

# HMMER web server: interactive sequence similarity search

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Finding Protein and Nucleotide Similarities with FASTA. <i>Current Protocols in Bioinformatics</i> , 2003, 4, Unit3.9.	25.8	55
4	Computational approaches to selecting and optimising targets for structural biology. <i>Methods</i> , 2011, 55, 3-11.	1.9	7
5	Complete Genome Sequence of the Soybean Symbiont <i>Bradyrhizobium japonicum</i> Strain USDA6T. <i>Genes</i> , 2011, 2, 763-787.	1.0	108
6	Evolution and Quantitative Comparison of Genome-Wide Protein Domain Distributions. <i>Genes</i> , 2011, 2, 912-924.	1.0	9
7	Context-dependent conservation of DNA methyltransferases in bacteria. <i>Nucleic Acids Research</i> , 2012, 40, 7066-7073.	6.5	60
8	Side-chain rotamer changes upon ligand binding: common, crucial, correlate with entropy and rearrange hydrogen bonding. <i>Bioinformatics</i> , 2012, 28, i423-i430.	1.8	61
9	Characterization and Prediction of Protein Phosphorylation Hotspots in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 207.	1.7	22
10	Whole Genome Analysis of <i>Leptospira icterohaemolyticum</i> Provides Insight into Leptospiral Evolution and Pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1853.	1.3	60
11	A common ancestry for BAP1 and Uch37 regulators. <i>Bioinformatics</i> , 2012, 28, 1953-1956.	1.8	48
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22	BIPS: BIANA Interolog Prediction Server. A tool for proteinâ€“protein interaction inference. <i>Nucleic Acids Research</i> , 2012, 40, W147-W151.	6.5	57
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24	BioJava: an open-source framework for bioinformatics in 2012. <i>Bioinformatics</i> , 2012, 28, 2693-2695.	1.8	160
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78	Variant surface antigens of malaria parasites: functional and evolutionary insights from comparative gene family classification and analysis. <i>BMC Genomics</i> , 2013, 14, 427.	1.2	65
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1482	<i>Labeledella phragmitis</i> sp. nov. and <i>Labeledella populi</i> sp. nov., two endophytic actinobacteria isolated from plants in the Taklamakan Desert and emended description of the genus <i>Labeledella</i> . <i>Systematic and Applied Microbiology</i> , 2019, 42, 126004.	1.2	20
1483	Complete chloroplast genome of <i>Prunus canescens</i> : an endemic shrub in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2381-2382.	0.2	1
1484	The complete chloroplast genome of <i>Vaccinium duclouxii</i> , an endemic species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2215-2216.	0.2	5
1485	The complete chloroplast genome of <i>Vaccinium fragile</i> (Vacciniaceae), a shrub endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2310-2311.	0.2	4
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1487	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019, 20, 663.	1.2	19
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1506	Genome-Wide Identification and Characterization of JAZ Protein Family in Two <i>Petunia</i> Progenitors. <i>Plants</i> , 2019, 8, 203.	1.6	8
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1508	Microbial life cycles link global modularity in regulation to mosaic evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 1184-1196.	3.4	18
1509	Switching of INCENP paralogs controls transitions in mitotic chromosomal passenger complex functions. <i>Cell Cycle</i> , 2019, 18, 2006-2025.	1.3	6
1510	Functional characterization of Gh_A08G1120 (GH3.5) gene reveal their significant role in enhancing drought and salt stress tolerance in cotton. <i>BMC Genetics</i> , 2019, 20, 62.	2.7	39

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1543	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	4.9	65
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1548	Genome-wide analysis of cotton C2H2-zinc finger transcription factor family and their expression analysis during fiber development. <i>BMC Plant Biology</i> , 2019, 19, 400.	1.6	27
1549	High-Throughput RNA Sequencing Reveals NDUFC2-AS lncRNA Promotes Adipogenic Differentiation in Chinese Buffalo ( <i>Bubalus bubalis</i> L). <i>Genes</i> , 2019, 10, 689.	1.0	32
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1566	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
1567	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
1568	NBS-Encoding Genes in <i>Brassica napus</i> Evolved Rapidly After Allopolyploidization and Co-localize With Known Disease Resistance Loci. <i>Frontiers in Plant Science</i> , 2019, 10, 26.	1.7	27
1569	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
1570	Comparative analysis of two sister <i>Erythrophleum</i> species (Leguminosae) reveal contrasting transcriptome-wide responses to early drought stress. <i>Gene</i> , 2019, 694, 50-62.	1.0	2
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1574	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
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1581	Diversity of circular RNAs and RNA ligases in archaeal cells. <i>Biochimie</i> , 2019, 164, 37-44.	1.3	6
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1584	Genomic analysis and lactose transporter expression in <i>Kluyveromyces marxianus</i> CCT 7735. <i>Fungal Biology</i> , 2019, 123, 687-697.	1.1	4
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1586	Mosaic origin of the eukaryotic kinetochore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12873-12882.	3.3	76
1587	The Transcriptome Landscape of Walnut Interspecies Hybrid ( <i>Juglans hindsii</i> × <i>Juglans regia</i> ) and Regulation of Cambial Activity in Relation to Grafting. <i>Frontiers in Genetics</i> , 2019, 10, 577.	1.1	9
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1603	Genome-Wide Identification of WRKY Genes and Their Response to Cold Stress in <i>Coffea canephora</i> . <i>Forests</i> , 2019, 10, 335.	0.9	15
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1894	Genome-wide identification and characterization of DCL, AGO and RDR gene families in <i>Saccharum spontaneum</i> . <i>Scientific Reports</i> , 2020, 10, 13202.	1.6	23
1895	FASTQINS and ANUBIS: two bioinformatic tools to explore facts and artifacts in transposon sequencing and essentiality studies. <i>Nucleic Acids Research</i> , 2020, 48, e102-e102.	6.5	15
1896	ARDEP, a Rapid Degenerate Primer Design Pipeline Based on k-mers for Amplicon Microbiome Studies. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 5958.	1.2	4
1897	SelfAT-Fold: protein fold recognition based on residue-based and motif-based self-attention networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	1.9	10
1898	Genome-Wide Identification and Capsaicinoid Biosynthesis-Related Expression Analysis of the R2R3-MYB Gene Family in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2020, 11, 598183.	1.1	23
1899	Isolation, Identification, and Complete Genome Assembly of an Endophytic <i>Bacillus velezensis</i> YB-130, Potential Biocontrol Agent Against <i>Fusarium graminearum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 598285.	1.5	38
1900	Identification, Phylogeny, and Comparative Expression of the Lipoxygenase Gene Family of the Aquatic Duckweed, <i>Spirodela polyrhiza</i> , during Growth and in Response to Methyl Jasmonate and Salt. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9527.	1.8	13
1901	Characterization of Prodiginine Pathway in Marine Sponge-Associated <i>Pseudoalteromonas</i> sp. PPB1 in Hilo, Hawai'i. <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	1.8	1
1902	Immunoproteomic Analysis Reveals Novel Candidate Antigens for the Diagnosis of Paracoccidioidomycosis Due to <i>Paracoccidioides lutzii</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 357.	1.5	19
1903	Genome-Wide Analysis of the Cyclin Gene Family and Their Expression Profile in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9430.	1.8	13
1904	Characterization of Metagenome-Assembled Genomes and Carbohydrate-Degrading Genes in the Gut Microbiota of Tibetan Pig. <i>Frontiers in Microbiology</i> , 2020, 11, 595066.	1.5	34
1905	Genome-wide identification and expression analysis of the CLC gene family in pomegranate ( <i>Punica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	12
1906	Identification and functional characterization of ABCC transporters for Cd tolerance and accumulation in <i>Sedum alfredii</i> Hance. <i>Scientific Reports</i> , 2020, 10, 20928.	1.6	14
1907	Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. <i>BMC Biology</i> , 2020, 18, 139.	1.7	17
1908	An Earliest Endosymbiont, <i>Wolbachia massiliensis</i> sp. nov., Strain PL13 from the Bed Bug ( <i>Cimex</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 8064.	1.8	23

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1909	The Transcriptome of <i>Cunninghamia lanceolata</i> male/female cone reveal the association between MIKC MADS-box genes and reproductive organs development. <i>BMC Plant Biology</i> , 2020, 20, 508.	1.6	15
1910	Characterization of the Topological Features of Catalytic Sites in Protein Coevolution Networks*. <i>Chinese Physics Letters</i> , 2020, 37, 068701.	1.3	2
1911	Identification and Expression Analysis of Sugar Transporter Gene Family in <i>Aspergillus oryzae</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-15.	0.8	6
1912	Hemiptera phylogenomic resources: Tree-based orthology prediction and conserved exon identification. <i>Molecular Ecology Resources</i> , 2020, 20, 1346-1360.	2.2	5
1913	A Review of Deep Learning Methods for Antibodies. <i>Antibodies</i> , 2020, 9, 12.	1.2	40
1914	Genome-Wide Identification and Characterization of Gene Families in <i>Arachis</i> : Methods and Strategies. <i>Frontiers in Genetics</i> , 2020, 11, 525.	1.1	9
1915	Chromosome-level assembly of the melon thrips genome yields insights into evolution of a sap-sucking lifestyle and pesticide resistance. <i>Molecular Ecology Resources</i> , 2020, 20, 1110-1125.	2.2	31
1916	Cloning, molecular and functional characterization by overexpression in <i>Arabidopsis</i> of MAPKK genes from grapevine ( <i>Vitis vinifera</i> ). <i>BMC Plant Biology</i> , 2020, 20, 194.	1.6	9
1917	Genomic Identification, Evolution, and Expression Analysis of Collagen Genes Family in Water Buffalo during Lactation. <i>Genes</i> , 2020, 11, 515.	1.0	11
1918	Review: Long non-coding RNA in livestock. <i>Animal</i> , 2020, 14, 2003-2013.	1.3	31
1919	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413.	2.3	40
1920	The Bioinformatic and In Vitro Studies of <i>Clostridioides Difficile</i> Aminopeptidase M24 Revealed the Immunoreactive KKGIK Peptide. <i>Cells</i> , 2020, 9, 1146.	1.8	2
1921	Classification and functional analyses of putative virulence factors of <i>Mycobacterium tuberculosis</i> : A combined sequence and structure based study. <i>Computational Biology and Chemistry</i> , 2020, 87, 107270.	1.1	0
1922	The Kernel Size-Related Quantitative Trait Locus <i>qKW9</i> Encodes a Pentatricopeptide Repeat Protein That Affects Photosynthesis and Grain Filling. <i>Plant Physiology</i> , 2020, 183, 1696-1709.	2.3	29
1923	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	0.8	34
1924	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. <i>Water Research</i> , 2020, 181, 115858.	5.3	37
1925	Dynamics of the transcriptional landscape during human fetal testis and ovary development. <i>Human Reproduction</i> , 2020, 35, 1099-1119.	0.4	22
1926	Predicting host taxonomic information from viral genomes: A comparison of feature representations. <i>PLoS Computational Biology</i> , 2020, 16, e1007894.	1.5	31

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1927	Engineered triply orthogonal pyrrolysyl-tRNA synthetase/tRNA pairs enable the genetic encoding of three distinct non-canonical amino acids. <i>Nature Chemistry</i> , 2020, 12, 535-544.	6.6	93
1928	Improved bacterial recombineering by parallelized protein discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13689-13698.	3.3	82
1929	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	4.3	22
1930	A Clone Resource of <i>Magnaporthe oryzae</i> Effectors That Share Sequence and Structural Similarities Across Host-Specific Lineages. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1032-1035.	1.4	20
1931	Genome-wide characterization of the abscisic acid-, stress- and ripening-induced (ASR) gene family in wheat ( <i>Triticum aestivum</i> L.). <i>Biological Research</i> , 2020, 53, 23.	1.5	20
1932	Screening and functional identification of lncRNAs in antler mesenchymal and cartilage tissues using high-throughput sequencing. <i>Scientific Reports</i> , 2020, 10, 9492.	1.6	5
1933	Pheromone biosynthetic pathway and chemoreception proteins in sex pheromone gland of <i>Eogystia hippophaecolus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100702.	0.4	1
1934	Higher-order Markov models for metagenomic sequence classification. <i>Bioinformatics</i> , 2020, 36, 4130-4136.	1.8	6
1935	Draft genomes of two outcrossing wild rice, <i>Oryza rufipogon</i> and <i>O. longistaminata</i> , reveal genomic features associated with mating system evolution. <i>Plant Direct</i> , 2020, 4, e00232.	0.8	9
1936	Pattern recognition receptors in grass carp <i>Ctenopharyngodon idella</i> : II. Organization and expression analysis of NOD-like receptors. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103734.	1.0	17
1937	CRISPRcasIdentifier: Machine learning for accurate identification and classification of CRISPR-Cas systems. <i>GigaScience</i> , 2020, 9, .	3.3	31
1938	Importance of <i>Deffluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	1.6	13
1939	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	2.1	13
1940	Disequilibrium evolution of the Fructose-1,6-bisphosphatase gene family leads to their functional biodiversity in <i>Gossypium</i> species. <i>BMC Genomics</i> , 2020, 21, 379.	1.2	13
1941	A cotton 1,3-/4-fucosyltransferase-encoding gene, <i>FucT4</i> , plays an important role in cell elongation and is significantly associated with fiber quality. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1141-1153.	1.0	3
1942	The nuclear and mitochondrial genomes of <i>Frieseomelitta varia</i> – a highly eusocial stingless bee ( <i>Meliponini</i> ) with a permanently sterile worker caste. <i>BMC Genomics</i> , 2020, 21, 386.	1.2	15
1943	Basic Helix-Loop-Helix (bHLH) transcription factor family in Yellow horn ( <i>Xanthoceras sorbifolia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 patterns. <i>International Journal of Biological Macromolecules</i> , 2020, 160, 711-723.	3.6	17
1944	An evolutionarily conserved motif is required for Plasmodium-located protein 5 to regulate cell-to-cell movement. <i>Communications Biology</i> , 2020, 3, 291.	2.0	15

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1945	Transcriptome Analysis of Maternal Gene Transcripts in Unfertilized Eggs of <i>Misgurnus anguillicaudatus</i> and Identification of Immune-Related Maternal Genes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3872.	1.8	4
1946	Identification of a chitosanase from the marine metagenome and its molecular improvement based on evolution data. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6647-6657.	1.7	7
1947	RNA Pol II Length and Disorder Enable Cooperative Scaling of Transcriptional Bursting. <i>Molecular Cell</i> , 2020, 79, 207-220.e8.	4.5	32
1948	Shifting evolutionary sands: transcriptome characterization of the <i>Aptostichus atomarius</i> species complex. <i>BMC Evolutionary Biology</i> , 2020, 20, 68.	3.2	1
1949	The Complete Chloroplast Genome Sequencing and Comparative Analysis of Reed Canary Grass ( <i>Phalaris arundinacea</i> ) and Hardinggrass ( <i>P. aquatica</i> ). <i>Plants</i> , 2020, 9, 748.	1.6	9
1950	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	1.1	13
1951	Genome-wide analysis of the U-box E3 ubiquitin ligase enzyme gene family in tomato. <i>Scientific Reports</i> , 2020, 10, 9581.	1.6	40
1952	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
1953	A case study of salivary microbiome in smokers and non-smokers in Hungary: analysis by shotgun metagenome sequencing. <i>Journal of Oral Microbiology</i> , 2020, 12, 1773067.	1.2	18
1954	Metabolic Engineering Strategies in Diatoms Reveal Unique Phenotypes and Genetic Configurations With Implications for Algal Genetics and Synthetic Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 513.	2.0	26
1955	Diversity and Evolutionary Dynamics of Antiphage Defense Systems in <i>Ralstonia solanacearum</i> Species Complex. <i>Frontiers in Microbiology</i> , 2020, 11, 961.	1.5	11
1956	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	1.7	10
1957	<i>Clostridioides difficile</i> Senses and Hijacks Host Heme for Incorporation into an Oxidative Stress Defense System. <i>Cell Host and Microbe</i> , 2020, 28, 411-421.e6.	5.1	36
1958	Characterization and Analysis of the Full-Length Transcriptomes of Multiple Organs in <i>Pseudotaxus chienii</i> (W.C.Cheng) W.C.Cheng. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4305.	1.8	4
1959	Genome mining and sequence analysis of chemosensory soluble proteins in arthropods. <i>Methods in Enzymology</i> , 2020, 642, 1-20.	0.4	5
1960	Evolution of Two Ubiquitin-like System of Autophagy in Orchid. <i>Horticultural Plant Journal</i> , 2020, 6, 321-334.	2.3	6
1961	NAC Family Transcription Factors in Carrot: Genomic and Transcriptomic Analysis and Responses to Abiotic Stresses. <i>DNA and Cell Biology</i> , 2020, 39, 816-827.	0.9	7
1962	Genome-wide identification and expression analysis of WRKY transcription factors in pearl millet ( <i>Pennisetum glaucum</i> ) under dehydration and salinity stress. <i>BMC Genomics</i> , 2020, 21, 231.	1.2	56



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1963	Mechanism of Antibacterial Activity of <i>Bacillus amyloliquefaciens</i> C-1 Lipopeptide toward Anaerobic <i>Clostridium difficile</i> . <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	23
1964	Portal of Juglandaceae: A comprehensive platform for Juglandaceae study. <i>Horticulture Research</i> , 2020, 7, 35.	2.9	22
1965	A novel thermostable cellulase cocktail enhances lignocellulosic bioconversion and biorefining in a broad range of pH. <i>International Journal of Biological Macromolecules</i> , 2020, 154, 349-360.	3.6	47
1966	Insights Into the Function of the NuA4 Complex in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 125.	1.7	21
1967	Comparison of Viromes in Ticks from Different Domestic Animals in China. <i>Virologica Sinica</i> , 2020, 35, 398-406.	1.2	15
1968	COST1 regulates autophagy to control plant drought tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7482-7493.	3.3	71
1969	Genome-Scale Identification, in Silico Characterization and Interaction Study Between Wheat SNARE and NPSN Gene Families Involved in Vesicular Transport. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2492-2501.	1.9	8
1970	Characterization of the Ch4CL gene family reveals a role of Ch4CL7 in drought tolerance. <i>BMC Plant Biology</i> , 2020, 20, 125.	1.6	40
1971	Genome Sequence and Comparative Analysis of <i>Colletotrichum gloeosporioides</i> Isolated from <i>Liriodendron</i> Leaves. <i>Phytopathology</i> , 2020, 110, 1260-1269.	1.1	13
1972	Transcriptome Analysis of the Cytokinin Response in <i>Medicago truncatula</i> . <i>Journal of Plant Biology</i> , 2020, 63, 189-202.	0.9	2
1973	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020, 7, 45.	2.9	35
1974	Genome-Wide Identification and Evolutionary Analysis of the Fruit-Weight 2.2-Like Gene Family in Polyploid Oilseed Rape ( <i>Brassica napus</i> L.). <i>DNA and Cell Biology</i> , 2020, 39, 766-782.	0.9	3
1975	Transcriptomic analysis of the mode of action of the candidate anti-fouling compound di(1H-indol-3-yl)methane (DIM) on a marine biofouling species, the bryozoan <i>Bugula neritina</i> . <i>Marine Pollution Bulletin</i> , 2020, 152, 110904.	2.3	3
1976	The Cytochrome P450 Monooxygenase Inventory of Grapevine ( <i>Vitis vinifera</i> L.): Genome-Wide Identification, Evolutionary Characterization and Expression Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 44.	1.1	35
1977	First Genome of the Brown Alga <i>Undaria pinnatifida</i> : Chromosome-Level Assembly Using PacBio and Hi-C Technologies. <i>Frontiers in Genetics</i> , 2020, 11, 140.	1.1	39
1978	Genome-wide characterization and expression analyses of the auxin/indole-3-acetic acid (Aux/IAA) gene family in barley ( <i>Hordeum vulgare</i> L.). <i>Scientific Reports</i> , 2020, 10, 10242.	1.6	15
1979	Genome-Wide Identification, Evolution, and Expression of GDSL-Type Esterase/Lipase Gene Family in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 726.	1.7	47
1980	Genome-wide analysis and comparison of the DNA-binding one zinc finger gene family in diploid and tetraploid cotton ( <i>Gossypium</i> ). <i>PLoS ONE</i> , 2020, 15, e0235317.	1.1	6



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1981	Genome-wide Identification and Expression Analysis of TALE Gene Family in Pomegranate ( <i>Punica</i> ) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	1.3	10
1982	Microbial succession during the transition from active to inactive stages of deep-sea hydrothermal vent sulfide chimneys. <i>Microbiome</i> , 2020, 8, 102.	4.9	62
1983	A bacterial cytidine deaminase toxin enables CRISPR-free mitochondrial base editing. <i>Nature</i> , 2020, 583, 631-637.	13.7	409
1984	Functional analysis of RXLR effectors from the New Zealand kauri dieback pathogen <i>Phytophthora agathidicida</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 1131-1148.	2.0	13
1985	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. <i>Cell Host and Microbe</i> , 2020, 28, 380-389.e9.	5.1	51
1986	The Gut Microbiota in Prediabetes and Diabetes: A Population-Based Cross-Sectional Study. <i>Cell Metabolism</i> , 2020, 32, 379-390.e3.	7.2	233
1987	Comparative study of the SBP-box gene family in rice siblings. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	2
1988	Improved reconstruction and comparative analysis of chromosome 12 to rectify Mis-assemblies in <i>Gossypium arboreum</i> . <i>BMC Genomics</i> , 2020, 21, 470.	1.2	0
1989	Pervasive duplication, biased molecular evolution and comprehensive functional analysis of the PP2C family in <i>Glycine max</i> . <i>BMC Genomics</i> , 2020, 21, 465.	1.2	9
1990	The auxin response factor gene family in wheat ( <i>Triticum aestivum</i> L.): Genome-wide identification, characterization and expression analyses in response to leaf rust. <i>South African Journal of Botany</i> , 2021, 140, 312-325.	1.2	13
1991	MetaRibo-Seq measures translation in microbiomes. <i>Nature Communications</i> , 2020, 11, 3268.	5.8	30
1992	Evolutionary History of the Globin Gene Family in Annelids. <i>Genome Biology and Evolution</i> , 2020, 12, 1719-1733.	1.1	8
1993	Signatures of adaptation to a monocot host in the plant-parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	2.8	9
1994	Complete transcriptome assembly and annotation of a critically important amphipod species in freshwater ecotoxicological risk assessment: <i>Gammarus fossarum</i> . <i>Environment International</i> , 2020, 137, 105319.	4.8	8
1995	Transcriptome-Wide Identification, Evolutionary Analysis, and GA Stress Response of the GRAS Gene Family in <i>Panax ginseng</i> C. A. Meyer. <i>Plants</i> , 2020, 9, 190.	1.6	13
1996	Systematic identification of long intergenic non-coding RNAs expressed in bovine oocytes. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 13.	1.4	11
1997	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	4.7	112
1998	Analysis of two Mexican <i>Pectobacterium brasiliense</i> strains reveals an inverted relationship between c-di-GMP levels with exopolysaccharide production and swarming motility. <i>Microbiological Research</i> , 2020, 235, 126427.	2.5	7

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1999	Genome-Wide Identification of the Auxin Response Factor (ARF) Gene Family and Their Expression Analysis during Flower Development of <i>Osmanthus fragrans</i> . <i>Forests</i> , 2020, 11, 245.	0.9	10
2000	Toward the Mechanistic Understanding of Enzymatic CO <sub>2</sub> Reduction. <i>ACS Catalysis</i> , 2020, 10, 3844-3856.	5.5	76
2001	Genome-wide annotation, comparison and functional genomics of carbohydrate-active enzymes in legumes infecting <i>Fusarium oxysporum</i> formae speciales. <i>Mycology</i> , 2020, 11, 56-70.	2.0	12
2002	Origin and Evolution of Polycyclic Triterpene Synthesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1925-1941.	3.5	38
2003	Genome-wide analysis of a putative lipid transfer protein LTP_2 gene family reveals CsLTP_2 genes involved in response of cucumber against root-knot nematode ( <i>Meloidogyne incognita</i> ). <i>Genome</i> , 2020, 63, 225-238.	0.9	11
2004	Characterizing ciguatoxin (CTX)- and Non-CTX-producing strains of <i>Gambierdiscus balechii</i> using comparative transcriptomics. <i>Science of the Total Environment</i> , 2020, 717, 137184.	3.9	12
2005	Genome of <i>Tripterygium wilfordii</i> and identification of cytochrome P450 involved in triptolide biosynthesis. <i>Nature Communications</i> , 2020, 11, 971.	5.8	103
2006	Genome-wide identification, phylogeny, and expression analysis of the <i>CA</i> gene family in tomato. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 70-83.	0.5	5
2007	De novo Transcriptome Reveals Gene Changes in the Development of the Endosperm Chalazal Haustorium in <i>Taxillus chinensis</i> (DC.) Danser. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	8
2008	Genome-Wide Profiling and Phylogenetic Analysis of the SWEET Sugar Transporter Gene Family in Walnut and Their Lack of Responsiveness to <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1251.	1.8	17
2009	Assembly-free single-molecule sequencing recovers complete virus genomes from natural microbial communities. <i>Genome Research</i> , 2020, 30, 437-446.	2.4	80
2010	Passion Fruit Green Spot Virus Genome Harbors a New Orphan ORF and Highlights the Flexibility of the 5'-End of the RNA2 Segment Across Cileviruses. <i>Frontiers in Microbiology</i> , 2020, 11, 206.	1.5	41
2011	Hookworms Evade Host Immunity by Secreting a Deoxyribonuclease to Degrade Neutrophil Extracellular Traps. <i>Cell Host and Microbe</i> , 2020, 27, 277-289.e6.	5.1	53
2012	TRPA1 modulates noxious odor responses in <i>Lygus hesperus</i> . <i>Journal of Insect Physiology</i> , 2020, 122, 104038.	0.9	6
2013	Comprehensive phylogenomic analysis of ERF genes in sorghum provides clues to the evolution of gene functions and redundancy among gene family members. <i>3 Biotech</i> , 2020, 10, 139.	1.1	16
2014	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , 2020, 18, 12.	1.7	95
2015	Structural Insights into the Unique Activation Mechanisms of a Non-classical Calpain and Its Disease-Causing Variants. <i>Cell Reports</i> , 2020, 30, 881-892.e5.	2.9	17
2016	Trimethylamine-N-Oxide Postprandial Response in Plasma and Urine Is Lower After Fermented Compared to Non-Fermented Dairy Consumption in Healthy Adults. <i>Nutrients</i> , 2020, 12, 234.	1.7	27

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2017	Tentacle Transcriptomes of the Speckled Anemone ( <i>Actiniaria: Actiniidae: Oulactis</i> sp.): Venom-Related Components and Their Domain Structure. <i>Marine Biotechnology</i> , 2020, 22, 207-219.	1.1	19
2018	Transcriptional regulation by $\sigma^f$ factor phosphorylation in bacteria. <i>Nature Microbiology</i> , 2020, 5, 395-406.	5.9	17
2019	The mirid bug <i>Apolygus lucorum</i> deploys a glutathione peroxidase as a candidate effector to enhance plant susceptibility. <i>Journal of Experimental Botany</i> , 2020, 71, 2701-2712.	2.4	30
2020	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2008-2016.	1.9	13
2021	Critiquing Protein Family Classification Models Using Sufficient Input Subsets. <i>Journal of Computational Biology</i> , 2020, 27, 1219-1231.	0.8	7
2022	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	1.5	12
2023	Highly efficient production of chitooligosaccharides by enzymes mined directly from the marine metagenome. <i>Carbohydrate Polymers</i> , 2020, 234, 115909.	5.1	23
2024	Plant Mitochondrial Carriers: Molecular Gatekeepers That Help to Regulate Plant Central Carbon Metabolism. <i>Plants</i> , 2020, 9, 117.	1.6	23
2025	De Novo Transcriptome Identifies Olfactory Genes in <i>Diachasmimorpha longicaudata</i> (Ashmead). <i>Genes</i> , 2020, 11, 144.	1.0	8
2026	Computationally Aided Discovery of LysEFm5 Variants with Improved Catalytic Activity and Stability. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	2
2027	Genome-Wide Identification, Expression Profile of the TIFY Gene Family in <i>Brassica oleracea</i> var. <i>capitata</i> , and Their Divergent Response to Various Pathogen Infections and Phytohormone Treatments. <i>Genes</i> , 2020, 11, 127.	1.0	31
2028	Draft Genome of the Asian Buffalo Leech <i>Hirudinaria manillensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1321.	1.1	11
2029	Genome Sequence Resource of <i>Magnaporthe oryzae</i> Laboratory Strain 2539. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1029-1031.	1.4	2
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2167	Genome-wide identification and expression profiling of chitinase genes in tea ( <i>Camellia sinensis</i> (L.) O.) Tj ETQq1 1 0,784314 rgBT /Over	1.4	16
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3854	iORbase: A database for the prediction of the structures and functions of insect olfactory receptors. <i>Insect Science</i> , 2023, 30, 1245-1254.	1.5	2
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3856	Identification, classification, and expression profile analysis of heat shock transcription factor gene family in <i>Salvia miltiorrhiza</i> . <i>PeerJ</i> , 0, 10, e14464.	0.9	1
3857	Mapping the FtsQBL divisome components in bacterial NTD pathogens as potential drug targets. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
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3859	Transcriptome profiling reveals the underlying mechanism of grape post-harvest pathogen <i>Penicillium olsonii</i> against the metabolites of <i>Bacillus velezensis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3860	Comprehensive Analysis of the lncRNA-miRNA-mRNA Regulatory Network for Intramuscular Fat in Pigs. <i>Genes</i> , 2023, 14, 168.	1.0	4
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3865	Genome-wide identification of acyl-CoA binding proteins and possible functional prediction in legumes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
3866	Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	0
3867	Potential for mercury methylation by Asgard archaea in mangrove sediments. <i>ISME Journal</i> , 2023, 17, 478-485.	4.4	6
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3870	The <i>Aphelenchoides</i> genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant-parasitic nematodes. <i>Molecular Ecology Resources</i> , 2023, 23, 905-919.	2.2	2
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3875	Diversity of viral communities in faecal samples of farmed red foxes. <i>Heliyon</i> , 2023, 9, e12826.	1.4	0
3876	Genome-wide identification, evolution, and expression analysis of carbonic anhydrases genes in soybean ( <i>Glycine max</i> ). <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	1
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3882	Genomic survey of NPF and NRT2 transporter gene families in five inbred maize lines and their responses to pathogens infection. <i>Genomics</i> , 2023, 115, 110555.	1.3	1
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3896	Deciphering the Genetic Basis of Silkworm Cocoon Colors Provides New Insights into Biological Coloration and Phenotypic Diversification. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	5
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3901	Killer Knots: Molecular Evolution of Inhibitor Cystine Knot Toxins in Wandering Spiders (Araneae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.5	4
3902	Coevolution and smFRET Enhances Conformation Sampling and FRET Experimental Design in Tandem PDZ1-2 Proteins. <i>Journal of Physical Chemistry B</i> , 2023, 127, 884-898.	1.2	2

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3920	Organelle genomes of <i>Indigofera amblyantha</i> and <i>Indigofera pseudotinctoria</i> : comparative genome analysis, and intracellular gene transfer. <i>Industrial Crops and Products</i> , 2023, 198, 116674.	2.5	2
3921	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. <i>Nature Communications</i> , 2023, 14, .	5.8	10
3922	Identification and characterization of ABC proteins in an important rice insect pest, <i>Cnaphalocrocis medinalis</i> unveil their response to Cry1C toxin. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 123949.	3.6	1
3923	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of <i>Poncirus polyandra</i> . <i>Genomics</i> , 2023, 115, 110617.	1.3	1
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3951	The Antidepressant Sertraline Affects Cell Signaling and Metabolism in <i>Trichophyton rubrum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 275.	1.5	1

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3996	Recovery of metagenomic data from the <i>Aedes aegypti</i> microbiome using a reproducible snakemake pipeline: MINUUR. <i>Wellcome Open Research</i> , 0, 8, 131.	0.9	1
3997	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. <i>PLoS Computational Biology</i> , 2023, 19, e1010966.	1.5	0
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4021	Dynamic Evolution of Retroviral Envelope Genes in Egg-Laying Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4
4023	The Complete Chloroplast Genomes of <i>Gynostemma</i> Reveal the Phylogenetic Relationships of Species within the Genus. <i>Genes</i> , 2023, 14, 929.	1.0	2
4024	Tilapia lake virus: A structured phylogenetic approach. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	3
4025	The <i>Dictyostelium discoideum</i> genome lacks significant DNA methylation and uncovers palindromic sequences as a source of false positives in bisulfite sequencing. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	1.5	1
4026	Regulation of Cell Proliferation and Nrf2-Mediated Antioxidant Defense: Conservation of Keap1 Cysteines and Nrf2 Binding Site in the Context of the Evolution of KLHL Family. <i>Life</i> , 2023, 13, 1045.	1.1	5
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4028	Mirusviruses link herpesviruses to giant viruses. <i>Nature</i> , 2023, 616, 783-789.	13.7	28
4029	Insights into the Molecular Basis of Huanglongbing Tolerance in Persian Lime ( <i>Citrus latifolia</i> Tan.) through a Transcriptomic Approach. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7497.	1.8	2
4030	Genome-wide identification and functional analysis of ICE genes reveal that <i>Gossypium thurberi</i> ICE2 is responsible for cold and drought stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2023, 199, 107708.	2.8	3
4031	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
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4237	Designing Efficient SIMD Kernels for High Performance Sequence Alignment. , 2023, , .		0
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4472	Role of Distributed Computing in Biology Research Field and Its Challenges. <i>Series in Bioengineering</i> , 2024, , 147-162.	0.3	0

#	ARTICLE	IF	CITATIONS
4488	Bioinformatic analysis of microbial type terpene synthase genes in plants. <i>Methods in Enzymology</i> , 2024, , .	0.4	0