D764-D772.	6.5	358
4	Identification of essential genes of the periodontal pathogen <i>Porphyromonas gingivalis</i> . <i>BMC Genomics</i> , 2012, 13, 578.	1.2	123
5	Genome-guided analysis of physiological and morphological traits of the fermentative acetate oxidizer <i>Thermacetogenium phaeum</i> . <i>BMC Genomics</i> , 2012, 13, 723.	1.2	64
6	Crystallization of the DdrB-DNA complex from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1534-1537.	0.7	4
7	SP-G, a Putative New Surfactant Protein Tissue Localization and 3D Structure. <i>PLoS ONE</i> , 2012, 7, e47789.	1.1	27
8	The Purine-Utilizing Bacterium <i>Clostridium acidurici</i> 9a: A Genome-Guided Metabolic Reconsideration. <i>PLoS ONE</i> , 2012, 7, e51662.	1.1	46
9	Comparative modeling of Rab6 proteins: identification of key residues and their interactions with guanine nucleotides. <i>Journal of Molecular Modeling</i> , 2013, 19, 1891-1900.	0.8	2
10	Computational Models of Algae Metabolism for Industrial Applications. <i>Industrial Biotechnology</i> , 2013, 9, 185-195.	0.5	7
11	Biological and Chemical Databases for Research into the Composition of Animal Source Foods. <i>Food Reviews International</i> , 2013, 29, 321-351.	4.3	19
12	Binding of G-quadruplexes to the N-terminal Recognition Domain of the RNA Helicase Associated with AU-rich Element (RHAU). <i>Journal of Biological Chemistry</i> , 2013, 288, 35014-35027.	1.6	53
13	Novel aquatic silk genes from <i>Simulium (Psilozia) vittatum</i> (Zett) Diptera: Simuliidae. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 1181-1188.	1.2	4
14	Phylogenomics of fescue grass-derived fungal endophytes based on selected nuclear genes and the mitochondrial gene complement. <i>BMC Evolutionary Biology</i> , 2013, 13, 270.	3.2	16
15	Intrinsically disordered regions of p53 family are highly diversified in evolution. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 725-738.	1.1	68
16	Mutated Desmoglein-2 Proteins are Incorporated into Desmosomes and Exhibit Dominant-Negative Effects in Arrhythmic Right Ventricular Cardiomyopathy. <i>Human Mutation</i> , 2013, 34, 697-705.	1.1	30
17	<i>Acinetobacter baylyi</i> long-term stationary-phase protein StiP is a protease required for normal cell morphology and resistance to tellurite. <i>Canadian Journal of Microbiology</i> , 2013, 59, 726-736.	0.8	4
18	Extensions to In Silico Bioactivity Predictions Using Pathway Annotations and Differential Pharmacology Analysis: Application to <i>Xenopus laevis</i> Phenotypic Readouts. <i>Molecular Informatics</i> , 2013, 32, 1009-1024.	1.4	13

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19	The stimulatory effect of mannitol on levan biosynthesis: Lessons from metabolic systems analysis of <i>Halomonas smyrnensis</i> AAD6 <sup>T</sup> . <i>Biotechnology Progress</i> , 2013, 29, 1386-1397.	1.3	38
20	Directed Multistep Biocatalysis Using Tailored Permeabilized Cells. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2013, 137, 185-234.	0.6	15
21	Binary Response Models for Recognition of Antimicrobial Peptides. , 2013, , .		11
22	Isolation and characterization of homologous TRBP cDNA for RNA interference in <i>Penaeus monodon</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 704-711.	1.6	11
23	<i>Lactobacillus helveticus</i> as a tool to change proteolysis and functionality in Swiss-type cheeses. <i>Journal of Dairy Science</i> , 2013, 96, 1455-1470.	1.4	39
24	Purification, characterisation and expression in <i>Saccharomyces cerevisiae</i> of LipG7 an enantioselective, cold-adapted lipase from the Antarctic filamentous fungus <i>Geomyces</i> sp. P7 with unusual thermostability characteristics. <i>Enzyme and Microbial Technology</i> , 2013, 53, 18-24.	1.6	42
25	Fusion of mApple and Venus fluorescent proteins to the Sindbis virus E2 protein leads to different cell-binding properties. <i>Virus Research</i> , 2013, 177, 138-146.	1.1	6
26	Early Folding Events Protect Aggregation-Prone Regions of a $\beta^2$ -Rich Protein. <i>Structure</i> , 2013, 21, 476-485.	1.6	14
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28	Evolutionary and mechanistic insights into substrate and product accommodation of <i>Ctp</i> :phosphocholine cytidyltransferase from <i>Plasmodium falciparum</i> . <i>FEBS Journal</i> , 2013, 280, 3132-3148.	2.2	16
29	Metabolic profiling reveals that time related physiological changes in mammalian cell perfusion cultures are bioreactor scale independent. <i>Metabolic Engineering</i> , 2013, 19, 1-9.	3.6	42
30	Human Protein Cluster Analysis Using Amino Acid Frequencies. <i>PLoS ONE</i> , 2013, 8, e60220.	1.1	5
31	Quantification of Human Kallikrein-2 in Clinical Samples by Selected Reaction Monitoring. <i>Journal of Proteome Research</i> , 2013, 12, 4612-4616.	1.8	9
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33	Reconstitution of a Kv Channel into Lipid Membranes for Structural and Functional Studies. <i>Journal of Visualized Experiments</i> , 2013, , e50436.	0.2	10
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35	Advancements in the Analysis of the Arabidopsis Plasma Membrane Proteome. <i>Frontiers in Plant Science</i> , 2013, 4, 86.	1.7	51
36	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	2.1	68

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37	Comprehensive Analysis of Transcriptome Variation Uncovers Known and Novel Driver Events in T-Cell Acute Lymphoblastic Leukemia. <i>PLoS Genetics</i> , 2013, 9, e1003997.	1.5	110
38	Pyranose Dehydrogenase from <i>Agaricus campestris</i> and <i>Agaricus xanthoderma</i> : Characterization and Applications in Carbohydrate Conversions. <i>Biomolecules</i> , 2013, 3, 535-552.	1.8	13
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42	Shrinking the FadE Proteome of <i>Mycobacterium tuberculosis</i> : Insights into Cholesterol Metabolism through Identification of an $\hat{I}^{\pm 2}$ $\hat{I}^2$ Heterotetrameric Acyl Coenzyme A Dehydrogenase Family. <i>Journal of Bacteriology</i> , 2013, 195, 4331-4341.	1.0	59
43	High-Throughput Methods for Combinatorial Drug Discovery. <i>Science Translational Medicine</i> , 2013, 5, 205rv1.	5.8	139
44	Residue-Level Prediction of HIV-1 Antibody Epitopes Based on Neutralization of Diverse Viral Strains. <i>Journal of Virology</i> , 2013, 87, 10047-10058.	1.5	64
45	Culture-dependent and independent approaches for identifying novel halogenases encoded by <i>Crambe crambe</i> (marine sponge) microbiota. <i>Scientific Reports</i> , 2013, 3, 2780.	1.6	41
46	Library of Apicomplexan Metabolic Pathways: a manually curated database for metabolic pathways of apicomplexan parasites. <i>Nucleic Acids Research</i> , 2013, 41, D706-D713.	6.5	61
47	Metabolomics and Network Biology for sensitive monitoring of how growth environment changes affect the physiology of industrial-scale perfusion cultures. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2013, 46, 227-232.	0.4	1
48	Analysis of Unannotated Equine Transcripts Identified by mRNA Sequencing. <i>PLoS ONE</i> , 2013, 8, e70125.	1.1	16
49	The Prevalence and Polymorphisms of Zonula Occluden Toxin Gene in Multiple <i>Campylobacter concisus</i> Strains Isolated from Saliva of Patients with Inflammatory Bowel Disease and Controls. <i>PLoS ONE</i> , 2013, 8, e75525.	1.1	39
50	Direct Repair in Mammalian Cells. , 2013, , .		1
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53	Rapid Purification of Recombinant Histones. <i>PLoS ONE</i> , 2014, 9, e104029.	1.1	45
54	Synthetic Biology Outside the Cell: Linking Computational Tools to Cell-Free Systems. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 66.	2.0	12

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56	Computational Strategies for a System-Level Understanding of Metabolism. <i>Metabolites</i> , 2014, 4, 1034-1087.	1.3	54
57	Characterisation of divergent flavivirus NS3 and NS5 protein sequences detected in Rhipicephalus microplus ticks from Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2014, 109, 38-50.	0.8	59
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60	Mining the Dark Matter of the Cancer Proteome for Novel Biomarkers. <i>Current Cancer Therapy Reviews</i> , 2014, 9, 265-277.	0.2	9
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63	Cyclic nucleotide-gated ion channel gene family in rice, identification, characterization and experimental analysis of expression response to plant hormones, biotic and abiotic stresses. <i>BMC Genomics</i> , 2014, 15, 853.	1.2	129
64	Overexpression of p49/STRAP alters cellular cytoskeletal structure and gross anatomy in mice. <i>BMC Cell Biology</i> , 2014, 15, 32.	3.0	20
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66	Diversity in the preimmune immunoglobulin repertoire of SHR lines susceptible and resistant to end-organ injury. <i>Genes and Immunity</i> , 2014, 15, 528-533.	2.2	15
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68	Subcellular localization and developmental regulation of cytosolic, soluble pyrophosphatase isoforms in <i>Arabidopsis thaliana</i> . <i>Turkish Journal of Botany</i> , 2014, 38, 1036-1049.	0.5	9
69	Databases and Datasources at SIB, Swiss Institute of Bioinformatics. , 2014, , 191-204.		2
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72	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	6.5	13

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73	Computational Approaches for Microalgal Biofuel Optimization: A Review. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	21
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75	Stable-isotope-labeled Histone Peptide Library for Histone Post-translational Modification and Variant Quantification by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2450-2466.	2.5	53
76	The crystal structure of human mitochondrial 3-ketoacyl-CoA thiolase (T1): insight into the reaction mechanism of its thiolase and thioesterase activities. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3212-3225.	2.5	29
77	Evolutionary Origins of a Bioactive Peptide Buried within Preproalbumin. <i>Plant Cell</i> , 2014, 26, 981-995.	3.1	51
78	Genetic mutations in early-onset Parkinson's disease Mexican patients: Molecular testing implications. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2014, 165, 235-244.	1.1	13
79	The newly characterized <i>Pl</i> is specifically expressed in skeletogenic cells of the <i>Paracentrotus lividus</i> sea urchin embryo. <i>FEBS Journal</i> , 2014, 281, 3828-3843.	2.2	21
80	Involvement of the Iron Regulatory Protein from <i>Eisenia andrei</i> Earthworms in the Regulation of Cellular Iron Homeostasis. <i>PLoS ONE</i> , 2014, 9, e109900.	1.1	1
81	Capillary isoelectric focusing of a difficult-to-denature tetrameric enzyme using alkylurea mixtures. <i>Analytical Biochemistry</i> , 2014, 465, 90-95.	1.1	18
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85	Tandem Mass Spectral Libraries of Peptides in Digests of Individual Proteins: Human Serum Albumin (HSA). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2435-2449.	2.5	21
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88	Dynamic condensation of linker histone C-terminal domain regulates chromatin structure. <i>Nucleic Acids Research</i> , 2014, 42, 7553-7560.	6.5	56
89	Reduced Culture Temperature Differentially Affects Expression and Biophysical Properties of Monoclonal Antibody Variants. <i>Antibodies</i> , 2014, 3, 253-271.	1.2	17
90	Identification of a Fourth Haplotype of <i>Bactericera cockerelli</i> (Hemiptera: Trioziidae) in the United States. <i>Journal of Insect Science</i> , 2014, 14, 161.	0.6	39

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95	Origin and function of the major royal jelly proteins of the honeybee ( <i>Apis mellifera</i> ) as members of the <i>yellow</i> gene family. <i>Biological Reviews</i> , 2014, 89, 255-269.	4.7	168
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97	The <i>Sinorhizobium meliloti</i> EmrAB Efflux System Is Regulated by Flavonoids Through a TetR-Like Regulator (EmrR). <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 379-387.	1.4	18
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103	Characterization of tomato Cycling Dof Factors reveals conserved and new functions in the control of flowering time and abiotic stress responses. <i>Journal of Experimental Botany</i> , 2014, 65, 995-1012.	2.4	161
104	Molecular functions of the iron-regulated metastasis suppressor, NDRG1, and its potential as a molecular target for cancer therapy. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014, 1845, 1-19.	3.3	88
105	Reduced effects of thyroid hormone on gene expression and metamorphosis in a paedomorphic plethodontid salamander. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 294-303.	0.6	13
106	Protein modeling and molecular dynamics simulation of the two novel surfactant proteins SP-G and SP-H. <i>Journal of Molecular Modeling</i> , 2014, 20, 2513.	0.8	16
107	Zinc Finger Endonuclease Targeting <i>PSIP1</i> Inhibits HIV-1 Integration. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4318-4327.	1.4	15
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110	Expression and characterization of an epoxide hydrolase from <i>Anopheles gambiae</i> with high activity on epoxy fatty acids. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 54, 42-52.	1.2	12
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112	The metallothionein gene from the white shrimp <i>Litopenaeus vannamei</i> : Characterization and expression in response to hypoxia. <i>Marine Environmental Research</i> , 2014, 101, 91-100.	1.1	25
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115	The phosphoinositide-dependent protein kinase 1 inhibitor, UCN-01, induces fragmentation: Possible role of metalloproteinases. <i>European Journal of Pharmacology</i> , 2014, 740, 88-96.	1.7	4
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121	Genomewide analysis of LATERAL ORGAN BOUNDARIES Domain gene family in <i>Zea mays</i> . <i>Journal of Genetics</i> , 2014, 93, 79-91.	0.4	48
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131	Resolution of the type material of the Asian elephant, <i>Elephas maximus</i> Linnaeus, 1758 (Proboscidea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 T</i>	1.6	22
132	Improving protein order-disorder classification using charge-hydrophathy plots. <i>BMC Bioinformatics</i> , 2014, 15, S4.	1.2	63
133	Novel human recombinant antibodies against <i>Mycobacterium tuberculosis</i> antigen 85B. <i>BMC Biotechnology</i> , 2014, 14, 68.	1.7	20
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730	Genome-wide identification of the expansin gene family reveals that expansin genes are involved in fibre cell growth in cotton. <i>BMC Plant Biology</i> , 2020, 20, 223.	1.6	32
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732	Genome-wide identification and expression analysis of StPP2C gene family in response to multiple stresses in potato ( <i>Solanum tuberosum</i> L.). <i>Journal of Integrative Agriculture</i> , 2020, 19, 1609-1624.	1.7	19
733	Flexibility of intrinsically disordered degrons in AUX/IAA proteins reinforces auxin co-receptor assemblies. <i>Nature Communications</i> , 2020, 11, 2277.	5.8	38
734	Genome-wide characterization of tea plant ( <i>Camellia sinensis</i> ) Hsf transcription factor family and role of CsHsfA2 in heat tolerance. <i>BMC Plant Biology</i> , 2020, 20, 244.	1.6	26
735	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , 2020, 181, 1062-1079.e30.	13.5	115
736	Expression and purification of soluble recombinant SapM from <i>Mycobacterium tuberculosis</i> . <i>Protein Expression and Purification</i> , 2020, 174, 105663.	0.6	3
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738	Biotechnology for Biofuels: A Sustainable Green Energy Solution. , 2020, , .		4
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742	DDIEM: drug database for inborn errors of metabolism. <i>Orphanet Journal of Rare Diseases</i> , 2020, 15, 146.	1.2	9
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744	A systematic strategy for the investigation of vaccines and drugs targeting bacteria. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1525-1538.	1.9	13
745	Determination of amyloid core regions of insulin analogues fibrils. <i>Prion</i> , 2020, 14, 149-162.	0.9	13
746	Identifying variation in red raspberry MLO genes thought to provide resistance to powdery mildew. <i>Acta Horticulturae</i> , 2020, , 25-32.	0.1	2

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748	META-BASE: A Novel Architecture for Large-Scale Genomic Metadata Integration. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 543-557.	1.9	19
749	Basic Helix-Loop-Helix (bHLH) transcription factor family in Yellow horn ( <i>Xanthoceras sorbifolia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 patterns. <i>International Journal of Biological Macromolecules</i> , 2020, 160, 711-723.	3.6	17
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753	CpG-creating mutations are costly in many human viruses. <i>Evolutionary Ecology</i> , 2020, 34, 339-359.	0.5	14
754	Akt and Src mediate the photocrosslinked fibroin-induced neural differentiation.. <i>NeuroReport</i> , 2020, 31, 770-775.	0.6	3
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789	Current Trends in Diagnostics of Viral Infections of Unknown Etiology. <i>Viruses</i> , 2020, 12, 211.	1.5	49
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1403	Genome-Wide Identification of Genes Encoding for Rho-Related Proteins in "Duli" Pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlap 10 Tf 5	1.6	1
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1412	The Fingerprints of Biomedical Science in Internal Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2022, , .	0.8	0
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1433	The interplay of DNA methyltransferases and demethylases with tuberization genes in potato ( <i>Solanum tuberosum</i> L.) genotypes under high temperature. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
1434	Evolutionary diversification of epidermal barrier genes in amphibians. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
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1442	Genome-wide identification and expression analysis of MATE gene family in citrus fruit ( <i>Citrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 107	1.8	3
1443	Genome-wide analysis of UGT gene family identified key gene for the biosynthesis of bioactive flavonol glycosides in <i>Epimedium pubescens</i> Maxim.. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 1095-1107.	1.8	12
1444	Neuropeptidomes of <i>Tenebrio molitor</i> L. and <i>Zophobas atratus</i> Fab. (Coleoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 107	1.8	4
1445	An LTR retrotransposon in the promoter of a <i>PsMYB10.2</i> gene associated with the regulation of fruit flesh color in Japanese plum. <i>Horticulture Research</i> , 0, , .	2.9	1
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1449	Genome-Wide Analysis of the WOX Transcription Factor Genes in <i>Dendrobium catenatum</i> Lindl.. <i>Genes</i> , 2022, 13, 1481.	1.0	4
1450	Evidence of circulation of beak and feather disease virus in captive psittacine and non-psittacine birds in Bangladesh. <i>Archives of Virology</i> , 2022, 167, 2567-2575.	0.9	2
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1457	Identification, characterization, and expression profiling of the putative U-box E3 ubiquitin ligase gene family in <i>Sorghum bicolor</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
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1460	Cytochrome P450 Genes Expressed in Phasmatodea Midguts. <i>Insects</i> , 2022, 13, 873.	1.0	1
1461	Genome-wide identification and analysis of anthocyanin synthesis-related R2R3-MYB genes in <i>Cymbidium goeringii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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1470	Genome-Wide Investigation and Expression Analysis of the Nitraria sibirica Pall. CIPK Gene Family. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11599.	1.8	3
1471	Phylogenetic Characterization of HIV-1 Sub-Subtype A1 in Karachi, Pakistan. <i>Viruses</i> , 2022, 14, 2307.	1.5	0
1472	Molecular Characterization of bHLH Transcription Factor Family in Rose ( <i>Rosa chinensis</i> Jacq.) under <i>Botrytis cinerea</i> Infection. <i>Horticulturae</i> , 2022, 8, 989.	1.2	3
1473	Sequence Characteristics and Expression Analysis of GhCIPK23 Gene in Upland Cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	0
1474	Genome-Wide Identification and Characterization of the Oat ( <i>Avena sativa</i> L.) WRKY Transcription Factor Family. <i>Genes</i> , 2022, 13, 1918.	1.0	6
1475	Genome-wide identification and expression analysis of BrAGC genes in <i>Brassica rapa</i> reveal their potential roles in sexual reproduction and abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
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1477	Identification and characterization of epicuticular proteins of nematodes sharing motifs with cuticular proteins of arthropods. <i>PLoS ONE</i> , 2022, 17, e0274751.	1.1	1
1478	Identification and characteristics of SnRK genes and cold stress-induced expression profiles in <i>Liriodendron chinense</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	5
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1480	Genome-wide characterization of the UDP-glycosyltransferase gene family reveals their potential roles in leaf senescence in cotton. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2648-2660.	3.6	6
1481	Specific <sc>IgE</sc> against the house dust mite allergens Der p 5, 20 and 21 influences the phenotype and severity of atopic diseases. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2023, 78, 731-742.	2.7	9
1482	Genome-Wide Identification of Auxin-Responsive GH3 Gene Family in <i>Saccharum</i> and the Expression of ScGH3-1 in Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12750.	1.8	6
1483	Genome-Wide Identification and Expression Analysis of AMT and NRT Gene Family in Pecan ( <i>Carya</i> ) Tj ETQq1 1 0.784314 rgBT /Overl <i>Sciences</i> , 2022, 23, 13314.	1.8	4

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1485	De Novo Transcriptome Analysis in <i>Hevea brasiliensis</i> to Unveil Genes Involved in Low Temperature Stress Response. <i>Phyton</i> , 2023, 92, 559-575.	0.4	0
1486	Genome-wide identification, phylogenetic, and expression analysis under abiotic stress conditions of Whirly (WHY) gene family in <i>Medicago sativa</i> L.. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
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1488	Identification of <i>Brachypodium distachyon</i> B3 genes reveals that Bdb3-54 regulates primary root growth. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
1489	<i>GmFtsH25</i> overexpression increases soybean seed yield by enhancing photosynthesis and photosynthates. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1026-1040.	4.1	7
1490	Genome-Wide Identification, Characterization, and Expression Analysis of CHS Gene Family Members in <i>Chrysanthemum nankingense</i> . <i>Genes</i> , 2022, 13, 2145.	1.0	3
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1495	Genome-wide characterization and expression profiling of GASA gene family in <i>Triticum turgidum</i> ssp. durum (desf.) husn. (Durum wheat) unveils its involvement in environmental stress responses. <i>Phytochemistry</i> , 2023, 206, 113544.	1.4	3
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1497	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. <i>Gene</i> , 2023, 855, 147127.	1.0	3
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1501	Genome-wide identification of calcium-dependent protein kinases (CDPKs) in pear ( <i>Pyrus bretschneideri</i> ) Tj ETQq1 1 0.784314 rgBT /Over Environment and Biotechnology, 2022, 63, 903-915.	0.7	2

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1506	Genome-wide identification of the VOZ transcription factors in tomato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td (lyco of Horticultural Science and Biotechnology, 2023, 98, 468-482.	0.9	1
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1513	Genome-wide analysis of the TCP gene family and their expression pattern in <i>Cymbidium goeringii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
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1521	Stereochemistry and Intermolecular Interactions Influence Carrier Peptide-Mediated Insulin Delivery. <i>Molecular Pharmaceutics</i> , 0, , .	2.3	5

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1525	Genome-Wide Comparative Analysis of the Fasciclin-like Arabinogalactan Proteins (FLAs) in Salicacea and Identification of Secondary Tissue Development-Related Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1481.	1.8	3
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1539	Identification of novel inhibitors against hantaviruses through 2D fingerprinting and molecular modeling approaches. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
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1570	Assembly, Characterization, and Phylogenetic Relationships of Mitogenomes of Two Species of Mexican Trout ( <i>Oncorhynchus chrysogaster</i> and <i>O. mykiss nelsoni</i> ). <i>Fishes</i> , 2023, 8, 178.	0.7	0
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1667	Current Biotechnological Advancements in Lignin Valorization For Value-added Products. , 2023, , 37-60.		0
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