

SMART: recent updates, new developments and status i

Nucleic Acids Research

43, D257-D260

DOI: [10.1093/nar/gku949](https://doi.org/10.1093/nar/gku949)

Citation Report

#	ARTICLE	IF	CITATIONS
1	“On the Power of Penetrating into Space”: The Telescopes of William Herschel. <i>Journal for the History of Astronomy</i> , 1976, 7, 75-108.	0.1	38
2	Prt199C Acts Together with Protamines and Safeguards Male Fertility in <i>Drosophila</i> . <i>Cell Reports</i> , 2015, 13, 2327-2335.	2.9	20
3	Molecular Cloning and Expression of a New Major Allergen, Anisakis simplex. <i>Shokuhin Eiseigaku Zasshi Journal of the Food Hygienic Society of Japan</i> , 2015, 56, 194-199.	0.1	19
4	Targeted silencing of the Aquaporin 2 gene of <i>Rhipicephalus (Boophilus) microplus</i> reduces tick fitness. <i>Parasites and Vectors</i> , 2015, 8, 618.	1.0	30
5	A bioinformatic survey of RNA-binding proteins in <i>Plasmodium</i> . <i>BMC Genomics</i> , 2015, 16, 890.	1.2	79
6	Experimental detection of short regulatory motifs in eukaryotic proteins: tips for good practice as well as for bad. <i>Cell Communication and Signaling</i> , 2015, 13, 42.	2.7	58
7	A NONOVARY-SPECIFIC VITELLOGENIN RECEPTOR FROM THE ORIENTAL FRUIT FLY, <i>Bactrocera dorsalis</i> (HENDEL). <i>Archives of Insect Biochemistry and Physiology</i> , 2015, 90, 169-180.	0.6	12
8	The <i>Psp</i> system of <i>Mycobacterium tuberculosis</i> integrates envelope stress-sensing and envelope-preserving functions. <i>Molecular Microbiology</i> , 2015, 97, 408-422.	1.2	42
9	Improving the consistency of domain annotation within the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	16
10	The Multifunctions of WD40 Proteins in Genome Integrity and Cell Cycle Progression. <i>Journal of Genomics</i> , 2015, 3, 40-50.	0.6	64
11	Identification and Characterization of 40 Isolated <i>Rehmannia glutinosa</i> MYB Family Genes and Their Expression Profiles in Response to Shading and Continuous Cropping. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15009-15030.	1.8	19
12	Structural Features of the ATP-Binding Cassette (ABC) Transporter ABCA3. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19631-19644.	1.8	17
13	Functional prediction of hypothetical proteins in human adenoviruses. <i>Bioinformatics</i> , 2015, 11, 466-473.	0.2	5
15	The Essential Role of Vitellogenin Receptor in Ovary Development and Vitellogenin Uptake in <i>Bactrocera dorsalis</i> (Hendel). <i>International Journal of Molecular Sciences</i> , 2015, 16, 18368-18383.	1.8	60
16	Cloning, Expression, and Characterization of a Thermophilic Endoglucanase, AcCel12B from <i>Acidothermus cellulolyticus</i> 11B. <i>International Journal of Molecular Sciences</i> , 2015, 16, 25080-25095.	1.8	22
17	Proteome profiling of heat, oxidative, and salt stress responses in <i>Thermococcus kodakarensis</i> KOD1. <i>Frontiers in Microbiology</i> , 2015, 6, 605.	1.5	40
18	Commentary: The absence of protein Y4yS affects negatively the abundance of T3SS Mesorhizobium loti secretin, RhcC2, in bacterial membranes. <i>Frontiers in Microbiology</i> , 2015, 6, 710.	1.5	2
19	Regulation of biofilm formation by BpfA, BpfD, and BpfG in <i>Shewanella oneidensis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 790.	1.5	42

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20	A Zinc-Dependent Protease AMZ-tk from a Thermophilic Archaeon is a New Member of the Archaemetzincin Protein Family. <i>Frontiers in Microbiology</i> , 2015, 6, 1380.	1.5	13
21	Computational Prediction of acyl-coA Binding Proteins Structure in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2015, 10, e0129650.	1.1	25
22	A Novel Matrix Protein Hic31 from the Prismatic Layer of <i>Hyriopsis cumingii</i> Displays a Collagen-Like Structure. <i>PLoS ONE</i> , 2015, 10, e0135123.	1.1	12
23	Evolution of a Novel Antiviral Immune-Signaling Interaction by Partial-Gene Duplication. <i>PLoS ONE</i> , 2015, 10, e0137276.	1.1	9
24	Transcriptator: An Automated Computational Pipeline to Annotate Assembled Reads and Identify Non Coding RNA. <i>PLoS ONE</i> , 2015, 10, e0140268.	1.1	14
25	Genome-Wide Identification, Evolutionary, and Expression Analyses of Histone H3 Variants in Plants. <i>BioMed Research International</i> , 2015, 2015, 1-7.	0.9	14
26	CDD: NCBI's conserved domain database. <i>Nucleic Acids Research</i> , 2015, 43, D222-D226.	6.5	3,022
27	The 2015 <i>Nucleic Acids Research</i> Database Issue and Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2015, 43, D1-D5.	6.5	79
28	<i>hecd-1</i> Modulates <i>Notch</i> Activity in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 353-359.	0.8	8
29	The Immunoglobulin-like Gene <i>spe-45</i> Acts during Fertilization in <i>Caenorhabditis elegans</i> like the Mouse <i>Izumo1</i> Gene. <i>Current Biology</i> , 2015, 25, 3225-3231.	1.8	37
30	Maize EMBRYO SAC family peptides interact differentially with pollen tubes and fungal cells. <i>Journal of Experimental Botany</i> , 2015, 66, 5205-5216.	2.4	16
31	The recombinant LIC10508 is a plasma fibronectin, plasminogen, fibrinogen and C4BP-binding protein of <i>Leptospira interrogans</i> . <i>Pathogens and Disease</i> , 2016, 74, ftv118.	0.8	11
32	KIAA0556 is a novel ciliary basal body component mutated in Joubert syndrome. <i>Genome Biology</i> , 2015, 16, 293.	3.8	56
33	CLPB Mutations Cause 3-Methylglutaconic Aciduria, Progressive Brain Atrophy, Intellectual Disability, Congenital Neutropenia, Cataracts, Movement Disorder. <i>American Journal of Human Genetics</i> , 2015, 96, 245-257.	2.6	111
34	Identification of a wheat polygalacturonase-inhibiting protein involved in <i>Fusarium</i> head blight resistance. <i>European Journal of Plant Pathology</i> , 2015, 141, 731-745.	0.8	17
35	FGF signaling repertoire of the indirect developing hemichordate <i>Ptychodera flava</i> . <i>Marine Genomics</i> , 2015, 24, 167-175.	0.4	6
36	Exome sequencing reveals a nonsense mutation in <i>TEX15</i> causing spermatogenic failure in a Turkish family. <i>Human Molecular Genetics</i> , 2015, 24, 5581-5588.	1.4	111
37	Databases for Microbiologists. <i>Journal of Bacteriology</i> , 2015, 197, 2458-2467.	1.0	39

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38	Complete genome sequence of a novel velarivirus infecting areca palm in China. Archives of Virology, 2015, 160, 2367-2370.	0.9	19
39	Transcriptome analysis reveals strong and complex antiviral response in a mollusc. Fish and Shellfish Immunology, 2015, 46, 131-144.	1.6	130
40	Identification and functional characterization of the TAB2 gene from Litopenaeus vannamei. Fish and Shellfish Immunology, 2015, 46, 206-216.	1.6	30
41	Defining the RNA-binding glycine-rich (RBC) gene superfamily: new insights into nomenclature, phylogeny, and evolutionary trends obtained by genome-wide comparative analysis of Arabidopsis, Chinese cabbage, rice and maize genomes. Molecular Genetics and Genomics, 2015, 290, 2279-2295.	1.0	16
42	A yeast two-hybrid approach for probing protein-protein interactions at the centrosome. Methods in Cell Biology, 2015, 129, 251-277.	0.5	25
43	Structural characterization and evolutionary analysis of fish-specific TLR27. Fish and Shellfish Immunology, 2015, 45, 940-945.	1.6	39
44	SELPHI: correlation-based identification of kinase-associated networks from global phospho-proteomics data sets. Nucleic Acids Research, 2015, 43, W276-W282.	6.5	24
45	Giving structure to the biofilm matrix: an overview of individual strategies and emerging common themes. FEMS Microbiology Reviews, 2015, 39, 649-669.	3.9	454
46	<i>Vibrio vulnificus</i> glycogen branching enzyme preferentially transfers very short chains: N1 domain determines the chain length transferred. FEBS Letters, 2015, 589, 1089-1094.	1.3	43
47	Discovery of novel <i>S. aureus</i> autolysins and molecular engineering to enhance bacteriolytic activity. Applied Microbiology and Biotechnology, 2015, 99, 6315-6326.	1.7	28
48	The single fgf receptor gene in the beetle <i>Tribolium castaneum</i> codes for two isoforms that integrate FGF8- and Branchless-dependent signals. Developmental Biology, 2015, 402, 264-275.	0.9	11
49	Identification and molecular characterization of a novel monopartite geminivirus associated with mulberry mosaic dwarf disease. Journal of General Virology, 2015, 96, 2421-2434.	1.3	67
50	Cancer/Testis Antigen PASD1 Silences the Circadian Clock. Molecular Cell, 2015, 58, 743-754.	4.5	51
51	Structural and evolutionary characteristics of fish-specific TLR19. Fish and Shellfish Immunology, 2015, 47, 271-279.	1.6	16
52	Characterization and manipulation of a DGAT2 from the diatom <i>Thalassiosira pseudonana</i> : Improved TAG accumulation without detriment to growth, and implications for chloroplast TAG accumulation. Algal Research, 2015, 12, 239-248.	2.4	41
53	Structural basis for amino-acid recognition and transmembrane signalling by tandem PerArntSim (tandem PAS) chemoreceptor sensory domains. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2127-2136.	2.5	56
54	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. Molecular and Cellular Proteomics, 2015, 14, 2833-2847.	2.5	100
55	The mysterious nature of bacterial surface (gliding) motility: A focal adhesion-based mechanism in <i>Mycococcus xanthus</i> . Seminars in Cell and Developmental Biology, 2015, 46, 143-154.	2.3	60

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56	Endothelial RhoGEFs: A systematic analysis of their expression profiles in VEGF-stimulated and tumor endothelial cells. <i>Vascular Pharmacology</i> , 2015, 74, 60-72.	1.0	43
57	Early Evolution of Vertebrate Mybs: An Integrative Perspective Combining Synteny, Phylogenetic, and Gene Expression Analyses. <i>Genome Biology and Evolution</i> , 2015, 7, 3009-3021.	1.1	19
58	De novo mutations in KIF1A cause progressive encephalopathy and brain atrophy. <i>Annals of Clinical and Translational Neurology</i> , 2015, 2, 623-635.	1.7	96
59	STAC—A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339.	2.0	17
60	Expression study of the hunchback ortholog in embryos of the onychophoran <i>Euperipatoides rowelli</i> . <i>Development Genes and Evolution</i> , 2015, 225, 207-219.	0.4	8
61	Genome-wide identification, expression profiling, and SSR marker development of the bZIP transcription factor family in <i>Medicago truncatula</i> . <i>Biochemical Systematics and Ecology</i> , 2015, 61, 218-228.	0.6	30
62	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1396-1410.	3.5	98
63	Membrane-Bound Selenoproteins. <i>Antioxidants and Redox Signaling</i> , 2015, 23, 795-813.	2.5	53
64	Establishment of Par-Polarized Cortical Domains via Phosphoregulated Membrane Motifs. <i>Developmental Cell</i> , 2015, 35, 199-210.	3.1	87
65	Diversity in protein domain superfamilies. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 40-49.	1.5	38
66	Proteomics of Schizophrenia. , 2016, , 195-209.		0
67	Insights into Ionizing-Radiation-Resistant Bacteria S-Layer Proteins and Nanobiotechnology for Bioremediation of Hazardous and Radioactive Waste. , 2016, , .		2
68	Scavenger Receptors. , 2016, , 371-380.		1
69	Bioinformatics analysis of the structural and evolutionary characteristics for toll-like receptor 15. <i>PeerJ</i> , 2016, 4, e2079.	0.9	13
70	Lymphangioliomyomatosis (LAM). , 2016, , 397-415.		0
71	Discovery of methylfarnesoate as the annelid brain hormone reveals an ancient role of sesquiterpenoids in reproduction. <i>ELife</i> , 2016, 5, .	2.8	34
72	A Genome-Wide Identification and Analysis of the Basic Helix-Loop-Helix Transcription Factors in Brown Planthopper, <i>Nilaparvata lugens</i> . <i>Genes</i> , 2016, 7, 100.	1.0	8
73	Expanding our Understanding of the Seaweed Holobiont: RNA Viruses of the Red Alga <i>Delisea pulchra</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1489.	1.5	49

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74	Integrated Information and Prospects for Gliding Mechanism of the Pathogenic Bacterium <i>Mycoplasma pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 960.	1.5	57
75	Novel Methyltransferase Recognition Motif Identified in <i>Chania multitudinisentens</i> RB-25T gen. nov., sp. nov.. <i>Frontiers in Microbiology</i> , 2016, 7, 1362.	1.5	9
76	Ultrastructure and Viral Metagenome of Bacteriophages from an Anaerobic Methane Oxidizing <i>Methylomirabilis</i> Bioreactor Enrichment Culture. <i>Frontiers in Microbiology</i> , 2016, 7, 1740.	1.5	13
77	Cloning of the GABAB Receptor Subunits B1 and B2 and their Expression in the Central Nervous System of the Adult Sea Lamprey. <i>Frontiers in Neuroanatomy</i> , 2016, 10, 118.	0.9	11
78	Functional Characterization of Soybean Glyma04g39610 as a Brassinosteroid Receptor Gene and Evolutionary Analysis of Soybean Brassinosteroid Receptors. <i>International Journal of Molecular Sciences</i> , 2016, 17, 897.	1.8	18
79	Genome-Wide Identification, Evolutionary Analysis, and Stress Responses of the GRAS Gene Family in Castor Beans. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1004.	1.8	65
80	Analysis of the Microprocessor in <i>Dictyostelium</i> : The Role of Rb dB, a dsRNA Binding Protein. <i>PLoS Genetics</i> , 2016, 12, e1006057.	1.5	16
81	Uncovering the Potential Pan Proteomes Encoded by Genomic Strand RNAs of Influenza A Viruses. <i>PLoS ONE</i> , 2016, 11, e0146936.	1.1	11
82	Glutathione S-Transferase Regulation in <i>Calanus finmarchicus</i> Feeding on the Toxic Dinoflagellate <i>Alexandrium fundyense</i> . <i>PLoS ONE</i> , 2016, 11, e0159563.	1.1	9
83	Cloning, Purification and Characterization of the Collagenase ColA Expressed by <i>Bacillus cereus</i> ATCC 14579. <i>PLoS ONE</i> , 2016, 11, e0162433.	1.1	17
84	Insights into the innate immunome of actiniarians using a comparative genomic approach. <i>BMC Genomics</i> , 2016, 17, 850.	1.2	42
85	Ternary WD40 Repeat-Containing Protein Complexes: Evolution, Composition and Roles in Plant Immunity. <i>Frontiers in Plant Science</i> , 2015, 6, 1108.	1.7	62
86	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 139.	1.7	81
87	VESPUCCI: Exploring Patterns of Gene Expression in Grapevine. <i>Frontiers in Plant Science</i> , 2016, 7, 633.	1.7	65
88	Geographically Distinct and Domain-Specific Sequence Variations in the Alleles of Rice Blast Resistance Gene <i>Pib</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 915.	1.7	12
89	Molecular Characterization of the 14-3-3 Gene Family in <i>Brachypodium distachyon</i> L. Reveals High Evolutionary Conservation and Diverse Responses to Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2016, 7, 1099.	1.7	43
90	Genome-Wide Investigation of Hsf Genes in Sesame Reveals Their Segmental Duplication Expansion and Their Active Role in Drought Stress Response. <i>Frontiers in Plant Science</i> , 2016, 7, 1522.	1.7	77
91	Comparative Analysis of DNA Methyltransferase Gene Family in Fungi: A Focus on Basidiomycota. <i>Frontiers in Plant Science</i> , 2016, 7, 1556.	1.7	12

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92	Ca ²⁺ /Cation Antiporters (CaCA): Identification, Characterization and Expression Profiling in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1775.	1.7	43
93	Genome-Wide Analysis of Soybean JmjC Domain-Containing Proteins Suggests Evolutionary Conservation Following Whole-Genome Duplication. <i>Frontiers in Plant Science</i> , 2016, 7, 1800.	1.7	51
94	<sc>WD</sc> Repeat-Containing Protein 73, A Novel Gene Correlated with Gonad Development in Large Yellow Croaker, <i>Larimichthys crocea</i>. <i>Journal of the World Aquaculture Society</i> , 2016, 47, 268-276.	1.2	3
95	Microform holoprosencephaly with bilateral congenital elbow dislocation; increasing the phenotypic spectrum of Steinfeld syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 754-759.	0.7	6
96	Further insight into BRUTUS domain composition and functionality. <i>Plant Signaling and Behavior</i> , 2016, 11, e1204508.	1.2	29
97	Bclqg1, a fungal IQGAP homolog, interacts with NADPH oxidase, MAP kinase and calcium signaling proteins and regulates virulence and development in <sc><i>B</i></sc> <i>otrytis cinerea</i>. <i>Molecular Microbiology</i> , 2016, 101, 281-298.	1.2	29
98	De novo annotation of the immune-enriched transcriptome provides insights into immune system genes of Chinese sturgeon (<i>Acipenser sinensis</i>). <i>Fish and Shellfish Immunology</i> , 2016, 55, 699-716.	1.6	40
99	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. <i>Expert Review of Proteomics</i> , 2016, 13, 757-769.	1.3	67
100	Evolution of the leucine-rich repeat receptor-like protein kinase gene family: Ancestral copy number and functional divergence of <i>BAM1</i> and <i>BAM2</i> in Brassicaceae. <i>Journal of Systematics and Evolution</i> , 2016, 54, 204-218.	1.6	7
101	Comparative and Transcriptome Analyses Uncover Key Aspects of Coding- and Long Noncoding RNAs in Flatworm Mitochondrial Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1191-1200.	0.8	30
102	Marriage shrines and worms impacting our understanding of mammalian fertilization. <i>Worm</i> , 2016, 5, e1184389.	1.0	4
103	Genome-wide identification of soybean WRKY transcription factors in response to salt stress. <i>SpringerPlus</i> , 2016, 5, 920.	1.2	76
104	Identification and characterization of histone lysine methylation modifiers in <i>Fragaria vesca</i> . <i>Scientific Reports</i> , 2016, 6, 23581.	1.6	28
105	Draft genome sequence of <i>Streptomyces</i> sp. TP-A0867, an alchivemycin producer. <i>Standards in Genomic Sciences</i> , 2016, 11, 85.	1.5	10
106	De-novo protein function prediction using DNA binding and RNA binding proteins as a test case. <i>Nature Communications</i> , 2016, 7, 13424.	5.8	22
107	A centrosome interactome provides insight into organelle assembly and reveals a non-duplication role for Plk4. <i>Nature Communications</i> , 2016, 7, 12476.	5.8	53
108	Genome-wide identification, phylogeny, and expression analysis of pectin methylesterases reveal their major role in cotton fiber development. <i>BMC Genomics</i> , 2016, 17, 1000.	1.2	42
109	The cell adhesion molecule Fasciclin2 regulates brush border length and organization in <i>Drosophila</i> renal tubules. <i>Nature Communications</i> , 2016, 7, 11266.	5.8	29

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110	Crystal structure of MytiLec, a galactose-binding lectin from the mussel <i>Mytilus galloprovincialis</i> with cytotoxicity against certain cancer cell types. <i>Scientific Reports</i> , 2016, 6, 28344.	1.6	39
111	A Preliminary Molecular and Phylogenetic Analysis of the Genome of a Novel Endogenous Retrovirus in the Sea Slug <i>Elysia chlorotica</i> . <i>Biological Bulletin</i> , 2016, 231, 236-244.	0.7	5
112	Ectodomain Architecture Affects Sequence and Functional Evolution of Vertebrate Toll-like Receptors. <i>Scientific Reports</i> , 2016, 6, 26705.	1.6	37
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114	Evolutionary and developmental analysis reveals KANK genes were co-opted for vertebrate vascular development. <i>Scientific Reports</i> , 2016, 6, 27816.	1.6	18
115	Identification and characterization of toll-like receptors (TLRs) in the Chinese tree shrew (<i>Tupaia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0 22	1.0	22
116	Recombinant preparation and functional studies of EspI ATP binding domain from <i>Mycobacterium tuberculosis</i> . <i>Protein Expression and Purification</i> , 2016, 123, 51-59.	0.6	1
117	Purification and characterization of thermostable serine proteases encoded by the genes <i>ttha0099</i> and <i>ttha01320</i> from <i>Thermus thermophilus</i> HB8. <i>Extremophiles</i> , 2016, 20, 493-502.	0.9	3
118	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , 2016, 30, 3-13.	0.4	164
119	A structured interdomain linker directs self-polymerization of human uromodulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1552-1557.	3.3	85
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122	In silico characterization of the citrate synthase family in <i>Mycobacterium tuberculosis</i> / <i>Mycobacterium tuberculosis</i> sitrat sentaz ailesinin in silico karakterizasyonu. <i>Turkish Journal of Biochemistry</i> , 2016, 41, .	0.3	0
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124	Amino Acid Substitutions of CrrB Responsible for Resistance to Colistin through CrrC in <i>Klebsiella pneumoniae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3709-3716.	1.4	112
125	In silico Identification and Characterization of Protein-Ligand Binding Sites. <i>Methods in Molecular Biology</i> , 2016, 1414, 1-21.	0.4	7
126	Characterization of a type I pullulanase from <i>Anoxybacillus</i> sp. SK3-4 reveals an unusual substrate hydrolysis. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6291-6307.	1.7	19
127	Identification, origin and evidence for retained functionality of two β paralogues in <i>Megalobrama amblycephala</i> . <i>Developmental and Comparative Immunology</i> , 2016, 62, 89-96.	1.0	10

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128	RNA helicase SACY-1 is required for longevity caused by various genetic perturbations in <i>Caenorhabditis elegans</i> . <i>Cell Cycle</i> , 2016, 15, 1821-1829.	1.3	11
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130	Evaluation of two novel leptospiral proteins for their interaction with human host components. <i>Pathogens and Disease</i> , 2016, 74, ftw040.	0.8	19
131	Characterization of two novel gadd45a genes in hybrid tilapia and their responses to the infection of <i>Streptococcus agalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2016, 54, 276-281.	1.6	14
132	Deep sequencing of banana bract mosaic virus from flowering ginger (<i>Alpinia purpurata</i>) and development of an immunocapture RT-LAMP detection assay. <i>Archives of Virology</i> , 2016, 161, 1783-1795.	0.9	10
133	Sperm <i>Bindin</i> Divergence under Sexual Selection and Concerted Evolution in Sea Stars. <i>Molecular Biology and Evolution</i> , 2016, 33, 1988-2001.	3.5	11
134	Homology-Based Annotation of Large Protein Datasets. <i>Methods in Molecular Biology</i> , 2016, 1415, 153-176.	0.4	0
135	PilZ Domain Protein FlgZ Mediates Cyclic Di-GMP-Dependent Swarming Motility Control in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1837-1846.	1.0	96
136	Genome-wide identification and evolutionary analysis of leucine-rich repeat receptor-like protein kinase genes in soybean. <i>BMC Plant Biology</i> , 2016, 16, 58.	1.6	73
137	Genome-wide identification and analysis of JHBP-domain family members in the silkworm <i>Bombyx mori</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 2159-2171.	1.0	13
138	Structure of the C-Terminal Helical Repeat Domain of Eukaryotic Elongation Factor 2 Kinase. <i>Biochemistry</i> , 2016, 55, 5377-5386.	1.2	4
139	Roles of Tetratricopeptide Repeat Proteins in Biogenesis of the Photosynthetic Apparatus. <i>International Review of Cell and Molecular Biology</i> , 2016, 324, 187-227.	1.6	40
140	Preparation, Biochemical Analysis, and Structure Determination of SET Domain Histone Methyltransferases. <i>Methods in Enzymology</i> , 2016, 573, 209-240.	0.4	5
141	Characterization and transcriptional profiles of <i>Engraulis encrasicolus</i> GnRH forms. <i>Reproduction</i> , 2016, 152, 727-739.	1.1	5
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563	Nuclear Pore Complex Components in the Malaria Parasite <i>Plasmodium berghei</i> . <i>Scientific Reports</i> , 2018, 8, 11249.	1.6	19
564	Genome-wide Characterization of <i>Brassica rapa</i> Genes Encoding Serine/arginine-rich Proteins: Expression and Alternative Splicing Events by Abiotic Stresses. <i>Journal of Plant Biology</i> , 2018, 61, 198-209.	0.9	14
565	A c-di-GMP-Modulating Protein Regulates Swimming Motility of <i>Burkholderia cenocepacia</i> in Response to Arginine and Glutamate. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 56.	1.8	16
566	Functional and Structural Diversity of Acyl-coA Binding Proteins in Oil Crops. <i>Frontiers in Genetics</i> , 2018, 9, 182.	1.1	14
567	Production of Calcium-Binding Proteins in <i>Crassostrea virginica</i> in Response to Increased Environmental CO ₂ Concentration. <i>Frontiers in Marine Science</i> , 2018, 5, .	1.2	14
568	Tomato Apical Leaf Curl Virus: A Novel, Monopartite Geminivirus Detected in Tomatoes in Argentina. <i>Frontiers in Microbiology</i> , 2017, 8, 2665.	1.5	43
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572	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
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574	FerA is a Membrane-Associating Four-Helix Bundle Domain in the Ferlin Family of Membrane-Fusion Proteins. <i>Scientific Reports</i> , 2018, 8, 10949.	1.6	19
575	ChHUB2, a ubiquitin ligase, is involved in cotton fiber development via the ubiquitin-26S proteasome pathway. <i>Journal of Experimental Botany</i> , 2018, 69, 5059-5075.	2.4	29
576	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018, 17, 43.	1.9	19
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1166	Evolutionary Significance of NHX Family and NHX1 in Salinity Stress Adaptation in the Genus <i>Oryza</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 2092.	1.8	19
1167	Genome-wide identification of the SWEET gene family in <i>Phaseolus vulgaris</i> L. and their patterns of expression under abiotic stress. <i>Journal of Plant Interactions</i> , 2022, 17, 390-403.	1.0	8
1168	Molecular Characterization, Evolutionary Analysis, and Expression Profiling of BOR Genes in Important Cereals. <i>Plants</i> , 2022, 11, 911.	1.6	14
1169	Hybrid Histidine Kinase Wela of <i>Sphingomonas</i> sp. WG Contributes to WL Gum Biosynthesis and Motility. <i>Frontiers in Microbiology</i> , 2022, 13, 792315.	1.5	1
1170	Increase in alpha-linolenic acid content by simultaneous expression of fatty acid metabolism genes in Sesame (<i>Sesamum indicum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 559-572.	1.4	5
1171	Genome-Wide Analysis of the GW2-Like Genes in <i>Gossypium</i> and Functional Characterization of the Seed Size Effect of GhGW2-2D. <i>Frontiers in Plant Science</i> , 2022, 13, 860922.	1.7	4
1172	Dynamic profiles of DNA methylation and the interaction with histone acetylation during fiber cell initiation of <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	2
1173	Cerato-platanin protein 1 is not critical for <i>Fusarium graminearum</i> growth and aggressiveness, but its overexpression provides an edge to <i>Fusarium</i> head blight in wheat. <i>Canadian Journal of Plant Pathology</i> , 2022, 44, 577-595.	0.8	4
1174	Molecular Epidemiology and Colistin-Resistant Mechanism of mcr-Positive and mcr-Negative <i>Escherichia coli</i> Isolated From Animal in Sichuan Province, China. <i>Frontiers in Microbiology</i> , 2022, 13, 818548.	1.5	9
1175	In-Silico Functional Annotation of <i>Plasmodium falciparum</i> Hypothetical Proteins to Identify Novel Drug Targets. <i>Frontiers in Genetics</i> , 2022, 13, 821516.	1.1	3
1177	Both Two CtACO3 Transcripts Promoting the Accumulation of the Flavonoid Profiles in Overexpressed Transgenic Safflower. <i>Frontiers in Plant Science</i> , 2022, 13, 833811.	1.7	3
1178	Aberrant RNA Splicing Is a Primary Link between Genetic Variation and Pancreatic Cancer Risk. <i>Cancer Research</i> , 2022, 82, 2084-2096.	0.4	14
1179	The WRKY transcription factor family in cowpea: Genomic characterization and transcriptomic profiling under root dehydration. <i>Gene</i> , 2022, 823, 146377.	1.0	5
1180	A novel molluscan TLR molecule engaged in inflammatory response through MyD88 adapter recruitment. <i>Developmental and Comparative Immunology</i> , 2022, 131, 104373.	1.0	6
1181	Silencing of GhKEA4 and GhKEA12 Revealed Their Potential Functions Under Salt and Potassium Stresses in Upland Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 789775.	1.7	10
1182	High Molecular Weight Kininogen: A Review of the Structural Literature. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13370.	1.8	15
1183	New insights into the evolution of SPX gene family from algae to legumes; a focus on soybean. <i>BMC Genomics</i> , 2021, 22, 915.	1.2	6

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1184	Phylogenetic Analysis with Prediction of Cofactor or Ligand Binding for <i>Pseudomonas aeruginosa</i> PAS and Cache Domains. <i>Microbiology Spectrum</i> , 2021, 9, e0102621.	1.2	4
1185	A Novel Agarase, Gaa16B, Isolated from the Marine Bacterium <i>Gilvimirinus agarilyticus</i> JEA5, and the Moisturizing Effect of Its Partial Hydrolysis Products. <i>Marine Drugs</i> , 2022, 20, 2.	2.2	5
1186	QTL and candidate gene identification of the node of the first fruiting branch (NFFB) by QTL-seq in upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2021, 22, 882.	1.2	11
1187	NLR diversity and candidate fusiform rust resistance genes in loblolly pine. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
1188	NHX Gene Family in <i>Camellia sinensis</i> : In-silico Genome-Wide Identification, Expression Profiles, and Regulatory Network Analysis. <i>Frontiers in Plant Science</i> , 2021, 12, 777884.	1.7	8
1189	BrCNGC gene family in field mustard: genome-wide identification, characterization, comparative synteny, evolution and expression profiling. <i>Scientific Reports</i> , 2021, 11, 24203.	1.6	3
1190	Functional Characterization of Cotton C-Repeat Binding Factor Genes Reveal Their Potential Role in Cold Stress Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 766130.	1.7	10
1191	Gene Sequence Clustering Based on the Profile Hidden Markov Model with Differential Identifiability. <i>Security and Communication Networks</i> , 2021, 2021, 1-9.	1.0	0
1192	Exonic splicing code and protein binding sites for calcium. <i>Nucleic Acids Research</i> , 2022, 50, 5493-5512.	6.5	3
1193	Genome-wide identification and characterization of terpene synthase genes in <i>Gossypium hirsutum</i> . <i>Gene</i> , 2022, 828, 146462.	1.0	5
1377	Genomes of leafy and leafless <i>Platanthera</i> orchids illuminate the evolution of mycoheterotrophy. <i>Nature Plants</i> , 2022, 8, 373-388.	4.7	36
1378	Genome-wide Characterization of the JmjC Domain-Containing Histone Demethylase Gene Family Reveals GhJM24 and GhJM49 Involving in Somatic Embryogenesis Process in Cotton. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 888983.	1.6	0
1379	Expression and Role of Vitellogenin Genes in Ovarian Development of <i>Zeugodacus cucurbitae</i> . <i>Insects</i> , 2022, 13, 452.	1.0	5
1380	Identification, diversity and domain structure analysis of mucin and mucin-like genes in sea anemone <i>Actinia tenebrosa</i> . <i>PeerJ</i> , 2022, 10, e13292.	0.9	2
1381	The Alternative Sigma Factor SigL Influences <i>Clostridioides difficile</i> Toxin Production, Sporulation, and Cell Surface Properties. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
1382	Interferon-Induced Protein 6-16 (IFI6-16) from <i>Litopenaeus vannamei</i> Regulate Antiviral Immunity via Apoptosis-Related Genes. <i>Viruses</i> , 2022, 14, 1062.	1.5	5
1383	The Dual Functions of a Bracovirus C-Type Lectin in Caterpillar Immune Response Manipulation. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	3
1385	P Starvation in Roses Leads to Strongly Genotype-Dependent Induction of P-Transporter Genes during Black Spot Leaf Disease. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 549.	1.5	0

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1387	Identification of ACC Synthetase Genes in <i>Saccharum</i> and their Expression Profiles During Plant Growth and in Response to Low-nitrogen Stress. <i>Tropical Plant Biology</i> , 2022, 15, 197-210.	1.0	2
1388	Expansion and Diversification of the 14-3-3 Gene Family in <i>Camellia sinensis</i> . <i>Journal of Molecular Evolution</i> , 2022, 90, 296-306.	0.8	7
1389	Genome-wide analysis of cowpea NAC transcription factor family elucidating the genetic & molecular relationships that interface stress and growth regulatory signals. <i>Plant Gene</i> , 2022, 31, 100363.	1.4	2
1391	Genome-Wide Identification and Characterization of the Abiotic-Stress-Responsive LACS Gene Family in Soybean (<i>Glycine max</i>). <i>Agronomy</i> , 2022, 12, 1496.	1.3	3
1392	Insight into the Roles of Proline-Rich Extensin-like Receptor Protein Kinases of Bread Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	1.1	5
1393	Megaviruses contain various genes encoding for eukaryotic vesicle trafficking factors. <i>Traffic</i> , 0, , .	1.3	5
1394	Mapping immunogenic epitopes of an adhesin-like protein from <i>Methanobrevibacter ruminantium</i> M1 and comparison of empirical data with in silico prediction methods. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
1395	Noncatalytic Domains in DNA Glycosylases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7286.	1.8	1
1396	The <i>Vibrio vulnificus</i> stressosome is an oxygen-sensor involved in regulating iron metabolism. <i>Communications Biology</i> , 2022, 5, .	2.0	6
1397	Evolution of Epidermal Growth Factor (EGF)-like and Zona Pellucida Domains Containing Shell Matrix Proteins in Mollusks. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
1398	In silico analyses of leptin and leptin receptor of spotted snakehead <i>Channa punctata</i> . <i>PLoS ONE</i> , 2022, 17, e0270881.	1.1	2
1399	The wheat (<i>Triticum aestivum</i> L.) MADS-box transcription factor <i>TaMADS32</i> plays a role in response to abiotic stresses. <i>Biotechnology and Biotechnological Equipment</i> , 2022, 36, 451-461.	0.5	3
1400	Genome-wide identification of the LBD transcription factor genes in common bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	1.0	6
1401	Genome-wide identification and expression analysis of mitogen-activated protein kinase (<sc>MAPK</sc>) genes in response to salinity stress in channel catfish (<i>Ictalurus punctatus</i>). <i>Journal of Fish Biology</i> , 2022, 101, 972-984.	0.7	3
1402	Genome-Wide Identification of Glutathione S-Transferase and Expression Analysis in Response to Anthocyanin Transport in the Flesh of the New Teinturier Grape Germplasm 'Zhongshan-HongYu'™. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7717.	1.8	4
1403	EF-hand domain-containing proteins in <i>Triticum aestivum</i> : Insight into their roles in stress response and signalling. <i>South African Journal of Botany</i> , 2022, 149, 663-681.	1.2	9
1404	Genome-wide analysis and identification of the PEBP genes of <i>Brassica juncea</i> var. <i>Tumida</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	1

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1405	Genome-wide identification and comparative analysis of MATE gene family in Cucurbitaceae species and their regulatory role in melon (<i>Cucumis melo</i>) under salt stress. <i>Horticulture Environment and Biotechnology</i> , 0, , .	0.7	9
1406	Characterization of Histone H3 Gene Family Reveals That GmHH3-3 is Associated With Higher Seed Weight in <i>Glycine max</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
1407	Identification of sugar transporter (SWEET) genes involved in pomegranate seed coat sugar accumulation. <i>3 Biotech</i> , 2022, 12, .	1.1	2
1408	Wheat heat shock factor TaHsfA2d contributes to plant responses to phosphate deficiency. <i>Plant Physiology and Biochemistry</i> , 2022, 185, 178-187.	2.8	7
1409	Expression of tyrosinase-like protein genes and their functional analysis in melanin synthesis of Pacific oyster (<i>Crassostrea gigas</i>). <i>Gene</i> , 2022, 840, 146742.	1.0	7
1410	Conformational Change of the Hairpin-like-structured Robo2 Ectodomain Allows NELL1/2 Binding. <i>Journal of Molecular Biology</i> , 2022, 434, 167777.	2.0	0
1411	Plant <i>N</i> -glycan breakdown by human gut <i>Bacteroides</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	6
1412	The common bean (<i>Phaseolus vulgaris</i>) SULTR gene family: genome-wide identification, phylogeny, evolutionary expansion and expression patterns. <i>Biotechnology and Biotechnological Equipment</i> , 2022, 36, 724-736.	0.5	2
1413	Genome-Wide Identification and Expression Patterns of the SWEET Gene Family in <i>Bletilla striata</i> and its Responses to Low Temperature and Oxidative Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10057.	1.8	5
1414	Prediction of RNA editing sites and genome-wide characterization of PERK gene family in maize (<i>Zea mays</i>). <i>Journal of Molecular Biology</i> , 2022, 434, 167777.	1.6	0
1415	Bioinformatics Resources, Tools, and Strategies in Designing Therapeutic Proteins. , 2022, , 91-123.		0
1416	Characterization of <i>CsWRKY29</i> and <i>CsWRKY37</i> ; transcription factors and their functional roles in cold tolerance of tea plant. <i>Beverage Plant Research</i> , 2022, 2, 1-13.	0.6	6
1417	Genome-wide identification of the trehalose-6-phosphate synthase gene family in sweet orange (<i>Citrus sinensis</i>) and expression analysis in response to phytohormones and abiotic stresses. <i>PeerJ</i> , 0, 10, e13934.	0.9	3
1418	Multiple roles of <i>TaCPP</i> family genes during growth and stress treatment. <i>Crop Science</i> , 0, , .	0.8	0
1419	TrpR-like protein PXO_00831, regulated by the sigma factor RpoD, is involved in motility, oxidative stress tolerance, and virulence in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	1.1	1
1420	Systematic analysis of the pectin methylesterase gene family in <i>Nicotiana tabacum</i> and reveal their multiple roles in plant development and abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1421	Chemosensory protein 4 is required for <i>Bradysia odoriphaga</i> to be olfactory attracted to sulfur compounds released from Chinese chives. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	1
1422	CRISPR/Cas9-mediated silencing of an egg-specific gene <i>Nllet1</i> results in hatch failure in the brown planthopper. <i>Pest Management Science</i> , 2023, 79, 415-427.	1.7	5

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1424	Targeting <i>Echinococcus multilocularis</i> PIM kinase for improving anti-parasitic chemotherapy. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010483.	1.3	3
1425	Identification of epigenetic histone modifications and analysis of histone lysine methyltransferases in <i>Alexandrium pacificum</i> . <i>Harmful Algae</i> , 2022, 119, 102323.	2.2	5
1426	Propagation, detection and correction of errors using the sequence database network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
1427	Genome-wide identification of biotin carboxyl carrier subunits of acetyl-CoA carboxylase in <i>Brassica</i> and their role in stress tolerance in oilseed <i>Brassica napus</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	9
1428	Identification and Investigation of the Genetic Variations and Candidate Genes Responsible for Seed Weight via GWAS in Paper Mulberry. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12520.	1.8	2
1429	Identification, characterization and nutritional regulation of fatty acid-binding protein (<i>fabp</i>) genes by vegetable oils in European seabass (<i>Dicentrarchus labrax</i>) reared in low water temperatures. <i>Aquaculture Research</i> , 0, , .	0.9	2
1430	Metabolome and transcriptome analysis of terpene synthase genes and their putative role in floral aroma production in <i>Litchi chinensis</i> . <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	9
1431	Genome and transcriptome-wide study of carbamoyltransferase genes in major fleshy fruits: A multi-omics study of evolution and functional significance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
1432	Ammonia nitrogen stress increases susceptibility to bacterial infection via blocking IL-1R-mediated antimicrobial peptides expression in shrimp. <i>Aquaculture</i> , 2023, 563, 738934.	1.7	5
1433	Orthologous genes Pm12 and Pm21 from two wild relatives of wheat show evolutionary conservation but divergent powdery mildew resistance. <i>Plant Communications</i> , 2023, 4, 100472.	3.6	15
1434	Identification of CAMTA Gene Family in <i>Heimia myrtifolia</i> and Expression Analysis under Drought Stress. <i>Plants</i> , 2022, 11, 3031.	1.6	1
1435	Bioinformatic analysis of WxL domain proteins. <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103526.	1.8	2
1436	OSCA Genes in Bread Wheat: Molecular Characterization, Expression Profiling, and Interaction Analyses Indicated Their Diverse Roles during Development and Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14867.	1.8	15
1437	Genome-Wide Identification and Expression Analysis of Fatty Acid Desaturase (FAD) Genes in <i>Camelina sativa</i> (L.) Crantz. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14550.	1.8	1
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1439	Evolution and functional analysis of the GRAS family genes in six Rosaceae species. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
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1441	Identification of WRKYs using in silico tools for unraveling the modulation during abiotic stress response in Tef [<i>Eragrostis tef</i> (Zucc.) Trotter] a super grain. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0
1442	Comprehensive Proteomic Analysis of <i>Brucella melitensis</i> ATCC23457 Strain Reveals Metabolic Adaptations in Response to Nutrient Stress. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
1443	The localization of Toll and Imd pathway and complement system components and their response to <i>Vibrio</i> infection in the nemertean <i>Lineus ruber</i> . <i>BMC Biology</i> , 2023, 21, .	1.7	2
1444	The effects of ERN1 on gene expression during early rhizobial infection in <i>Lotus japonicus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
1445	Genome-Wide Identification and Expression Analysis of Response Regulators Family Genes in Chinese Hickory (<i>Carya cathayensis</i>) Suggests Their Potential Roles during Grafting. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 5099-5115.	2.8	2
1446	Fatty acid-binding protein genes in gilthead seabream: Molecular cloning and nutritional regulation under low water temperatures. <i>Journal of Fish Biology</i> , 0, , .	0.7	0
1447	Wide-Range Portrayal of AP2/ERF Transcription Factor Family in Maize (<i>Zea mays</i> L.) Development and Stress Responses. <i>Genes</i> , 2023, 14, 194.	1.0	12
1448	An AhR-Caspase Axis Mediated Antiviral Apoptosis in an Arthropod. <i>Journal of Immunology</i> , 2022, 209, 2022-2032.	0.4	3
1449	Cas9/gRNA-Mediated Mutations in PtrFLA40 and PtrFLA45 Reveal Redundant Roles in Modulating Wood Cell Size and SCW Synthesis in Poplar. <i>International Journal of Molecular Sciences</i> , 2023, 24, 427.	1.8	5
1450	Phylogenetic, Structural and Functional Evolution of the LHC Gene Family in Plant Species. <i>International Journal of Molecular Sciences</i> , 2023, 24, 488.	1.8	2
1451	Identification of the BcLEA Gene Family and Functional Analysis of the BcLEA73 Gene in Wucai (<i>Brassica</i>) Tj ETQq0 0.0 rgBT /Qverlock 10	1.0	2
1452	Oat AsDA1-2D enhances heat stress tolerance and negatively regulates seed-storage globulin. <i>Journal of Plant Physiology</i> , 2023, 284, 153981.	1.6	2
1454	Genome-wide analysis of Catalase gene family reveal insights into abiotic stress response mechanism in <i>Brassica juncea</i> and <i>B. rapa</i> . <i>Plant Science</i> , 2023, 330, 111620.	1.7	7
1455	ChGTG1 enhances cold stress tolerance by improving sensitivity to ABA in cotton and <i>Arabidopsis</i> . <i>Environmental and Experimental Botany</i> , 2023, 208, 105256.	2.0	2
1456	The Bcl-2-associated athanogene gene family in tobacco (<i>Nicotiana tabacum</i>) and the function of NtBAG5 in leaf senescence. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
1457	The genome of <i>Magnolia hypoleuca</i> provides a new insight into cold tolerance and the evolutionary position of magnoliids. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
1458	Identification, Characterization and Functional Analysis of Fibroblast Growth Factors in Black Rockfish (<i>Sebastes schlegelii</i>). <i>International Journal of Molecular Sciences</i> , 2023, 24, 3626.	1.8	2
1459	Uncovering the involvement of DoDELLA1-interacting proteins in development by characterizing the DoDELLA gene family in <i>Dendrobium officinale</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1

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1461	Life Continuously Acquires New Information in Dialogue with the Environment. , 2023, , 159-170.		0
1462	The MksG nuclease is the executing part of the bacterial plasmid defense system MksBEFG. <i>Nucleic Acids Research</i> , 2023, 51, 3288-3306.	6.5	8
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1464	Genome-wide characterization of trichome birefringence-like genes provides insights into fiber yield improvement. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
1465	Genome-wide identification of the TIFY family reveals JAZ subfamily function in response to hormone treatment in <i>Betula platyphylla</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
1466	Evolution of tetraspanin antigens in the zoonotic Asian blood fluke <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2023, 16, .	1.0	0
1468	Exploration of Piezo Channels in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Agriculture (Switzerland)</i> , 2023, 13, 783.	1.4	6
1469	Genome-wide identification of the soybean cytokinin oxidase/dehydrogenase gene family and its diverse roles in response to multiple abiotic stress. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	8