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Citation Report

#	ARTICLE	IF	CITATIONS
3	TRANSPARENT TESTA GLABRA 1-Dependent Regulation of Flavonoid Biosynthesis. <i>Plants</i> , 2017, 6, 65.	1.6	62
4	A sequence family database built on ECOD structural domains. <i>Bioinformatics</i> , 2018, 34, 2997-3003.	1.8	5
5	An ancient Sec10â€‘formin fusion provides insights into actin-mediated regulation of exocytosis. <i>Journal of Cell Biology</i> , 2018, 217, 945-957.	2.3	23
6	The 2018 Nucleic Acids Research database issue and the online molecular biology database collection. <i>Nucleic Acids Research</i> , 2018, 46, D1-D7.	6.5	106
7	Comparative systems analysis of the secretome of the opportunistic pathogen <i>Aspergillus fumigatus</i> and other <i>Aspergillus</i> species. <i>Scientific Reports</i> , 2018, 8, 6617.	1.6	42
8	Reactive-site-centric chemoproteomics identifies a distinct class of deubiquitinase enzymes. <i>Nature Communications</i> , 2018, 9, 1162.	5.8	85
9	Distinctive Nuclear Features of Dinoflagellates with A Particular Focus on Histone and Histone-Replacement Proteins. <i>Microorganisms</i> , 2018, 6, 128.	1.6	15
10	Dual expression of plastidial GPAT1 and LPAT1 regulates triacylglycerol production and the fatty acid profile in <i>Phaeodactylum tricornutum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 318.	6.2	64
11	Comparative evolutionary histories of fungal proteases reveal gene gains in the mycoparasitic and nematode-parasitic fungus <i>Clonostachys rosea</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 171.	3.2	31
12	Genome-wide identification and analysis of WD40 proteins in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2018, 19, 803.	1.2	46
13	Photoperiod response-related gene <i>SiCOL1</i> contributes to flowering in sesame. <i>BMC Plant Biology</i> , 2018, 18, 343.	1.6	17
14	Putative Interaction Proteins of the Ubiquitin Ligase <i>Hrd1</i> in <i>Magnaporthe oryzae</i> . <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431881099.	0.6	3
15	Cloning and characterization of a <i>Mimulus lewisii</i> NPR1 gene involved in regulating plant resistance to <i>Rhizoctonia solani</i> . <i>Plant Biotechnology</i> , 2018, 35, 349-356.	0.5	2
16	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. <i>BMC Genomics</i> , 2018, 19, 851.	1.2	59
17	Digenic Inheritance of Shortened Repeat Units of the D4Z4 Region and a Loss-of-Function Variant in <i>SMCHD1</i> in a Family With FSHD. <i>Frontiers in Neurology</i> , 2018, 9, 1027.	1.1	8
18	A Mechanically Weak Extracellular Membrane-Adjacent Domain Induces Dimerization of Protocadherin-15. <i>Biophysical Journal</i> , 2018, 115, 2368-2385.	0.2	27
19	Genome-Wide Identification and Expression Profiling Analysis of the Galactinol Synthase Gene Family in Cassava ( <i>Manihot esculenta</i> Crantz). <i>Agronomy</i> , 2018, 8, 250.	1.3	14
20	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	6.0	805

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21	CHESS: a new human gene catalog curated from thousands of large-scale RNA sequencing experiments reveals extensive transcriptional noise. <i>Genome Biology</i> , 2018, 19, 208.	3.8	263
22	Two Novel Short Peptidoglycan Recognition Proteins (PGRPs) From the Deep Sea Vesicomidae Clam <i>Archivesica packardana</i> : Identification, Recombinant Expression and Bioactivity. <i>Frontiers in Physiology</i> , 2018, 9, 1476.	1.3	8
23	Introduction to Bioinformatics in Microbiology. <i>Learning Materials in Biosciences</i> , 2018, , .	0.2	5
24	Databases and Protein Structures. <i>Learning Materials in Biosciences</i> , 2018, , 25-50.	0.2	0
25	The Roles of E93 and Kr-h1 in Metamorphosis of <i>Nilaparvata lugens</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1677.	1.3	30
26	Genome-wide analysis of the plant-specific PLATZ proteins in maize and identification of their general role in interaction with RNA polymerase III complex. <i>BMC Plant Biology</i> , 2018, 18, 221.	1.6	37

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39	<i>Xrp1</i> genetically interacts with the ALS-associated <i>FUS</i> orthologue <i>caz</i> and mediates its toxicity. <i>Journal of Cell Biology</i> , 2018, 217, 3947-3964.	2.3	23
40	The <i>PedS2/PedR2</i> Two-Component System Is Crucial for the Rare Earth Element Switch in <i>Pseudomonas putida</i> KT2440. <i>MSphere</i> , 2018, 3, .	1.3	27
41	Molecular characterization, expression profile, and preliminary evaluation of diagnostic potential of CD63 in <i>Schistosoma japonicum</i> . <i>Parasitology Research</i> , 2018, 117, 3625-3631.	0.6	6
42	Structure of a Novel Dimeric SET Domain Methyltransferase that Regulates Cell Motility. <i>Journal of Molecular Biology</i> , 2018, 430, 4209-4229.	2.0	3
43	A gene-rich fraction analysis of the <i>Passiflora edulis</i> genome reveals highly conserved microsyntenic regions with two related Malpighiales species. <i>Scientific Reports</i> , 2018, 8, 13024.	1.6	18
44	Anti-haemostatic compounds from the vampire snail <i>Cumia reticulata</i> : Molecular cloning and in-silico structure-function analysis. <i>Computational Biology and Chemistry</i> , 2018, 75, 168-177.	1.1	5
45	The Maternal Effect Gene <i>Wds</i> Controls <i>Wolbachia</i> Titer in <i>Nasonia</i> . <i>Current Biology</i> , 2018, 28, 1692-1702.e6.	1.8	51
46	LEA Proteins and the Evolution of the <i>WHy</i> Domain. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	48
47	An antifungal polyketide associated with horizontally acquired genes supports symbiont-mediated defense in <i>Lagria villosa</i> beetles. <i>Nature Communications</i> , 2018, 9, 2478.	5.8	86
48	Genome-wide identification and comprehensive analysis of the NAC transcription factor family in <i>Sesamum indicum</i> . <i>PLoS ONE</i> , 2018, 13, e0199262.	1.1	29
49	A Tangled Web: Origins of Reproductive Parasitism. <i>Genome Biology and Evolution</i> , 2018, 10, 2292-2309.	1.1	47
50	Sex- and Tissue-Specific Expression Profiles of Odorant Binding Protein and Chemosensory Protein Genes in <i>Bradysia odoriphaga</i> (Diptera: Sciaridae). <i>Frontiers in Physiology</i> , 2018, 9, 107.	1.3	46
51	PASTA sequence composition is a predictive tool for protein class identification. <i>Amino Acids</i> , 2018, 50, 1441-1450.	1.2	4
52	Identification and transcriptional analysis of dehydrin gene family in cucumber ( <i>Cucumis sativus</i> ). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	8
53	Cork Oak Young and Traumatic Periderms Show PCD Typical Chromatin Patterns but Different Chromatin-Modifying Genes Expression. <i>Frontiers in Plant Science</i> , 2018, 9, 1194.	1.7	23
54	Identification of DEAD-Box RNA Helicase DDX41 as a Trafficking Protein That Involves in Multiple Innate Immune Signaling Pathways in a Zebrafish Model. <i>Frontiers in Immunology</i> , 2018, 9, 1327.	2.2	29
55	Identification and Characterization of Wheat Yellow Striate Virus, a Novel Leafhopper-Transmitted Nucleorhabdovirus Infecting Wheat. <i>Frontiers in Microbiology</i> , 2018, 9, 468.	1.5	43
56	Genome-Wide Identification, Characterization, and Expression Profiling of Glutathione S-Transferase (GST) Family in Pumpkin Reveals Likely Role in Cold-Stress Tolerance. <i>Genes</i> , 2018, 9, 84.	1.0	56

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57	Complete Genome Sequence of the Novel Virulent Phage PMBT28 with Lytic Activity against Thermotolerant <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Senftenberg ATCC 43845. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
58	Antibacterial Evaluation and Virtual Screening of New Thiazolyl-Triazole Schiff Bases as Potential DNA-Gyrase Inhibitors. <i>International Journal of Molecular Sciences</i> , 2018, 19, 222.	1.8	38
59	Positive selection adaptation of two-domain arginine kinase (AK) from cold seep <i>Vesicomysidae</i> clams. <i>Molecular Biology Reports</i> , 2018, 45, 1527-1532.	1.0	4
60	Sequences of Circadian Clock Proteins in the Nudibranch Molluscs <i>Hermisenda crassicornis</i> , <i>Melibe leonina</i> , and <i>Tritonia diomedea</i> . <i>Biological Bulletin</i> , 2018, 234, 207-218.	0.7	20
61	A recombinant <i>Fasciola gigantica</i> 14-3-3 epsilon protein (rFg14-3-3e) modulates various functions of goat peripheral blood mononuclear cells. <i>Parasites and Vectors</i> , 2018, 11, 152.	1.0	26
62	Genome-wide identification and characterization of cysteine-rich polycomb-like protein (CPP) family genes in cucumber ( <i>Cucumis sativus</i> ) and their roles in stress responses. <i>Biologia (Poland)</i> , 2018, 73, 425-435.	0.8	16
63	Molecular characterization of three toll-like receptors (TLR21, TLR22, and TLR25) from a primitive ray-finned fish Dabry's sturgeon ( <i>Acipenser dabryanus</i> ). <i>Fish and Shellfish Immunology</i> , 2018, 82, 200-211.	1.6	26
64	OrthoList 2: A New Comparative Genomic Analysis of Human and <i>Caenorhabditis elegans</i> Genes. <i>Genetics</i> , 2018, 210, 445-461.	1.2	233
65	Positive and Negative Regulation of Angiogenesis by Soluble Vascular Endothelial Growth Factor Receptor-1. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1306.	1.8	67
66	Genome-wide identification of the auxin/indole-3-acetic acid (Aux/IAA) gene family in pepper, its characterisation, and comprehensive expression profiling under environmental and phytohormones stress. <i>Scientific Reports</i> , 2018, 8, 12008.	1.6	17
67	Identification of Antifungal Targets Based on Computer Modeling. <i>Journal of Fungi (Basel)</i> , 2018, 10, 342.	1.5	12
68	The myosin light-chain kinase MLCK-1 relocalizes during <i>Caenorhabditis elegans</i> ovulation to promote actomyosin bundle assembly and drive contraction. <i>Molecular Biology of the Cell</i> , 2018, 29, 1975-1991.	0.9	14
69	Evidence for interaction between Hsp90 and the ER membrane complex. <i>Cell Stress and Chaperones</i> , 2018, 23, 1101-1115.	1.2	11
70	Agrin has a pathological role in the progression of oral cancer. <i>British Journal of Cancer</i> , 2018, 118, 1628-1638.	2.9	28
71	The Uba4 domain interplay is mediated via a thioester that is critical for tRNA thiolation through Urm1 thiocarboxylation. <i>Nucleic Acids Research</i> , 2018, 46, 5171-5181.	6.5	25
72	Toll-Like Receptor Evolution in Birds: Gene Duplication, Pseudogenization, and Diversifying Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 2170-2184.	3.5	107
73	Sec16A, a key protein in COPII vesicle formation, regulates the stability and localization of the novel ubiquitin ligase RNF183. <i>PLoS ONE</i> , 2018, 13, e0190407.	1.1	5
74	Overexpression of <i>TaCML20</i> , a calmodulin-like gene, enhances water soluble carbohydrate accumulation and yield in wheat. <i>Physiologia Plantarum</i> , 2019, 165, 790-799.	2.6	17

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75	Novel mutation in <sc>MBTPS</sc>2 causes keratosis follicularis spinulosa decalvans in a large Chinese family. International Journal of Dermatology, 2019, 58, 493-496.	0.5	7
76	Phylo-PFP: improved automated protein function prediction using phylogenetic distance of distantly related sequences. Bioinformatics, 2019, 35, 753-759.	1.8	29
77	Landscape of ROD9 Island: Functional annotations and biological network of hypothetical proteins in Salmonella enterica. Computational Biology and Chemistry, 2019, 83, 107110.	1.1	1
78	<i>In Silico</i> Phylogenetic and Structural Analyses of Plant Endogenous Danger Signaling Molecules upon Stress. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-14.	1.9	8
79	Clinical Persistence of Chlamydia trachomatis Sexually Transmitted Strains Involves Novel Mutations in the Functional Î±Î²Î²Î± Tetramer of the Tryptophan Synthase Operon. MBio, 2019, 10, .	1.8	20
80	Genome-wide identification of GRAS genes in Brachypodium distachyon and functional characterization of BdSLR1 and BdSLRL1. BMC Genomics, 2019, 20, 635.	1.2	24
81	Marchantia polymorpha, a New Model Plant for Autophagy Studies. Frontiers in Plant Science, 2019, 10, 935.	1.7	19
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83	The multi <sc>PAM</sc> 2 protein Upa2 functions as novel core component of endosomal <sc>mRNA</sc> transport. EMBO Reports, 2019, 20, e47381.	2.0	11
84	Databases: A Weapon from the Arsenal of Bioinformatics for Plant Abiotic Stress Research. , 2019, , 135-169.		15
85	Identification and expression analysis of the GDSL esterase/lipase family genes, and the characterization of <i>SaGLIP8</i> in <i>Sedum alfredii</i> Hance under cadmium stress. PeerJ, 2019, 7, e6741.	0.9	18
86	Type II Ice-Binding Proteins Isolated from an Arctic Microalga Are Similar to Adhesin-Like Proteins and Increase Freezing Tolerance in Transgenic Plants. Plant and Cell Physiology, 2019, 60, 2744-2757.	1.5	10
87	Identification of cells expressing two peptidoglycan recognition proteins in the gill of the vent mussel, Bathymodiolus septemdierum. Fish and Shellfish Immunology, 2019, 93, 815-822.	1.6	20
88	The F-Box Protein SAGL1 and ECERIFERUM3 Regulate Cuticular Wax Biosynthesis in Response to Changes in Humidity in Arabidopsis. Plant Cell, 2019, 31, 2223-2240.	3.1	58
89	Three <i>GLI2</i> mutations combined potentially underlie non-Î©syndromic cleft lip with or without cleft palate in a Chinese pedigree. Molecular Genetics & Genomic Medicine, 2019, 7, e714.	0.6	10
90	Shootins mediate collective cell migration and organogenesis of the zebrafish posterior lateral line system. Scientific Reports, 2019, 9, 12156.	1.6	6
91	Predicting Sequence Features, Function, and Structure of Proteins Using MESSA. Current Protocols in Bioinformatics, 2019, 67, e84.	25.8	0
92	Using MARRVEL v1.2 for Bioinformatics Analysis of Human Genes and Variant Pathogenicity. Current Protocols in Bioinformatics, 2019, 67, e85.	25.8	14

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94	Ligand Binding and Signaling of HARE/Stabilin-2. <i>Biomolecules</i> , 2019, 9, 273.	1.8	21
95	The Med31 Conserved Component of the Divergent Mediator Complex in <i>Tetrahymena thermophila</i> Participates in Developmental Regulation. <i>Current Biology</i> , 2019, 29, 2371-2379.e6.	1.8	13
96	Environmental conditions shape the nature of a minimal bacterial genome. <i>Nature Communications</i> , 2019, 10, 3100.	5.8	43
97	Membrane-Deformation Ability of ANKHD1 Is Involved in the Early Endosome Enlargement. <i>IScience</i> , 2019, 17, 101-118.	1.9	15
98	Structural insight into the fungal $\beta$ -glucosidases and their interactions with organics. <i>International Journal of Biological Macromolecules</i> , 2019, 138, 1019-1028.	3.6	6
99	Genomic Characterization of the Emerging Pathogen <i>Streptococcus pseudopneumoniae</i> . <i>MBio</i> , 2019, 10, .	1.8	18
100	Comparative genomics of <i>Mycobacterium mucogenicum</i> and <i>Mycobacterium neoaurum</i> clade members emphasizing tRNA and non-coding RNA. <i>BMC Evolutionary Biology</i> , 2019, 19, 124.	3.2	10
101	Thymol Mediates Bactericidal Activity against <i>Staphylococcus aureus</i> by Targeting an Aldo-Keto Reductase and Consequent Depletion of NADPH. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8382-8392.	2.4	28
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103	Systematic Analysis and Functional Validation of Citrus XTH Genes Reveal the Role of Csxth04 in Citrus Bacterial Canker Resistance and Tolerance. <i>Frontiers in Plant Science</i> , 2019, 10, 1109.	1.7	15
104	Identification of a candidate gene underlying qKRN5b for kernel row number in <i>Zea mays</i> L.. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3439-3448.	1.8	12
105	Genome-wide investigation of superoxide dismutase (SOD) gene family and their regulatory miRNAs reveal the involvement in abiotic stress and hormone response in tea plant ( <i>Camellia sinensis</i> ). <i>PLoS ONE</i> , 2019, 14, e0223609.	1.1	69
106	The variability of SMCHD1 gene in FSHD patients: evidence of new mutations. <i>Human Molecular Genetics</i> , 2019, 28, 3912-3920.	1.4	9
107	Functional characterization of poplar WRKY75 in salt and osmotic tolerance. <i>Plant Science</i> , 2019, 289, 110259.	1.7	48
108	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	6.5	126
109	The long non-coding RNA lncRNA973 is involved in cotton response to salt stress. <i>BMC Plant Biology</i> , 2019, 19, 459.	1.6	70
110	Expansion of LINEs and species-specific DNA repeats drives genome expansion in Asian Gypsy Moths. <i>Scientific Reports</i> , 2019, 9, 16413.	1.6	8

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111	A Single Transcription Factor (PDD1) Determines Development and Yield of Winter Mushroom ( <i>Tricholoma matsutake</i> )	1.4	33
112	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
113	Sex- and tissue-specific transcriptome analyses and expression profiling of olfactory-related genes in <i>Ceracris nigricornis</i> Walker (Orthoptera: Acrididae). <i>BMC Genomics</i> , 2019, 20, 808.	1.2	12
114	Diverse cell junctions with unique molecular composition in tissues of a sponge (Porifera). <i>EvoDevo</i> , 2019, 10, 26.	1.3	16
115	Venom Diversity and Evolution in the Most Divergent Cone Snail Genus <i>Profundiconus</i> . <i>Toxins</i> , 2019, 11, 623.	1.5	16
116	IFN-Stimulated Genes in Zebrafish and Humans Define an Ancient Arsenal of Antiviral Immunity. <i>Journal of Immunology</i> , 2019, 203, 3361-3373.	0.4	59
117	KMT2C, a histone methyltransferase, is mutated in a family segregating non-syndromic primary failure of tooth eruption. <i>Scientific Reports</i> , 2019, 9, 16469.	1.6	15
118	Rapid Tagging of Human Proteins with Fluorescent Reporters by Genome Engineering using Double-Stranded DNA Donors. <i>Current Protocols in Molecular Biology</i> , 2019, 129, e102.	2.9	9
119	Induction of DNA methyltransferase genes in <i>Helicoverpa armigera</i> following injection of pathogenic bacteria modulates expression of antimicrobial peptides and affects bacterial proliferation. <i>Journal of Insect Physiology</i> , 2019, 118, 103939.	0.9	15
120	Machine learning-based chemical binding similarity using evolutionary relationships of target genes. <i>Nucleic Acids Research</i> , 2019, 47, e128-e128.	6.5	13
121	Genome-Wide Identification and Characterization of Cucumber BPC Transcription Factors and Their Responses to Abiotic Stresses and Exogenous Phytohormones. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5048.	1.8	11
122	VEGF and FGF signaling during head regeneration in hydra. <i>Gene</i> , 2019, 717, 144047.	1.0	16
123	An amino-terminal threonine/serine motif is necessary for activity of the Crp/Fnr homolog, MrpC and for <i>Myxococcus xanthus</i> developmental robustness. <i>Molecular Microbiology</i> , 2019, 112, 1531-1551.	1.2	5
124	The finger loop of the SRA domain in the E3 ligase UHRF1 is a regulator of ubiquitin targeting and is required for the maintenance of DNA methylation. <i>Journal of Biological Chemistry</i> , 2019, 294, 15724-15732.	1.6	12
125	Identification and Functional Analysis of the CLAVATA3/EMBRYO SURROUNDING REGION (CLE) Gene Family in Wheat. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4319.	1.8	18
126	In silico and expression analyses of fasciclin-like arabinogalactan proteins reveal functional conservation during embryo and seed development. <i>Plant Reproduction</i> , 2019, 32, 353-370.	1.3	27
127	Molecular characterization and computational structure prediction of activin receptor type IIB in aeseel and broiler chicken. <i>Research in Veterinary Science</i> , 2019, 126, 139-149.	0.9	0
128	Expression Analysis of the NAC Transcription Factor Family of <i>Populus</i> in Response to Salt Stress. <i>Forests</i> , 2019, 10, 688.	0.9	10



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129	ECM alterations in Fndc3a (Fibronectin Domain Containing Protein 3A) deficient zebrafish cause temporal fin development and regeneration defects. <i>Scientific Reports</i> , 2019, 9, 13383.	1.6	8
130	Allosteric regulation of a prokaryotic small Ras-like GTPase contributes to cell polarity oscillations in bacterial motility. <i>PLoS Biology</i> , 2019, 17, e3000459.	2.6	22
131	Hexa-Longin domain scaffolds for inter-Rab signalling. <i>Bioinformatics</i> , 2020, 36, 990-993.	1.8	5
132	Further Elucidation of the Argonaute and Dicer Protein Families in the Model Grass Species <i>Brachypodium distachyon</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1332.	1.7	7
133	Evaluation of clan CD C11 peptidase PNT1 and other <i>Leishmania mexicana</i> cysteine peptidases as potential drug targets. <i>Biochimie</i> , 2019, 166, 150-160.	1.3	13
134	Genome-Wide Identification, Evolution, and Expression Analysis of RING Finger Gene Family in <i>Solanum lycopersicum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4864.	1.8	17
135	Investigation of the Possible Role of RAD9 in Post-Diapaused Embryonic Development of the Brine Shrimp <i>Artemia sinica</i> . <i>Genes</i> , 2019, 10, 768.	1.0	18
136	Comparative Genome Analyses Reveal the Genomic Traits and Host Plant Adaptations of <i>Flavobacterium akiainvivens</i> IK-1T. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4910.	1.8	1
137	Cadherin switch marks germ layer formation in the diploblastic sea anemone <i>Nematostella vectensis</i> . <i>Development (Cambridge)</i> , 2019, 146, .	1.2	14
138	Heterologous biosynthesis of a fungal macrocyclic polylactone requires only two iterative polyketide synthases. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 374-379.	1.5	12
139	Systematic domain-based aggregation of protein structures highlights DNA-, RNA- and other ligand-binding positions. <i>Nucleic Acids Research</i> , 2019, 47, 582-593.	6.5	16
140	Genome-wide identification, phylogeny, and expression profile of the sucrose transporter multigene family in tobacco. <i>Canadian Journal of Plant Science</i> , 2019, 99, 312-323.	0.3	6
141	Genome-wide characterization and expression profiling of SWEET genes in cabbage ( <i>Brassica oleracea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 93.	1.2	51
142	Genome-Wide Identification and Expression Profiling of Sugar Transporter Protein (STP) Family Genes in Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> L.) Reveals their Involvement in Clubroot Disease Responses. <i>Genes</i> , 2019, 10, 71.	1.0	29
143	Genome-wide identification of genes involved in carbon fixation in <i>Saccharina japonica</i> and responses of putative C4-related genes to bicarbonate concentration and light intensity. <i>Plant Physiology and Biochemistry</i> , 2019, 137, 75-83.	2.8	8
144	Genome-Wide Identification, Characterization and Expression Analysis of Xyloglucan Endotransglucosylase/Hydrolase Genes Family in Barley ( <i>Hordeum vulgare</i> ). <i>Molecules</i> , 2019, 24, 1935.	1.7	29
145	A de novo transcriptome assembly approach elucidates the dynamics of ovarian maturation in the swordfish ( <i>Xiphias gladius</i> ). <i>Scientific Reports</i> , 2019, 9, 7375.	1.6	12
146	Deletion of the Nonribosomal Peptide Synthetase Gene <i>nps1</i> in the Fungus <i>Clonostachys rosea</i> Attenuates Antagonism and Biocontrol of Plant Pathogenic <i>Fusarium</i> and Nematodes. <i>Phytopathology</i> , 2019, 109, 1698-1709.	1.1	25

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147	Intra- and interspecies comparison of EYS transcripts highlights its characteristics in the eye. <i>FASEB Journal</i> , 2019, 33, 9422-9433.	0.2	6
148	<i>Plasmodium berghei</i> serine/threonine protein phosphatase PP5 plays a critical role in male gamete fertility. <i>International Journal for Parasitology</i> , 2019, 49, 685-695.	1.3	13
149	Genetic basis of ruminant headgear and rapid antler regeneration. <i>Science</i> , 2019, 364, .	6.0	121
150	Genome-wide mining of respiratory burst homologs and its expression in response to biotic and abiotic stresses in <i>Triticum aestivum</i> . <i>Genes and Genomics</i> , 2019, 41, 1027-1043.	0.5	17
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1332	Genome-wide characterization of aldehyde dehydrogenase gene family members in groundnut ( <i>Arachis</i> ) Tj ETQq1 1.0.784314 rgBT /Overlock 10	1.7	4
1333	<i>Sorghum bicolor</i> <i>SbHSP110</i> has an elongated shape and is able of protecting against aggregation and replacing human <i>HSPH1</i> in refolding and disaggregation assays. <i>Biopolymers</i> , 2023, 114, .	1.2	0
1334	Evidence for Extensive Duplication and Subfunctionalization of FCRL6 in Armadillo ( <i>Dasypus</i> ) Tj ETQq1 1.0.784314 rgBT /Overlock 10	1.8	1
1336	Genome-Wide Identification, Characterization and Experimental Expression Analysis of CNGC Gene Family in <i>Gossypium</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4617.	1.8	0
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1338	Genome-Wide Identification and Expression Analysis of RCC1 Gene Family under Abiotic Stresses in Rice ( <i>Oryza sativa</i> L.). <i>Agronomy</i> , 2023, 13, 703.	1.3	1
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1342	Transposon-derived transcription factors across metazoans. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2
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1346	Identification of <i>Camellia oleifera</i> WRKY transcription factor genes and functional characterization of CoWRKY78. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
1347	Genome-wide identification and characterization of tomato <i>SlTFT6</i> ( <i>SlTFT6</i> ) genes and functional analysis of <i>SlTFT6</i> under heat stress. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	4
1348	Neofunctionalization of tandem duplicate genes encoding putative $\beta$ -arabinofuranosidases in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 0, , .	2.3	1
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1351	Modeling of Protein Complexes. <i>Methods in Molecular Biology</i> , 2023, , 349-371.	0.4	1
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1353	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	13
1354	Large-scale analysis of putative Euphorbiaceae R2R3-MYB transcription factors identifies a MYB involved in seed oil biosynthesis. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	5
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