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SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads

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766	Combining transcriptome assemblies from multiple de novo assemblers in the allo-tetraploid plant Nicotiana benthamiana. <b>2014</b> , 9, e91776		108
765	Genomic Takeover by Transposable Elements in the Strawberry Poison Frog. <b>2018</b> , 35, 2913-2927		27
764	Temporal genomic evolution of bird sex chromosomes. <b>2014</b> , 14, 250		31
763	Evaluation of de novo transcriptome assemblies from RNA-Seq data. <i>Genome Biology</i> , <b>2014</b> , 15, 553	18.3	170
762	Quality control of next-generation sequencing data without a reference. <b>2014</b> , 5, 111		38
761	De novo transcriptome assemblies and annotation for pacifie whiteleg shrimp. 2014,		
760	Data access for the 1,000 Plants (1KP) project. <b>2014</b> , 3, 17		403
759	Phylogenomics resolves the timing and pattern of insect evolution. <b>2014</b> , 346, 763-7		1489
75 <sup>8</sup>	Analysis considerations for utilizing RNA-Seq to characterize the brain transcriptome. <b>2014</b> , 116, 21-54		3
757	Multiplex sequencing of pooled mitochondrial genomes-a crucial step toward biodiversity analysis using mito-metagenomics. <b>2014</b> , 42, e166		188
756	Identification and characterization of CYP79D16 and CYP71AN24 catalyzing the first and second steps in L-phenylalanine-derived cyanogenic glycoside biosynthesis in the Japanese apricot, Prunus mume Sieb. et Zucc. <b>2014</b> , 86, 215-23		38
755	LTR retroelements are intrinsic components of transcriptional networks in frogs. <b>2014</b> , 15, 626		4
754	Transcriptome profiling and comparative analysis of Panax ginseng adventitious roots. <b>2014</b> , 38, 278-88	3	48
753	Integrative workflows for metagenomic analysis. <b>2014</b> , 2, 70		28
75 <sup>2</sup>	Combined de novo and genome guided assembly and annotation of the Pinus patula juvenile shoot transcriptome. <b>2015</b> , 16, 1057		34
75 <sup>1</sup>	Microfluidic PCR-based target enrichment: A case study in two rapid radiations of Commiphora (Burseraceae) from Madagascar. <b>2015</b> , 53, 411-431		19
75°	Omics Analysis and Databases for Plant Science. <b>2015</b> , 150-159		2

#### (2015-2015)

749	De novo transcriptome assembly databases for the central nervous system of the medicinal leech. <b>2015</b> , 2, 150015	15
748	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, Hypothenemus hampei. <b>2015</b> , 5, 12525	44
747	Transcriptomes of parents identify parenting strategies and sexual conflict in a subsocial beetle. <b>2015</b> , 6, 8449	61
746	TRUFA: A User-Friendly Web Server for de novo RNA-seq Analysis Using Cluster Computing. <b>2015</b> , 11, 97-104	30
745	Heuristic pairwise alignment of de Bruijn graphs to facilitate simultaneous transcript discovery in related organisms from RNA-Seq data. <b>2015</b> , 16 Suppl 11, S5	4
744	Genome of the facultative scuticociliatosis pathogen Pseudocohnilembus persalinus provides insight into its virulence through horizontal gene transfer. <b>2015</b> , 5, 15470	33
743	Optimizing and benchmarking de novo transcriptome sequencing: from library preparation to assembly evaluation. <b>2015</b> , 16, 977	56
742	High quality draft genomic sequence of Flavobacterium enshiense DK69(T) and comparison among Flavobacterium genomes. <b>2015</b> , 10, 92	1
741	First complete mitochondrial genome of the South American annual fish Austrolebias charrua (Cyprinodontiformes: Rivulidae): peculiar features among cyprinodontiforms mitogenomes. <b>2015</b> , 16, 879	4
740	Eco-genomic analysis of the poleward range expansion of the wasp spider Argiope bruennichi shows rapid adaptation and genomic admixture. <b>2015</b> , 21, 4320-32	41
739	Transcription analysis of neonicotinoid resistance in Mediterranean (MED) populations of B. tabaci reveal novel cytochrome P450s, but no nAChR mutations associated with the phenotype. <b>2015</b> , 16, 939	36
738	The origin and genetic differentiation of the socially parasitic aphid Tamalia inquilinus. <b>2015</b> , 24, 5751-66	7
737	CRCDAComprehensive resources for cancer NGS data analysis. <b>2015</b> , 2015,	3
736	High-throughput monitoring of wild bee diversity and abundance via mitogenomics. <b>2015</b> , 6, 1034-1043	97
735	Transcriptome Characterization for Non-Model Endangered Lycaenids, Protantigius superans and Spindasis takanosis, Using Illumina HiSeq 2500 Sequencing. <i>International Journal of Molecular Sciences</i> , <b>2015</b> , 16, 29948-70	7
734	The transcriptome of equine peripheral blood mononuclear cells. <b>2015</b> , 10, e0122011	14
733	An improved fruit transcriptome and the identification of the candidate genes involved in fruit abscission induced by carbohydrate stress in litchi. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 439	34
732	Bermuda. <b>2015</b> ,	

731	Phylogenetic relationship of some "accessory" helicases of plant positive-stranded RNA viruses: toward understanding the evolution of triple gene block. <b>2015</b> , 6, 508	20
730	RNA-Seq Data Analysis for Studying Abiotic Stress in Horticultural Plants. <b>2015</b> , 197-220	2
729	Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. <i>Bioinformatics</i> , <b>2015</b> , 31, 3938-45	63
728	Early transcriptional events linked to induction of diapause revealed by RNAseq in larvae of drosophilid fly, Chymomyza costata. <b>2015</b> , 16, 720	60
727	Genome sequencing of herb Tulsi (Ocimum tenuiflorum) unravels key genes behind its strong medicinal properties. <b>2015</b> , 15, 212	60
726	Highlights. <b>2015</b> , 102, 1009-1010	
725	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. 2015, 563-612	3
724	De novo transcriptome assembly for a non-model species, the blood-sucking bug Triatoma brasiliensis, a vector of Chagas disease. <b>2015</b> , 143, 225-39	17
723	De novo assembly and comprehensive characterization of the skeletal muscle transcriptomes of the European anchovy (Engraulis encrasicolus). <b>2015</b> , 20, 7-9	3
722	De novo transcriptome assembly of a fern, Lygodium japonicum, and a web resource database, Ljtrans DB. <b>2015</b> , 56, e5	28
721	Abiotic Stress Biology in Horticultural Plants. <b>2015</b> ,	10
720	CHAPTER 3:Venoms-Based Drug Discovery: Proteomic and Transcriptomic Approaches. <b>2015</b> , 80-96	5
719	Pathways associated with lignin biosynthesis in lignomaniac jute fibres. <b>2015</b> , 290, 1523-42	33
718	Optimal assembly strategies of transcriptome related to ploidies of eukaryotic organisms. <b>2015</b> , 16, 65	24
717	Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. <i>Genome Biology</i> , <b>2015</b> , 16, 30	190
716	Elucidation of the growth delimitation of Dunaliella tertiolecta under nitrogen stress by integrating transcriptome and peptidome analysis. <b>2015</b> , 194, 57-66	32
715	Optimized deep-targeted proteotranscriptomic profiling reveals unexplored Conus toxin diversity and novel cysteine frameworks. <b>2015</b> , 112, E3782-91	70
714	Transcriptome profiling of in vitro lines propagated from corm bud tip of elephant foot yam (Amorphophallus paeoniifolius) approves complete potyviruses elimination. <b>2015</b> , 143, 363-371	3

#### (2015-2015)

713	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <b>2015</b> , 102, 1089-107	114
712	Numerous transitions of sex chromosomes in Diptera. <b>2015</b> , 13, e1002078	186
711	Maternal and zygotic transcriptomes in the appendicularian, Oikopleura dioica: novel protein-encoding genes, intra-species sequence variations, and trans-spliced RNA leader. <b>2015</b> , 225, 149-59	17
710	Saccharina genomes provide novel insight into kelp biology. <b>2015</b> , 6, 6986	154
709	Thermophiles in the genomic era: Biodiversity, science, and applications. <b>2015</b> , 33, 633-47	89
708	Comprehensive analysis of transcriptome response to salinity stress in the halophytic turf grass Sporobolus virginicus. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 241	58
707	The nervous system of Xenacoelomorpha: a genomic perspective. <b>2015</b> , 218, 618-28	25
706	Peptidomics of Circular Cysteine-Rich Plant Peptides: Analysis of the Diversity of Cyclotides from Viola tricolor by Transcriptome and Proteome Mining. <b>2015</b> , 14, 4851-62	62
705	An efficient transcriptome analysis pipeline to accelerate venom peptide discovery and characterisation. <b>2015</b> , 107, 282-9	12
704	De novo assembly of the Carcinus maenas transcriptome and characterization of innate immune system pathways. <b>2015</b> , 16, 458	39
703	Novel insights into the insect trancriptome response to a natural DNA virus. <b>2015</b> , 16, 310	21
702	De novo assembly and characterisation of the field pea transcriptome using RNA-Seq. <b>2015</b> , 16, 611	37
701	We can@all be supermodels: the value of comparative transcriptomics to the study of non-model insects. <b>2015</b> , 24, 139-54	49
700	. 2015,	
699	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <b>2015</b> , 49, 12628-40	45
698	Analysis of amino acid and codon usage in Paramecium bursaria. <b>2015</b> , 589, 3113-8	3
697	Genomic variant annotation and prioritization with ANNOVAR and wANNOVAR. 2015, 10, 1556-66	459
696	Early genome duplications in conifers and other seed plants. <b>2015</b> , 1, e1501084	167

695	Characterization of a second secologanin synthase isoform producing both secologanin and secoxyloganin allows enhanced de novo assembly of a Catharanthus roseus transcriptome. <b>2015</b> , 16, 619	35
694	Use of genome sequencing to assess nucleotide structure variation of Staphylococcus aureus strains cultured in spaceflight on Shenzhou-X, under simulated microgravity and on the ground. <b>2015</b> , 170, 61-8	10
693	Identification and distribution of SIFamide in the nervous system of the desert locust Schistocerca gregaria. <b>2015</b> , 523, 108-25	16
692	The complete mitochondrial genome of the ruby-topaz hummingbird Chrysolampis mosquitus through Illumina sequencing. <b>2016</b> , 27, 769-70	2
691	SeqDev: An Algorithm for Constructing Genetic Elements Using Comparative Assembly. <b>2016</b> , 26, 105-121	
690	. 2016,	6
689	Generation and Characterisation of a Reference Transcriptome for Lentil (Lens culinaris Medik.).  International Journal of Molecular Sciences, 2016, 17,  6.3	33
688	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. <b>2016</b> ,	4
687	Pseudo-Reference-Based Assembly of Vertebrate Transcriptomes. <b>2016</b> , 7,	2
686	Interactive knowledge discovery and data mining on genomic expression data with numeric formal concept analysis. <b>2016</b> , 17, 374	6
685	BinPacker: Packing-Based De Novo Transcriptome Assembly from RNA-seq Data. <b>2016</b> , 12, e1004772	91
684	De Novo Transcriptome Analysis of the Common New Zealand Stick Insect Clitarchus hookeri (Phasmatodea) Reveals Genes Involved in Olfaction, Digestion and Sexual Reproduction. <b>2016</b> , 11, e0157783	11
683	De Novo Transcriptomes of Forsythia koreana Using a Novel Assembly Method: Insight into Tissue-and Species-Specific Expression of Lignan Biosynthesis-Related Gene. <b>2016</b> , 11, e0164805	17
682	High-throughput sequencing and de novo transcriptome assembly of Swertia japonica to identify genes involved in the biosynthesis of therapeutic metabolites. <b>2016</b> , 35, 2091-111	26
681	TransRate: reference-free quality assessment of de novo transcriptome assemblies. <b>2016</b> , 26, 1134-44	406
680	Gene coevolution and regulation lock cyclic plant defence peptides to their targets. <b>2016</b> , 210, 717-30	41
679	Draft Genome Sequences of Rhodosporidium toruloides Strains ATCC 10788 and ATCC 10657 with Compatible Mating Types. <b>2016</b> , 4,	16
678	Complete Genome Sequence of a Marine Bacterium, Pseudomonas pseudoalcaligenes Strain S1, with High Mercury Resistance and Bioaccumulation Capacity. <b>2016</b> , 4,	2

677	Positive Selection in Rapidly Evolving Plastid-Nuclear Enzyme Complexes. <b>2016</b> , 204, 1507-1522		44
676	Genome Sequence of Pandoraea sp. ISTKB, a Lignin-Degrading Betaproteobacterium, Isolated from Rhizospheric Soil. <b>2016</b> , 4,		13
675	Complete mitochondrial genomes of the Laotian Rock Rat () confirm deep divergence within the species. <b>2016</b> , 1, 479-482		
674	The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in Chenopodium rubrum. <b>2016</b> , 6, 3065-3076		9
673	Lazer: Distributed memory-efficient assembly of large-scale genomes. 2016,		3
672	Analysis of ethanol fermentation mechanism of ethanol producing white-rot fungus Phlebia sp. MG-60 by RNA-seq. <b>2016</b> , 17, 616		17
671	A new method for decontamination of de novo transcriptomes using a hierarchical clustering algorithm. <i>Bioinformatics</i> , <b>2017</b> , 33, 1293-1300	7.2	12
670	Evolution of Chemosensory Gene Families in Arthropods: Insight from the First Inclusive Comparative Transcriptome Analysis across Spider Appendages. <b>2017</b> , 9, 178-196		31
669	Single-cell TCRseq: paired recovery of entire T-cell alpha and beta chain transcripts in T-cell receptors from single-cell RNAseq. <b>2016</b> , 8, 80		74
668	The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. <b>2016</b> , 6, 24501		66
667	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <b>2016</b> , 6, 34589		30
666	Canine genome assembly correction facilitates identification of a MAP9 deletion as a potential age of onset modifier for RPGRIP1-associated canine retinal degeneration. <b>2016</b> , 27, 237-45		17
665	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <b>2016</b> , 30, 3-13		97
664	De novo assembly of transcriptome from next-generation sequencing data. <b>2016</b> , 4, 94-105		3
663	Back to solitude: Solving the phylogenetic position of the Diazonidae using molecular and developmental characters. <b>2016</b> , 100, 51-56		17
662	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. <b>2016</b> , 12, 1		20
661	Transcriptome reveals senescing callus tissue of Aquilaria malaccensis, an endangered tropical tree, triggers similar response as wounding with respect to terpenoid biosynthesis. <b>2016</b> , 12, 1		10
660	rnaQUAST: a quality assessment tool for de novo transcriptome assemblies. <i>Bioinformatics</i> , <b>2016</b> , 32, 2210-2	7.2	65

659	The influence of trematode parasite burden on gene expression in a mammalian host. <b>2016</b> , 17, 600		4
658	An Overview And Comparison of Tools for RNA-Seq Assembly. <b>2016</b> , 269-286		
657	Comprehensive evaluation of de novo transcriptome assembly programs and their effects on differential gene expression analysis. <i>Bioinformatics</i> , <b>2017</b> , 33, 327-333	7.2	41
656	Post-transcriptional mending of gene sequences: Looking under the hood of mitochondrial gene expression in diplonemids. <b>2016</b> , 13, 1204-1211		12
655	The mitochondrial genome of the pelagic chaetognath,. <b>2016</b> , 1, 515-516		2
654	Theoretical model of circular RNA prediction and classification. 2016,		
653	Analysis RNA-seq and Noncoding RNA. <b>2016</b> , 1480, 125-35		14
652	Synergies and antagonisms in virus interactions. <b>2016</b> , 252, 176-192		56
651	Molecular Evolution and Functional Characterization of a Bifunctional Decarboxylase Involved in Lycopodium Alkaloid Biosynthesis. <b>2016</b> , 171, 2432-44		29
650	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <b>2016</b> , 11, 1650-67		2264
650 649			2264
	2016, 11, 1650-67  De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic	18.3	25
649	2016, 11, 1650-67  De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic Daphnia galeata. 2016, 8, 3120-3139  A novel codon-based de Bruijn graph algorithm for gene construction from unassembled	18.3	25
649 648	2016, 11, 1650-67  De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic Daphnia galeata. 2016, 8, 3120-3139  A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232	18.3	25
649 648 647	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic Daphnia galeata. 2016, 8, 3120-3139  A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232  Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. 2016, 3, 160030  De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan	18.3	25 11 62
649 648 647	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic Daphnia galeata. 2016, 8, 3120-3139  A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232  Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. 2016, 3, 160030  De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. 2016, 6, 28199  Transcriptome profiling of two olive cultivars in response to infection by the CoDiRO strain of	18.3	25 11 62 9
<ul><li>649</li><li>648</li><li>647</li><li>646</li><li>645</li></ul>	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic Daphnia galeata. 2016, 8, 3120-3139  A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232  Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. 2016, 3, 160030  De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. 2016, 6, 28199  Transcriptome profiling of two olive cultivars in response to infection by the CoDiRO strain of Xylella fastidiosa subsp. pauca. 2016, 17, 475  Genome Sequence of Carbon Dioxide-Sequestering Serratia sp. Strain ISTD04 Isolated from Marble	18.3	25 11 62 9

641	The complete mitochondrial genome of horn-nosed boxfish (). <b>2016</b> , 1, 100-102		1
640	Evolution of neuropeptides in non-pterygote hexapods. <b>2016</b> , 16, 51		41
639	Differential mRNA Alternative Splicing. <b>2016</b> , 105-119		4
638	Informed kmer selection for de novo transcriptome assembly. <i>Bioinformatics</i> , <b>2016</b> , 32, 1670-7	7.2	20
637	A new resource for the development of SSR markers: Millions of loci from a thousand plant transcriptomes. <b>2016</b> , 4, 1600024		23
636	Illumina next-generation sequencing reveals the mitochondrial genome of (Orthoptera: Tettigoniidae). <b>2016</b> , 1, 361-362		1
635	Mitochondrial metagenomics: letting the genes out of the bottle. <b>2016</b> , 5, 15		75
634	High-throughput identification of novel conotoxins from the Chinese tubular cone snail (Conus betulinus) by multi-transcriptome sequencing. <b>2016</b> , 5, 17		39
633	Novel modes of RNA editing in mitochondria. <b>2016</b> , 44, 4907-19		42
632	Analyses of transcriptome sequences reveal multiple ancient large-scale duplication events in the ancestor of Sphagnopsida (Bryophyta). <b>2016</b> , 211, 300-18		32
631	Management of Insect Pests to Agriculture. <b>2016</b> ,		5
630	Plant-Herbivore Interactions in the Era of Big Data. <b>2016</b> , 3-48		2
629	Molecular evolution of antioxidant and hypoxia response in long-lived, cancer-resistant blind mole rats: The Nrf2-Keap1 pathway. <i>Gene</i> , <b>2016</b> , 577, 293-8	3.8	14
628	Evaluation of potential candidate genes involved in salinity tolerance in striped catfish (Pangasianodon hypophthalmus) using an RNA-Seq approach. <b>2016</b> , 25, 75-88		23
627	Mesophyll Chloroplast Investment in C3, C4 and C2 Species of the Genus Flaveria. <b>2016</b> , 57, 904-18		20
626	Parallel tagged amplicon sequencing of relatively long PCR products using the Illumina HiSeq platform and transcriptome assembly. <b>2016</b> , 16, 91-102		18
625	Mitochondrial capture enriches mito-DNA 100 fold, enabling PCR-free mitogenomics biodiversity analysis. <b>2016</b> , 16, 470-9		64
624	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , <b>2016</b> , 17, 13	18.3	1203

623	Genomics of the hop pseudo-autosomal regions. <b>2016</b> , 209, 171-179	7
622	RNA-Seq identifies SPGs as a ventral skeletal patterning cue in sea urchins. <b>2016</b> , 143, 703-14	14
621	Complete mitochondrial genome sequence of the pelagic chaetognath, sagitta ferox. <b>2016</b> , 27, 4699-4700	3
620	The mitochondrial genome of the winter stonefly Apteroperla tikumana (Plecoptera, Capniidae). <b>2016</b> , 27, 3030-2	8
619	Mitochondrial genome of Hylaeus dilatatus (Hymenoptera: Colletidae). <b>2016</b> , 27, 3975-3976	8
618	Complete mitochondrial genome of Spiniphilus spinicornis (Coleoptera: Vesperidae: Philinae) and phylogenetic analysis among Cerambycoidea. <b>2017</b> , 28, 145-146	2
617	AmphiBase: A new genomic resource for non-model amphibian species. <b>2017</b> , 55, e23010	1
616	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. <b>2017</b> , 27, 793-800	20
615	Shared characteristics underpinning C4 leaf maturation derived from analysis of multiple C3 and C4 species of Flaveria. <b>2017</b> , 68, 177-189	13
614	Issues with RNA-seq analysis in non-model organisms: A salmonid example. <b>2017</b> , 75, 38-47	4
613	Lineage-Specific and Highly Derived Gene Sequences Among Amoebozoa, Revealed by the Comparative Analysis of Transcriptomes from Twelve Amoebozoan Species. <b>2017</b> , 64, 622-631	
612	Towards a higher-level Ensifera phylogeny inferred from mitogenome sequences. <b>2017</b> , 108, 22-33	30
611	High-confidence coding and noncoding transcriptome maps. <b>2017</b> , 27, 1050-1062	40
610	Updated Reference Genome Sequence and Annotation of AF2122/97. <b>2017</b> , 5,	31
609	Transcriptomic responses to conspecific and congeneric competition in co-occurring Trifolium. <b>2017</b> , 105, 602-615	18
608	Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. <b>2017</b> , 91,	34
607	Bioresources and Bioprocess in Biotechnology. 2017,	1
606	Biodiversity Mining Through Transcriptome Analysis. <b>2017</b> , 207-246	

605	Recent advances in sequence assembly: principles and applications. <b>2017</b> , 16, 361-378	9
604	Insights into the Evolution of Hydroxyproline-Rich Glycoproteins from 1000 Plant Transcriptomes. <b>2017</b> , 174, 904-921	36
603	Next-generation sequencing data used to determine the mitochondrial genomes and a preliminary phylogeny of Verophasmatodea insects. <b>2017</b> , 20, 713-719	9
602	Pipeline to Identify Hydroxyproline-Rich Glycoproteins. <b>2017</b> , 174, 886-903	35
601	DBH: A de Bruijn graph-based heuristic method for clustering large-scale 16S rRNA sequences into OTUs. <b>2017</b> , 425, 80-87	8
600	Identification of the abiotic stress-related transcription in little Neptune grass Cymodocea nodosa with RNA-seq. <b>2017</b> , 34, 47-56	7
599	Transcriptome of Pterospermum kingtungense provides implications on the mechanism underlying its rapid vegetative growth and limestone adaption. <b>2017</b> , 7, 3198	4
598	A survey of the complex transcriptome from the highly polyploid sugarcane genome using full-length isoform sequencing and de novo assembly from short read sequencing. <b>2017</b> , 18, 395	115
597	Genomic inferences of domestication events are corroborated by written records in Brassica rapa. <b>2017</b> , 26, 3373-3388	38
596	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. <b>2017</b> , 91, 3-21	53
595	Deep reticulation and incomplete lineage sorting obscure the diploid phylogeny of rain-lilies and allies (Amaryllidaceae tribe Hippeastreae). <b>2017</b> , 111, 231-247	40
594	Evolutionary History of the Hymenoptera. <b>2017</b> , 27, 1013-1018	372
593	A physiologically-oriented transcriptomic analysis of the midgut of Tenebrio molitor. 2017, 99, 58-66	12
592	Pharmacological screening technologies for venom peptide discovery. <b>2017</b> , 127, 4-19	24
591	EXPath tool-a system for comprehensively analyzing regulatory pathways and coexpression networks from high-throughput transcriptome data. <b>2017</b> , 24, 371-375	9
590	Identification and evolution of a plant cell wall specific glycoprotein glycosyl transferase, ExAD. <b>2017</b> , 7, 45341	22
589	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. <b>2017</b> , 27, 958-967	289
588	Transcriptomic imprints of adaptation to fresh water: parallel evolution of osmoregulatory gene expression in the Alewife. <b>2017</b> , 26, 831-848	37

587 RNA-seq Analysis in Plant**E**ungus Interactions. **2017**, 1-25

586	Avian Genomes Revisited: Hidden Genes Uncovered and the Rates versus Traits Paradox in Birds. <b>2017</b> , 34, 3123-3131	54
585	Abiotic Stress of Seagrasses: Recent Advances in Transcriptomics, Genomics, and Systems Biology. <b>2017</b> , 119-132	О
584	Deep transcriptome profiling sheds light on key players in nucleus implantation induced immune response in the pearl oyster Pinctada martensii. <b>2017</b> , 69, 67-77	18
583	Reference transcriptome assembly and annotation for perennial ryegrass. 2017, 60, 1086-1088	6
582	An expanded mammal mitogenome dataset from Southeast Asia. <b>2017</b> , 6, 1-8	20
581	Transcriptomic Analysis of L. Roots during the Early Infection Process. <b>2017</b> , 10, plantgenome2016.07.0060	26
580	De novo transcriptome assembly for the spiny mouse (Acomys cahirinus). <b>2017</b> , 7, 8996	24
579	FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. <b>2017</b> , 7, 10430	22
578	The transcriptome database, SuperbaSE: An online, open resource for researchers. <b>2017</b> , 7, 6060-6077	7
577	HopBase: a unified resource for Humulus genomics. <b>2017</b> , 2017,	19
576	Genomic and Transcriptomic Analyses of Avian Sex Chromosomes and Sex-Linked Genes. <b>2017</b> , 1650, 69-85	
575	Reducing the number of artifactual repeats in de novo assembly of RNA-Seq data by optimizing the assembly pipeline. <b>2017</b> , 9, 7-12	1
574	The complete mitochondrial transcript of the red tail loach as assembled from RNAseq (Teleostei: Botiidae). <b>2017</b> , 2, 46-47	2
573	Plant Bioinformatics. <b>2017</b> ,	2
572	Concept, Development, and Application of Computational Methods for the Analysis and Integration of Omics Data. <b>2017</b> , 241-266	1
571	The unexpected depths of genome-skimming data: A case study examining Goodeniaceae floral symmetry genes. <b>2017</b> , 5, 1700042	15
570	A novel feature selection for RNA-seq analysis. <b>2017</b> , 71, 245-257	7

## (2017-2017)

569	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. <b>2017</b> , 8, 59		130
568	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <b>2017</b> , 49, 1099-1106		421
567	A scalable and memory-efficient algorithm for de novo transcriptome assembly of non-model organisms. <b>2017</b> , 18, 387		6
566	Improved annotation with de novo transcriptome assembly in four social amoeba species. <b>2017</b> , 18, 120		4
565	Systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change. <b>2017</b> , 17, 42		22
564	T-Cell Differentiation. <b>2017</b> ,		4
563	Next-Generation Sequencing Analysis of Long Noncoding RNAs in CD4+ T Cell Differentiation. <b>2017</b> , 1514, 173-185		19
562	Nonreciprocal complementation of KNOX gene function in land plants. <b>2017</b> , 216, 591-604		26
561	Phylotranscriptomics resolves ancient divergences in the Lepidoptera. <b>2017</b> , 42, 305-316		28
560	De novo transcriptome assembly and characterization of nine tissues of Lonicera japonica to identify potential candidate genes involved in chlorogenic acid, luteolosides, and secoiridoid biosynthesis pathways. <b>2017</b> , 71, 1-15		41
559	Removal of glucuronic acid from xylan is a strategy to improve the conversion of plant biomass to sugars for bioenergy. <b>2017</b> , 10, 224		33
558	Transcriptome assembly strategies for precision medicine. <b>2017</b> , 5, 280-290		2
557	Tools for building de novo transcriptome assembly. <b>2017</b> , 11-12, 41-45		31
556	The Evolutionary Dynamics of the Odorant Receptor Gene Family in Corbiculate Bees. <b>2017</b> , 9, 2023-2036		28
555	Global Dosage Compensation Is Ubiquitous in Lepidoptera, but Counteracted by the Masculinization of the Z Chromosome. <b>2017</b> , 34, 2637-2649		24
554	A Dramatic Difference in Global Gene Expression between TCDD-Treated Atlantic Tomcod Larvae from the Resistant Hudson River and a Nearby Sensitive Population. <b>2017</b> , 9, 2251-2264		1
553	Assembly of the Transcriptome Reveals Key Genes of Flower Pigment Biosynthesis. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 1545	.2	25
552	Transcriptome Assembly and Comparison of C, C-C, and C Species of Tribe Salsoleae (Chenopodiaceae). <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 1939	.2	8

551	ExUTR: a novel pipeline for large-scale prediction of 3GUTR sequences from NGS data. 2017, 18, 847		17
550	De novo assembly of Phlomis purpurea after challenging with Phytophthora cinnamomi. <b>2017</b> , 18, 700		
549	A genome-wide transcriptome map of pistachio (Pistacia vera L.) provides novel insights into salinity-related genes and marker discovery. <b>2017</b> , 18, 627		20
548	DeepBound: accurate identification of transcript boundaries via deep convolutional neural fields. <i>Bioinformatics</i> , <b>2017</b> , 33, i267-i273	7.2	8
547	From Marine Venoms to Drugs: Efficiently Supported by a Combination of Transcriptomics and Proteomics. <b>2017</b> , 15,		21
546	De Novo RNA Sequencing and Expression Analysis of Aconitum carmichaelii to Analyze Key Genes Involved in the Biosynthesis of Diterpene Alkaloids. <b>2017</b> , 22,		24
545	Generation and Characterisation of a Reference Transcriptome for Phalaris (Phalaris aquatica L.). <b>2017</b> , 7, 14		5
544	Characterisation of Faba Bean (Vicia faba L.) Transcriptome Using RNA-Seq: Sequencing, De Novo Assembly, Annotation, and Expression Analysis. <b>2017</b> , 7, 53		10
543	Sequencing and De Novo Assembly of the Toxicodendron radicans (Poison Ivy) Transcriptome. <b>2017</b> , 8,		12
542	Radiogenomic Analysis of Oncological Data: A Technical Survey. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	70
541	An rbcL mRNA-binding protein is associated with C3 to C4 evolution and light-induced production of Rubisco in Flaveria. <b>2017</b> , 68, 4635-4649		4
540	De novo transcriptome analysis shows differential expression of genes in salivary glands of edible bird@nest producing swiftlets. <b>2017</b> , 18, 504		7
539	De novo assembly and comparative transcriptome analysis of the foot from Chinese green mussel (Perna viridis) in response to cadmium stimulation. <b>2017</b> , 12, e0176677		9
538	Transcriptomics technologies. <b>2017</b> , 13, e1005457		385
537	K-mer clustering algorithm using a MapReduce framework: application to the parallelization of the Inchworm module of Trinity. <b>2017</b> , 18, 467		9
536	Venomics of Remipede Crustaceans Reveals Novel Peptide Diversity and Illuminates the Venom <b>®</b> Biological Role. <i>Toxins</i> , <b>2017</b> , 9,	4.9	23
535	Transcriptome Analysis for Non-Model Organism: Current Status and Best-Practices. 2017,		6
534	A divide-and-conquer algorithm for large-scale de novo transcriptome assembly through combining small assemblies from existing algorithms. <b>2017</b> , 18, 895		

533	Comparison of Gene Expression Profiles in Nonmodel Eukaryotic Organisms with RNA-Seq. <b>2018</b> , 1751, 3-16	5
532	Evolution of pyrrolizidine alkaloid biosynthesis in Apocynaceae: revisiting the defence de-escalation hypothesis. <b>2018</b> , 218, 762-773	17
531	Molecular evolution and diversification of the SMXL gene family. <b>2018</b> , 69, 2367-2378	23
530	Functional Characterization of a Glycosyltransferase from the Moss Involved in the Biosynthesis of a Novel Cell Wall Arabinoglucan. <b>2018</b> , 30, 1293-1308	12
529	Next-Generation Sequencing and Data Analysis. 2018, 191-207	2
528	An annotated transcriptome of highly inbred Thuja plicata (Cupressaceae) and its utility for gene discovery of terpenoid biosynthesis and conifer defense. <b>2018</b> , 14, 1	12
527	Transcriptome of the bivalve Limecola balthica L. from Western Pacific: A new resource for studies of European populations. <b>2018</b> , 40, 58-63	2
526	Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. <b>2018</b> , 18, 1020	70
525	Characterization of viral RNA splicing using whole-transcriptome datasets from host species. <b>2018</b> , 8, 3273	4
524	Genetic diversity of K-antigen gene clusters of Escherichia coli and their molecular typing using a suspension array. <b>2018</b> , 64, 231-241	5
523	Genome assembly of the Pink Ip[(Handroanthus impetiginosus, Bignoniaceae), a highly valued, ecologically keystone Neotropical timber forest tree. <b>2018</b> , 7, 1-16	16
522	A Single Mutation Unlocks Cascading Exaptations in the Origin of a Potent Pitviper Neurotoxin. <b>2018</b> , 35, 887-898	17
521	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. <i>Bioinformatics</i> , <b>2018</b> , 34, 1697-1704	2
520	Extensive mitochondrial gene rearrangements in Ctenophora: insights from benthic Platyctenida. <b>2018</b> , 18, 65	10
519	SQUID: transcriptomic structural variation detection from RNA-seq. <i>Genome Biology</i> , <b>2018</b> , 19, 52 18.3	14
518	NGScloud: RNA-seq analysis of non-model species using cloud computing. <i>Bioinformatics</i> , <b>2018</b> , 34, 3405-3407	7 5
517	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. <b>2018</b> , 2, 859-866	39
516	assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. <b>2018</b> , 4, e00583	9

515	IDP-denovo: de novo transcriptome assembly and isoform annotation by hybrid sequencing. <i>Bioinformatics</i> , <b>2018</b> , 34, 2168-2176	25
514	A resource provisioning framework for bioinformatics applications in multi-cloud environments. <b>2018</b> , 78, 379-391	15
513	Cytochrome P450 diversity in the tree of life. <b>2018</b> , 1866, 141-154	136
512	Defective Kernel 39 encodes a PPR protein required for seed development in maize. <b>2018</b> , 60, 45-64	33
511	The roles of mucus-forming mucins, peritrophins and peritrophins with mucin domains in the insect midgut. <b>2018</b> , 27, 46-60	28
510	Phylogeny and the colourful history of jewel bugs (Insecta: Hemiptera: Scutelleridae). <b>2018</b> , 34, 502-516	6
509	Peculiar features of the plastids of the colourless alga Euglena longa and photosynthetic euglenophytes unveiled by transcriptome analyses. <b>2018</b> , 8, 17012	23
508	Phylogenomics and the evolution of hemipteroid insects. <b>2018</b> , 115, 12775-12780	121
507	TransFlow: a modular framework for assembling and assessing accurate de novo transcriptomes in non-model organisms. <b>2018</b> , 19, 416	7
506	Comprehensive evaluation of RNA-seq analysis pipelines in diploid and polyploid species. <b>2018</b> , 7,	14
505	TraRECo: a greedy approach based de novo transcriptome assembler with read error correction using consensus matrix. <b>2018</b> , 19, 653	1
504	A fast detection of fusion genes from paired-end RNA-seq data. <b>2018</b> , 19, 786	15
503	Transcriptomic basis for reinforcement of elm antiherbivore defence mediated by insect egg deposition. <b>2018</b> , 27, 4901-4915	8
502	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy, and Tools. <b>2020</b> , 17, 566-586	9
501	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. <b>2018</b> , 11, 79	8
500	Identification and comparison of key RNA interference machinery from western corn rootworm, fall armyworm, and southern green stink bug. <b>2018</b> , 13, e0203160	19
499	A Bioinformatics Pipeline for the Analysis and Target Prediction of RNA Effectors in Bidirectional Communication During Plant-Microbe Interactions. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1212	9
498	A Computational Protocol to Analyze Metatranscriptomic Data Capturing Fungal-Host Interactions. <b>2018</b> , 1848, 207-233	1

497	The assembled transcriptome of the adult horn fly,. 2018, 19, 1933-1940	4
496	De novo transcriptome assembly of the coral Agaricia lamarcki (Lamarck@ sheet coral) from mesophotic depth in southwest Puerto Rico. <b>2018</b> , 41, 6-11	5
495	De novo assembly and comparative transcriptome characterization of Poecilobdella javanica provide insight into blood feeding of medicinal leeches. <b>2018</b> , 14, 352-361	4
494	Three-Finger Toxin Diversification in the Venoms of Cat-Eye Snakes (Colubridae: Boiga). <b>2018</b> , 86, 531-545	9
493	Plant Pathogenic Fungi and Oomycetes. 2018,	1
492	Transcriptome profiling uncovers Egalactosidases of diverse domain classes influencing hypocotyl development in jute (Corchorus capsularis L.). <b>2018</b> , 156, 20-32	8
491	Differential gene expression in the evolution of sex pheromone communication in New Zealand@ endemic leafroller moths of the genera Ctenopseustis and Planotortrix. <b>2018</b> , 19, 94	5
490	Comparative analysis of mitochondrial genomes of the superfamily Grylloidea (Insecta, Orthoptera) reveals phylogenetic distribution of gene rearrangements. <b>2018</b> , 120, 1048-1054	6
489	The complete mitochondrial genome of the cowpea weevil, (Coleoptera: Chrysomelidae: Bruchinae) and a related phylogenetic analysis of Chrysomelidae. <b>2018</b> , 3, 645-647	2
488	A Guide for Designing and Analyzing RNA-Seq Data. <b>2018</b> , 1783, 35-80	13
487	Gene Expression Analysis. 2018,	1
486	High Throughput Sequencing-Based Approaches for Gene Expression Analysis. <b>2018</b> , 1783, 299-323	5
485	Improving amphibian genomic resources: a multitissue reference transcriptome of an iconic invader. <b>2018</b> , 7, 1-7	12
484	De Novo Transcriptome Assembly and Characterization of Lithospermum officinale to Discover Putative Genes Involved in Specialized Metabolites Biosynthesis. <b>2018</b> , 84, 920-934	17
483	Anticancer Plants: Mechanisms and Molecular Interactions. 2018,	1
482	Guidelines for RNA-seq projects: applications and opportunities in non-model decapod crustacean species. <b>2018</b> , 825, 5-27	10
	species. <b>2010</b> , 023, 3-21	
481	Exploiting the Catalytic Diversity of Short-Chain Dehydrogenases/Reductases: Versatile Enzymes from Plants with Extended Imine Substrate Scope. <b>2018</b> , 19, 1849-1852	15

479	Cyclopropane fatty acid biosynthesis in plants: phylogenetic and biochemical analysis of Litchi Kennedy pathway and acyl editing cycle genes. <b>2018</b> , 37, 1571-1583		1
47 <sup>8</sup>	Expressions of Olfactory Proteins in Locust Olfactory Organs and a Palp Odorant Receptor Involved in Plant Aldehydes Detection. <b>2018</b> , 9, 663		11
477	Full-length transcriptome of Misgurnus anguillicaudatus provides insights into evolution of genus Misgurnus. <b>2018</b> , 8, 11699		20
476	Evaluating the Performance of De Novo Assembly Methods for Venom-Gland Transcriptomics. <i>Toxins</i> , <b>2018</b> , 10,	4.9	29
475	Light-regulated PAS-containing histidine kinases delay gametophore formation in the moss Physcomitrella patens. <b>2018</b> , 69, 4839-4851		9
474	Functional Shifts in Bat Dim-Light Visual Pigment Are Associated with Differing Echolocation Abilities and Reveal Molecular Adaptation to Photic-Limited Environments. <b>2018</b> , 35, 2422-2434		12
473	Bioinformatics Approaches for Genomics and Post Genomics Applications of Anticancer Plants. <b>2018</b> , 283-317		2
472	Functional characterization of the hawkmoth transcriptome reveals strong expression of phorbol ester detoxification and seasonal cold hardiness genes. <b>2018</b> , 15, 20		10
471	Genome sequencing of Lawrence exposes an early branch of the Coleoptera. 2018, 15, 21		25
470	A software tool @roCodetects pervasive cross-species contamination in next generation sequencing data. <b>2018</b> , 16, 28		48
469	Complete mitochondrial genome of the darkling beetle Gonocephalum outreyi (Coleoptera: Tenebrionidae) with phylogenetic implications. <b>2018</b> , 21, 721-730		6
468	Anchored phylogenomics unravels the evolution of spider flies (Diptera, Acroceridae) and reveals discordance between nucleotides and amino acids. <b>2018</b> , 128, 233-245		25
467	Studying Smaller and Neglected Organisms in Modern Evolutionary Venomics Implementing RNASeq (Transcriptomics)-A Critical Guide. <i>Toxins</i> , <b>2018</b> , 10,	4.9	21
466	Mobile Elements Shape Plastome Evolution in Ferns. <b>2018</b> , 10, 2558-2571		14
465	Next-Generation Transcriptome Assembly: Strategies and Performance Analaysis. 2018,		11
464	JUM is a computational method for comprehensive annotation-free analysis of alternative pre-mRNA splicing patterns. <b>2018</b> , 115, E8181-E8190		29
463	Venom-gland transcriptomics and venom proteomics of the giant Florida blue centipede, Scolopendra viridis. <b>2018</b> , 152, 121-136		9
462	Transcriptome Sequencing Approaches to Elucidate Host-Microbe Interactions in Opportunistic Human Fungal Pathogens. <b>2019</b> , 422, 193-235		5

461	Rapid evolution of a voltage-gated sodium channel gene in a lineage of electric fish leads to a persistent sodium current. <b>2018</b> , 16, e2004892	7
460	The Plasmodium falciparum transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigen-encoding var genes. <b>2018</b> , 16, e2004328	38
459	Genome-Wide Scanning of Gene Expression. <b>2019</b> , 452-462	
458	Sequence Analysis. <b>2019</b> , 292-322	3
457	Next Generation Sequence Analysis. <b>2019</b> , 352-363	1
456	Differential Expression From Microarray and RNA-seq Experiments. <b>2019</b> , 372-387	
455	Transcriptome Analysis. <b>2019</b> , 792-805	3
454	A transcriptome-based resolution for a key taxonomic controversy in Cupressaceae. <b>2019</b> , 123, 153-167	11
453	Telomerase RNAs in land plants. <b>2019</b> , 47, 9842-9856	27
452	RNA sequencing: the teenage years. <b>2019</b> , 20, 631-656	519
451	Speciation in Howea Palms Occurred in Sympatry, Was Preceded by Ancestral Admixture, and Was Associated with Edaphic and Phenological Adaptation. <b>2019</b> , 36, 2682-2697	10
450	First mitochondrial genomes of five hoverfly species of the genus s (Diptera: Syrphidae). <b>2019</b> , 62, 677-687	7
449	iMicrobe: Tools and data-dreaiven discovery platform for the microbiome sciences. <b>2019</b> , 8,	11
448	Genome-skimming provides accurate quantification for pollen mixtures. <b>2019</b> , 19, 1433-1446	20
448	Genome-skimming provides accurate quantification for pollen mixtures. <b>2019</b> , 19, 1433-1446  Impact of sequencing depth and technology on de novo RNA-Seq assembly. <b>2019</b> , 20, 604	20 17
447	Impact of sequencing depth and technology on de novo RNA-Seq assembly. <b>2019</b> , 20, 604  Identification and Evaluations of Novel Insecticidal Proteins from Plants of the Class	17

443	Deep Instability in the Phylogenetic Backbone of Heteroptera is Only Partly Overcome by Transcriptome-Based Phylogenomics. <b>2019</b> , 3,	2
442	Optimized sequencing depth and de novo assembler for deeply reconstructing the transcriptome of the tea plant, an economically important plant species. <b>2019</b> , 20, 553	4
441	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <b>2019</b> , 8,	52
440	Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects. <b>2019</b> , 7,	31
439	The Complete Mitochondrial Genome and Expression Profile of Mitochondrial Protein-Coding Genes in the Bisexual and Parthenogenetic. <b>2019</b> , 10, 982	4
438	The Evolution of the Gene Family and Leaf Development in Lycophytes and Ferns. 2019, 8,	18
437	Fungal Physiology and Immunopathogenesis. 2019,	1
436	Advances and Challenges in Metatranscriptomic Analysis. <b>2019</b> , 10, 904	132
435	Proteogenomics: From next-generation sequencing (NGS) and mass spectrometry-based proteomics to precision medicine. <b>2019</b> , 498, 38-46	25
434	RNA-Seq analysis and de novo transcriptome assembly of Cry toxin susceptible and tolerant Achaea janata larvae. <b>2019</b> , 6, 159	5
433	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. 2019, 8,	170
432	Virus- and Interferon Alpha-Induced Transcriptomes of Cells from the Microbat Myotis daubentonii. <b>2019</b> , 19, 647-661	17
431	Sex-based venom variation in the eastern bark centipede (Hemiscolopendra marginata). <b>2019</b> , 169, 45-58	4
430	Gene expression during the early stages of host perception and attachment in adult female Rhipicephalus microplus ticks. <b>2019</b> , 79, 107-124	
429	PepSAVI-MS Reveals a Proline-rich Antimicrobial Peptide in. <b>2019</b> , 82, 2744-2753	10
428	Laying the Foundation for Crassulacean Acid Metabolism (CAM) Biodesign: Expression of the C Metabolism Cycle Genes of CAM in. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 101	17
427	Mitogenomes Uncover Extinct Penguin Taxa and Reveal Island Formation as a Key Driver of Speciation. <b>2019</b> , 36, 784-797	23
426	Identifying similar transcripts in a related organism from de Bruijn graphs of RNA-Seq data, with applications to the study of salt and waterlogging tolerance in Melilotus. <b>2019</b> , 20, 425	

425	Transcriptional profiles of early stage red sea urchins (Mesocentrotus franciscanus) reveal differential regulation of gene expression across development. <b>2019</b> , 48, 100692		8	
424	Convergent recruitment of adamalysin-like metalloproteases in the venom of the red bark centipede (Scolopocryptops sexspinosus). <b>2019</b> , 168, 1-15		5	
423	Uncovering genome wide novel allelic variants for eating and cooking quality in a popular Indian rice cultivar, Samba Mahsuri. <b>2019</b> , 18, 100111		1	
422	Effect of de novo transcriptome assembly on transcript quantification. <b>2019</b> , 9, 8304		20	
421	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <b>2019</b> , 11,		15	
420	Transcriptome assembly for a colour-polymorphic grasshopper (Gomphocerus sibiricus) with a very large genome size. <b>2019</b> , 20, 370		5	
419	Sex-Biased Gene Expression and Dosage Compensation on the Artemia franciscana Z-Chromosome. <b>2019</b> , 11, 1033-1044		14	
418	The first draft genomes of the ant Formica exsecta, and its Wolbachia endosymbiont reveal extensive gene transfer from endosymbiont to host. <b>2019</b> , 20, 301		9	
417	De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. <b>2019</b> , 8,		78	
416	Charting oat (Avena sativa) embryo and endosperm transcription factor expression reveals differential expression of potential importance for seed development. <b>2019</b> , 294, 1183-1197		7	
415	De novo transcriptome assembly of the digitate morphotype of Briareum asbestinum (Octocorallia: Alcyonacea) from the southwest shelf of Puerto Rico. <b>2019</b> , 47, 100676		1	
414	Comparative RNA-seq analysis of the drought-sensitive lentil (Lens culinaris) root and leaf under short- and long-term water deficits. <b>2019</b> , 19, 715-727		16	
413	Two Independent Plastid accD Transfers to the Nuclear Genome of Gnetum and Other Insights on Acetyl-CoA Carboxylase Evolution in Gymnosperms. <b>2019</b> , 11, 1691-1705		8	
412	phylostratr: a framework for phylostratigraphy. <i>Bioinformatics</i> , <b>2019</b> , 35, 3617-3627	7.2	16	
411	Transcriptome-wide identification of WRKY family genes and their expression under cold acclimation in Eucalyptus globulus. <b>2019</b> , 33, 1313-1327		6	
410	Phylogenomic analysis resolves the relationships among net-winged beetles (Coleoptera: Lycidae) and reveals the parallel evolution of morphological traits. <b>2019</b> , 44, 911-925		14	
409	TransLiG: a de novo transcriptome assembler that uses line graph iteration. <i>Genome Biology</i> , <b>2019</b> , 20, 81	18.3	14	
408	The Significance of Comparative Genomics in Modern Evolutionary Venomics. <b>2019</b> , 7,		14	

407	O-Antigen Gene Clusters of Serogroups and Its Application in Development of a Molecular Serotyping Scheme. <b>2019</b> , 10, 741	4
406	Gene Selection and Evolutionary Modeling Affect Phylogenomic Inference of Neuropterida Based on Transcriptome Data. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	5
405	Duplication and selection in Eketoacyl-ACP synthase gene lineages in the sexually deceptive Chiloglottis (Orchidaceace). <b>2019</b> , 123, 1053-1066	3
404	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. 2019, 47, e63	272
403	The Genome of Drosophila innubila Reveals Lineage-Specific Patterns of Selection in Immune Genes. <b>2019</b> , 36, 1405-1417	16
402	Plastome based phylogenetics and younger crown node age in Pelargonium. <b>2019</b> , 137, 33-43	11
401	High-Throughput Identification and Analysis of Novel Conotoxins from Three Vermivorous Cone Snails by Transcriptome Sequencing. <b>2019</b> , 17,	10
400	Genomic and phenotypic analyses of exopolysaccharide biosynthesis in Streptococcus thermophilus S-3. <b>2019</b> , 102, 4925-4934	18
399	Phylogenomic analysis of Calyptratae: resolving the phylogenetic relationships within a major radiation of Diptera. <b>2019</b> , 35, 605-622	29
398	Comparison of gal-lac operons in wild-type galactose-positive and -negative Streptococcus thermophilus by genomics and transcription analysis. <b>2019</b> , 46, 751-758	9
397	Physiological and Genomic Characterization of a Nitrate-Reducing Fe(II)-Oxidizing Bacterium Isolated from Paddy Soil. <b>2019</b> , 36, 433-442	7
396	The complete mitochondrial genome of Tetraphleps aterrimus (Hemiptera: Anthocoridae): Genomic comparisons and phylogenetic analysis of Cimicomorpha. <b>2019</b> , 130, 369-377	6
395	The Reference Genome and Transcriptome Assemblies of the Wild Tomato Species Highlights Birth and Death of NLR Genes Between Tomato Species. <b>2019</b> , 9, 3933-3941	16
394	Next generation sequencing and proteomics in plant virology: how is Colombia doing?. <b>2019</b> , 24, 423-438	3
393	Structural and functional insights into the Diabrotica virgifera virgifera ATP-binding cassette transporter gene family. <b>2019</b> , 20, 899	5
392	Genome draft of the Arabidopsis relative Pachycladon cheesemanii reveals novel strategies to tolerate New Zealand@high ultraviolet B radiation environment. <b>2019</b> , 20, 838	1
391	DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. <b>2019</b> , 20, 698	2
390	Comparative Analysis of Strategies for Transcriptome Assembly in Prokaryotes: as a Case Study. <b>2019</b> , 8,	1

### (2020-2019)

389	Mitochondrial genome characterization of the family Trigonidiidae (Orthoptera) reveals novel structural features and nad1 transcript ends. <b>2019</b> , 9, 19092	2
388	Toward a Common Coordinate Framework for the Human Body. <b>2019</b> , 179, 1455-1467	38
387	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <b>2019</b> , 47, D637-D648	33
386	RNA splicing analysis in genomic medicine. <b>2019</b> , 108, 61-71	13
385	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. <b>2019</b> , 8,	39
384	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. <b>2019</b> , 61, 12-31	16
383	Complex reproductive secretions occur in all extant gymnosperm lineages: a proteomic survey of gymnosperm pollination drops. <b>2019</b> , 32, 153-166	9
382	Phylotranscriptomic Insights into the Diversification of Endothermic Thunnus Tunas. <b>2019</b> , 36, 84-96	11
381	Computational analysis of alternative splicing in plant genomes. <i>Gene</i> , <b>2019</b> , 685, 186-195 3.8	7
380	Transcriptome Sequencing (RNA-Seq). <b>2019</b> , 33-49	O
379	The relapsing fever spirochete Borrelia turicatae persists in the highly oxidative environment of its soft-bodied tick vector. <b>2019</b> , 21, e12987	9
378	Theory and A Heuristic for the Minimum Path Flow Decomposition Problem. <b>2019</b> , 16, 658-670	6
377	IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. <b>2020</b> , 17, 938-948	3
376	Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. <b>2020</b> , 21, 1164-1181	19
375	Next-generation transcriptome assembly and analysis: Impact of ploidy. <b>2020</b> , 176, 14-24	13
374	Muscle transcriptome signature and gene regulatory network analysis in two divergent lines of a hilly bovine species Mithun (Bos frontalis). <b>2020</b> , 112, 252-262	9
373	Microarray-Based Quality Assessment as a Supporting Criterion for de novo Transcriptome Assembly Selection. <b>2020</b> , 17, 198-206	
372	The sweet side of venom: Glycosylated prothrombin activating metalloproteases from Dispholidus typus (boomslang) and Thelotornis mossambicanus (twig snake). <b>2020</b> , 227, 108625	5

371	Phylogenomics of Auchenorrhyncha (Insecta: Hemiptera) using transcriptomes: examining controversial relationships via degeneracy coding and interrogation of gene conflict. <b>2020</b> , 45, 85-113	16
370	The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. <b>2020</b> , 45, 188-204	25
369	Convergent evolution of the UbiA prenyltransferase family underlies the independent acquisition of furanocoumarins in plants. <b>2020</b> , 225, 2166-2182	10
368	Disentangling sRNA-Seq data to study RNA communication between species. <b>2020</b> , 48, e21	5
367	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <b>2020</b> , 71, 741-765	22
366	Bioinformatics-assisted, integrated omics studies on medicinal plants. <b>2020</b> , 21, 1857-1874	14
365	Organellomic data sets confirm a cryptic consensus on (unrooted) land-plant relationships and provide new insights into bryophyte molecular evolution. <b>2020</b> , 107, 91-115	18
364	Transcriptome analysis of Haematococcus pluvialis of multiple defensive systems against nitrogen starvation. <b>2020</b> , 134, 109487	15
363	The developmental transcriptome for Lytechinus variegatus exhibits temporally punctuated gene expression changes. <b>2020</b> , 460, 139-154	4
362	The Expansion and Diversification of Pentatricopeptide Repeat RNA-Editing Factors in Plants. <b>2020</b> , 13, 215-230	28
361	Venom Peptides with Dual Modulatory Activity on the Voltage-Gated Sodium Channel Na1.1 Provide Novel Leads for Development of Antiepileptic Drugs. <b>2020</b> , 3, 119-134	9
360	Transcriptomic analysis of root specific drought mediated response of G. arboreum and G. hirsutum. <b>2020</b> , 75, 627-636	2
359	RNA-seq and ChIP-seq as Complementary Approaches for Comprehension of Plant Transcriptional Regulatory Mechanism. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 21,	13
358	A promiscuous coenzyme A ligase provides benzoyl-coenzyme A for xanthone biosynthesis in Hypericum. <b>2020</b> , 104, 1472-1490	6
357	Transcriptomics of the Rooibos (Aspalathus linearis) Species Complex. <b>2020</b> , 9, 19	2
356	Comparative transcriptome analysis suggests convergent evolution of desiccation tolerance in Selaginella species. <b>2020</b> , 20, 468	4
355	Liver transcriptome resources of four commercially exploited teleost species. <b>2020</b> , 7, 214	1
354	Sequencing and analysis of gerbera daisy leaf transcriptomes reveal disease resistance and susceptibility genes differentially expressed and associated with powdery mildew resistance. <b>2020</b> , 20, 539	6

#### (2020-2020)

353	Transcriptional variation of sensory-related genes in natural populations of Aedes albopictus. <b>2020</b> , 21, 547	3
352	A new classification of Carex (Cyperaceae) subgenera supported by a HybSeq backbone phylogenetic tree. <b>2020</b> , 194, 141-163	23
351	Cathepsins L and B in Dysdercus peruvianus, Rhodnius prolixus, and Mahanarva fimbriolata. Looking for enzyme adaptations to digestion. <b>2020</b> , 127, 103488	1
350	Raw transcriptomics data to gene specific SSRs: a validated free bioinformatics workflow for biologists. <b>2020</b> , 10, 18236	2
349	Sympatric speciation in mountain roses () on an oceanic island. <b>2020</b> , 375, 20190542	5
348	Characterization of a Lytic Bacteriophage vB_EfaS_PHB08 Harboring Endolysin Lys08 Against Biofilms. <b>2020</b> , 8,	9
347	Short k-mer abundance profiles yield robust machine learning features and accurate classifiers for RNA viruses. <b>2020</b> , 15, e0239381	4
346	TransBorrow: genome-guided transcriptome assembly by borrowing assemblies from different assemblers. <b>2020</b> , 30, 1181-1190	9
345	Characterization and analysis of full-length transcriptomes from two grasshoppers, Gomphocerus licenti and Mongolotettix japonicus. <b>2020</b> , 10, 14228	1
344	A LINE-1 insertion situated in the promoter of IMPG2 is associated with autosomal recessive progressive retinal atrophy in Lhasa Apso dogs. <b>2020</b> , 21, 100	4
343	The Use of Bioinformatic Tools in Symbiosis and Co-Evolution Studies. <b>2020</b> ,	
342	Deadly Proteomes: A Practical Guide to Proteotranscriptomics of Animal Venoms. <b>2020</b> , 20, e1900324	10
341	Statistical Optimisation of Phenol Degradation and Pathway Identification through Whole Genome Sequencing of the Cold-Adapted Antarctic Bacterium, sp. Strain AQ5-07. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	4
340	TagSeq for gene expression in non-model plants: A pilot study at the Santa Rita Experimental Range NEON core site. <b>2020</b> , 8, e11398	2
339	Gene Sequences of Potential Targets of Insecticidal PF2 Lectin Identified from the Larval De Novo Transcriptome of the Mexican Bean Weevil (; Boheman 1833). <b>2020</b> , 11,	1
338	Multiomics-based characterization of specialized metabolites biosynthesis in Cornus Officinalis. <b>2020</b> , 27,	6
337	Transcriptional Sequencing and Gene Expression Analysis of Various Genes in Fruit Development of Three Different Black Pepper (L.) Varieties. <b>2020</b> , 2020, 1540915	3
336	Nuclear phylogenomic analyses of asterids conflict with plastome trees and support novel relationships among major lineages. <b>2020</b> , 107, 790-805	29

335	Ampliconic Genes on the Great Ape Y Chromosomes: Rapid Evolution of Copy Number but Conservation of Expression Levels. <b>2020</b> , 12, 842-859		3
334	Evolution of multiple sex-chromosomes associated with dynamic genome reshuffling in Leptidea wood-white butterflies. <b>2020</b> , 125, 138-154		8
333	RefShannon: A genome-guided transcriptome assembler using sparse flow decomposition. <b>2020</b> , 15, e0232946		6
332	Lineage Divergence of in Southern China Based on Mitochondrial Genome. <b>2020</b> , 11, 65		2
331	Complete genome sequence of a novel rhabdo-like virus from the Chinese black cutworm Agrotis ipsilon (Lepidoptera: Noctuidae). <b>2020</b> , 165, 989-991		1
330	A putative AGAMOUS ortholog is a candidate for the gene determining ease of dehulling in Tartary buckwheat (Fagopyrum tataricum). <b>2020</b> , 251, 85		3
329	A Phylogenomic Perspective on Evolution and Discordance in the Alpine-Arctic Plant Clade (Saxifragaceae). <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 1773	5.2	15
328	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <b>2020</b> , 15, 2-16		5
327	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (Silurus asotus). <b>2020</b> , 112, 2603-2614		6
326	Transcriptional profiling and physiological roles of Aedes aegypti spermathecal-related genes. <b>2020</b> , 21, 143		9
325	The genome of the sea anemone Actinia equina (L.): Meiotic toolkit genes and the question of sexual reproduction. <b>2020</b> , 53, 100753		9
324	Tentacle Transcriptomes of the Speckled Anemone (Actiniaria: Actiniidae: Oulactis sp.): Venom-Related Components and Their Domain Structure. <b>2020</b> , 22, 207-219		8
323	iPAC: a genome-guided assembler of isoforms via phasing and combing paths. <i>Bioinformatics</i> , <b>2020</b> , 36, 2712-2717	7.2	2
322	Tools for Analysis of the Microbiome. <b>2020</b> , 65, 674-685		22
321	Compression-induced dedifferentiation of adipocytes promotes tumor progression. <b>2020</b> , 6, eaax5611		24
320	Roles of BdUNICULME4 and BdLAXATUM-A in the non-domesticated grass Brachypodium distachyon. <b>2020</b> , 103, 645-659		5
319	Combining independent de novo assemblies to optimize leaf transcriptome of Persian walnut. <b>2020</b> , 15, e0232005		8
318	Genomics of algae: Its challenges and applications. <b>2020</b> , 261-283		

### (2021-2020)

317	Crossing the Border: From Keto- to Imine Reduction in Short-Chain Dehydrogenases/Reductases. <b>2020</b> , 21, 2615-2619	7
316	Phylogenomic Evidence for the Monophyly of Bryophytes and the Reductive Evolution of Stomata. <b>2020</b> , 30, 2001-2012.e2	59
315	Next Generation Sequencing Methods: Pushing the Boundaries. <b>2021</b> , 19-46	
314	Phylogenomics reveals accelerated late Cretaceous diversification of bee flies (Diptera: Bombyliidae). <b>2021</b> , 37, 276-297	6
313	Drought responsiveness in black pepper (Piper nigrum L.): Genes associated and development of a web-genomic resource. <b>2021</b> , 172, 669-683	2
312	Comparative transcriptomics of ice-crawlers demonstrates cold specialization constrains niche evolution in a relict lineage. <b>2021</b> , 14, 360-382	1
311	Plant-herbivorous insect networks: who is eating what revealed by long barcodes using high-throughput sequencing and Trinity assembly. <b>2021</b> , 28, 127-143	3
310	Next Generation Sequencing: Transcriptomics. <b>2021</b> , 1-11	
309	Revising transcriptome assemblies with phylogenetic information. <b>2021</b> , 16, e0244202	4
308	A Guide to RNAseq Data Analysis Using Bioinformatics Approaches. <b>2021</b> , 243-260	
307	Relevance of Bioinformatics and Database in Omics Study. <b>2021</b> , 19-39	
306	Bioinformatics Approaches for Fungal Biotechnology. <b>2021</b> , 536-554	
305	MultiTrans: an algorithm for path extraction through mixed integer linear programming for transcriptome assembly. <b>2021</b> , PP,	2
304	A Comprehensive Guide to Potato Transcriptome Assembly. <b>2021</b> , 2354, 155-192	
303	Mushroom Transcriptome. <b>2021</b> , 572-591	О
302	RNA sequencing: a revolutionary tool for transcriptomics. <b>2021</b> , 61-73	
301	Pilot RNA-seq data from 24 species of vascular plants at Harvard Forest. <b>2021</b> , 9, e11409	1
300	Beyond Drosophila: resolving the rapid radiation of schizophoran flies with phylotranscriptomics. <b>2021</b> , 19, 23	4

299	Jumper Enables Discontinuous Transcript Assembly in Coronaviruses.	О
298	TransPi 🖟 comprehensive TRanscriptome ANalysiS PIpeline for de novo transcriptome assembly.	4
297	FINDER: An automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences.	1
296	Electric Blue: Molecular Evolution of Three-Finger Toxins in the Long-Glanded Coral Snake Species.  Toxins, <b>2021</b> , 13,	3
295	Comparative transcriptome analysis of Rheum australe, an endangered medicinal herb, growing in its natural habitat and those grown in controlled growth chambers. <b>2021</b> , 11, 3702	6
294	Improving the quality of barley transcriptome de novo assembling by using a hybrid approach for lines with varying spike and stem coloration <b>2021</b> , 25, 30-38	1
293	Phylotranscriptomics points to multiple independent origins of multicellularity and cellular differentiation in the volvocine algae.	
292	The mitochondrial genome of a leaf insect (Phasmatodea: Phylliidae) in Southeast Asia. <b>2021</b> , 6, 888-890	2
291	Plant Transcriptome Assembly: Review and Benchmarking. 109-130	
290	Comparing de novo transcriptome assembly tools in di- and autotetraploid non-model plant species. <b>2021</b> , 22, 146	2
289	Crop pangenomes <b>2021</b> , 25, 57-63	5
288	Cytosolic aromatic aldehyde dehydrogenase provides benzoic acid for xanthone biosynthesis in Hypericum. <b>2021</b> , 160, 82-93	2
287	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <b>2021</b> , 31, 713-720	2
286	An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes.	
285	Genomic features underlying the evolutionary transitions of Apibacter to honey bee gut symbionts. <b>2021</b> ,	3
284	Common virulence gene expression in adult first-time infected malaria patients and severe cases. <b>2021</b> , 10,	3
283	FINDER: an automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences. <b>2021</b> , 22, 205	5
282	Transcriptomic analysis of resistant and susceptible responses in a new model root-knot nematode infection system using Solanum torvum and Meloidogyne arenaria.	

281	NGScloud2: optimized bioinformatic analysis using Amazon Web Services. <b>2021</b> , 9, e11237		2
280	Phylotranscriptomic insights into Asteraceae diversity, polyploidy, and morphological innovation. <b>2021</b> , 63, 1273-1293		3
279	Transcriptomic Analysis of Resistant and Susceptible Responses in a New Model Root-Knot Nematode Infection System Using and. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 680151	6.2	2
278	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <b>2021</b> , 184, 3542-3558.e16		45
277	The Evolutionary Patterns of Genome Size in Ensifera (Insecta: Orthoptera). 2021, 12, 693541		4
276	Schistosome W-Linked Genes Inform Temporal Dynamics of Sex Chromosome Evolution and Suggest Candidate for Sex Determination. <b>2021</b> , 38, 5345-5358		2
275	Gene count from target sequence capture places three whole genome duplication events in Hibiscus L. (Malvaceae). <b>2021</b> , 21, 107		О
274	Underwater CAM photosynthesis elucidated by Isoetes genome.		O
273	Chloroplast genome features of Moricandia arvensis (Brassicaceae), a C3-C4 intermediate photosynthetic species. <b>2021</b> , 16, e0254109		
272	Genotype-Specific Expression and NLR Repertoire Contribute to Phenotypic Resistance Diversity in. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 675760	6.2	O
271	Research Progress and Future Development Trends in Medicinal Plant Transcriptomics. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 691838	6.2	3
270	Isolation, Characterization, and Genome Sequence Analysis of a Novel Lytic Phage, Xoo-sp15 Infecting Xanthomonas oryzae pv. oryzae. <b>2021</b> , 78, 3192-3200		3
269	Combining molecular datasets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of stoneflies (Insecta: Plecoptera). <b>2021</b> , 46, 952-967		3
268	Metatranscriptomic Analysis of Bacterial Communities on Laundered Textiles: A Pilot Case Study. <b>2021</b> , 9,		1
267	SAUTE: sequence assembly using target enrichment. <b>2021</b> , 22, 375		O
266	TransRef enables accurate transcriptome assembly by redefining accurate neo-splicing graphs. <b>2021</b> , 22,		1
265	Demystifying emerging bulk RNA-Seq applications: the application and utility of bioinformatic methodology. <b>2021</b> , 22,		3
264	Phylogenomic and mitogenomic data can accelerate inventorying of tropical beetles during the current biodiversity crisis.		

263	Phylotranscriptomics points to multiple independent origins of multicellularity and cellular differentiation in the volvocine algae. <b>2021</b> , 19, 182	5	
262	Can functional genomic diversity provide novel insights into mechanisms of community assembly? A pilot study from an invaded alpine streambed. <b>2021</b> , 11, 12075-12091		
261	Gene-Metabolite Network Analysis Revealed Tissue-Specific Accumulation of Therapeutic Metabolites in. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	5.3 3	
260	Chromosome-scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. <b>2021</b> , 108, 1174-1192	2	
259	A high-quality genome assembly of Jasminum sambac provides insight into floral trait formation and Oleaceae genome evolution. <b>2021</b> ,	2	
258	An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. <b>2021</b> , 17, e1008949		
257	Comparative Genomic Analysis of Strains Isolated from Different Niches. <b>2021</b> , 12,	1	
256	A Bayesian approach for accurate de novo transcriptome assembly. <b>2021</b> , 11, 17663	O	
255	Transitions to asexuality and evolution of gene expression in brine shrimp. <b>2021</b> , 288, 20211720	0	
254	Response process and adaptation mechanism of estuarine benthic microbiota to polyvinyl chloride microplastics with and without phthalates. <b>2022</b> , 806, 150693	o	
253	Prospects and challenges of cancer systems medicine: from genes to disease networks. 2021,	3	
252	Non-coding Natural Antisense Transcripts: Analysis and Application. <b>2021</b> , 340, 75-101	4	
251	Computational and functional annotation at genomic scale: gene expression and analysis. <b>2021</b> , 361-387		
250	A Pipeline for Non-model Organisms for Transcriptome Assembly, Annotation, and Gene Ontology Analysis Using Open Tools: Case Study with Scots Pine. <b>2021</b> , 11, e3912	3	
249	Genomics and Transcriptomics Advance in Plant Sciences. <b>2019</b> , 419-448	2	
248	Euzebya rosea sp. nov., a rare actinobacterium isolated from the East China Sea and analysis of two genome sequences in the genus Euzebya. <b>2018</b> , 68, 2900-2905	6	
247	sp. nov., from phycosphere microbiota of toxic marine dinoflagellate. <b>2020</b> , 70, 4390-4397	2	
246	Isolation and characterization of a novel phage Xoo-sp2 that infects Xanthomonas oryzae pv. oryzae. <b>2018</b> , 99, 1453-1462	1	6

245	Benchmark Analysis of Algorithms for Determining and Quantifying Full-length mRNA Splice Forms from RNA-Seq Data.	3
244	The Junction Usage Model (JUM): A method for comprehensive annotation-free analysis of alternative pre-mRNA splicing patterns.	4
243	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention.	2
242	Scallop enables accurate assembly of transcripts through phasing-preserving graph decomposition.	1
241	The Oyster River Protocol: A Multi Assembler and Kmer Approach For de novo Transcriptome Assembly.	1
240	Progress Towards Plant Community Transcriptomics: Pilot RNA-Seq Data from 24 Species of Vascular Plants at Harvard Forest.	2
239	TagSeq for gene expression in non-model plants: a pilot study at the Santa Rita Experimental Range NEON core site.	1
238	MINTIE: identifying novel structural and splice variants in transcriptomes using RNA-seq data.	3
237	A consensus-based ensemble approach to improve transcriptome assembly.	1
236	Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of the enigmatic genusEmbletonia.	1
235	Genomic features underlying the evolutionary transitions of Apibacter to honey bee gut symbionts.	0
234	Gene expression profiling of malaria parasites reveals common virulence gene expression in adult first-time infected patients and severe cases.	1
233	Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes.	5
232	phylostratr: A framework for phylostratigraphy.	1
231	The genome of Drosophila innubila reveals lineage-specific patterns of selection in immune genes.	5
230	Comparative assessment of long-read error-correction software applied to RNA-sequencing data.	4
229	MitoZ: A toolkit for mitochondrial genome assembly, annotation and visualization.	2
228	Disentangling sRNA-Seq data to study RNA communication between species.	1

227	SPIKEPIPE: A metagenomic pipeline for the accurate quantification of eukaryotic species occurrences and abundances using DNA barcodes or mitogenomes.	2
226	Longest protein, longest transcript or most expression, for accurate gene reconstruction of transcriptomes?.	13
225	Sequence Analysis of a Jumbo Bacteriophage, That Infects Xanthomonas oryzae pv. oryzae. <b>2020</b> , 9,	6
224	Big Omics Data Experience. <b>2015</b> , 2015,	8
223	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. <b>2016</b> , 12, e1005224	29
222	Comparisons of de novo transcriptome assemblers in diploid and polyploid species using peanut (Arachis spp.) RNA-Seq data. <b>2014</b> , 9, e115055	48
221	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <b>2016</b> , 11, e0146062	76
220	Sequencing, De Novo Assembly, and Annotation of the Transcriptome of the Endangered Freshwater Pearl Bivalve, Cristaria plicata, Provides Novel Insights into Functional Genes and Marker Discovery. <b>2016</b> , 11, e0148622	40
219	A Deep Insight into the Sialome of Male and Female Aedes aegypti Mosquitoes. <b>2016</b> , 11, e0151400	44
218	Comparison of De Novo Transcriptome Assemblers and k-mer Strategies Using the Killifish, Fundulus heteroclitus. <b>2016</b> , 11, e0153104	26
217	KrillDB: A de novo transcriptome database for the Antarctic krill (Euphausia superba). <b>2017</b> , 12, e0171908	16
216	Differential genomic arrangements in Caryophyllales through deep transcriptome sequencing of A. hypochondriacus. <b>2017</b> , 12, e0180528	4
215	Identification of Immediate Early Genes in the Nervous System of Snail. <b>2019</b> , 6,	7
214	Hardware Performance Evaluation of De novo Transcriptome Assembly Software in Amazon Elastic Compute Cloud. <b>2020</b> , 15, 420-430	2
213	Eupolybothrus cavernicolus Komerilli & Stoev sp. n. (Chilopoda: Lithobiomorpha: Lithobiidae): the first eukaryotic species description combining transcriptomic, DNA barcoding and micro-CT imaging data. <b>2013</b> , e1013	41
212	Transcriptional signatures of somatic neoblasts and germline cells in. <b>2016</b> , 5,	33
211	Genetic analysis of the Arabidopsis TIR1/AFB auxin receptors reveals both overlapping and specialized functions. <b>2020</b> , 9,	45
210	Augmenting transcriptome assembly by combining de novo and genome-guided tools. <b>2013</b> , 1, e133	19

209	Assessing the utility of the Oxford Nanopore MinION for snake venom gland cDNA sequencing. <b>2015</b> , 3, e1441	29
208	The myogenic electric organ of Sternopygus macrurus: a non-contractile tissue with a skeletal muscle transcriptome. <b>2016</b> , 4, e1828	9
207	Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. 2017, 5, e3486	5
206	Transcriptome sequencing reveals high isoform diversity in the ant. <b>2017</b> , 5, e3998	4
205	The Oyster River Protocol: a multi-assembler and kmer approach for de novo transcriptome assembly. <b>2018</b> , 6, e5428	37
204	Characterization of the mitochondrial genome of Wei & Du sp. nov. (Hymenoptera: Argidae). <b>2018</b> , 6, e6131	4
203	Genes of the pig, , reconstructed with EvidentialGene. <b>2019</b> , 7, e6374	19
202	MINTIE: identifying novel structural and splice variants in transcriptomes using RNA-seq data.  Genome Biology, <b>2021</b> , 22, 296	5
201	A consensus-based ensemble approach to improve transcriptome assembly. <b>2021</b> , 22, 513	0
200	Development of a metatranscriptomic analysis method for multiple intestinal sites and its application to the common marmoset intestine.	
199	Assessing Host-Pathogen Interaction Networks via RNA-Seq Profiling: A Systems Biology Approach.	
198	References. <b>2016</b> , 213-236	
197	Improved Annotation with de novo Transcriptome Assembly in Four Social Amoeba Species.	
196	HySA: A Hybrid Structural variant Assembly approach using next generation and single-molecule sequencing technologies.	1
195	Glutton: large-scale integration of non-model organism transcriptome data for comparative analysis.	2
194	De novo transcriptome assembly for the spiny mouse (Acomys cahirinus).	
193	Efficient Heuristic for Decomposing a Flow with Minimum Number of Paths.	1
192	Updated reference genome sequence and annotation of Mycobacterium bovis AF2122/97.	

191	Workflow Integration and Orchestration, Opportunities and the Challenges. <b>2017</b> , 137-156	
190	High-confidence Coding and Noncoding Transcriptome Maps.	
189	Genomic inferences of domestication events are corroborated by written records in Brassica rapa.	
188	DeepBound: Accurate Identification of Transcript Boundaries via Deep Convolutional Neural Fields.	1
187	The evolutionary dynamics of the odorant receptor gene family in corbiculate bees.	1
186	K-mer clustering algorithm using a MapReduce framework: application to the parallelization of the Inchworm module of Trinity.	
185	SQUID: Transcriptomic Structural Variation Detection from RNA-seq.	
184	A novel feature selection for RNA-seq analysis.	
183	TraRECo: A Greedy Approach based de novo Transcriptome Assembler with Read Error Correction using Consensus Matrix.	
182	DTAST: A Novel Radical Framework for de Novo Transcriptome Assembly Based on Suffix Trees. <b>2018</b> , 740-745	
181	Peculiar features of the plastids of the colourless algaEuglena longaand photosynthetic euglenophytes unveiled by transcriptome analyses.	
180	Effect of de novo transcriptome assembly on transcript quantification.	
179	Genes of the Pig, Sus scrofa, reconstructed with EvidentialGene.	1
178	Genome-skimming provides accurate quantification for pollen mixtures Authors.	
177	Bacillus acanthi sp. nov., isolated from the rhizosphere soil of a mangrove plant Acanthus ilicifolius. <b>2018</b> , 68, 3047-3051	5
176	Acuticoccus kandeliae sp. nov., isolated from rhizosphere soil of the mangrove plant Kandelia, and emended description of Acuticoccus yangtzensis. <b>2018</b> , 68, 3316-3321	2
175	The first draft genomes of the ant Formica exsecta, and its Wolbachia endosymbiont reveal extensive gene transfer from endosymbiont to host.	0
174	Genetic analysis of the Arabidopsis TIR1/AFB auxin receptors reveals both overlapping and specialized functions.	

173	The Developmental Transcriptome for Lytechinus variegatus Exhibits Temporally Punctuated Gene Expression Changes.	
172	The de novo reference genome and transcriptome assemblies of the wild tomato species Solanum chilense.	1
171	In silico analysis of drought responsive transposons and transcription factors in Solanum tuberosum L <b>2019</b> , 23, 189-195	
170	sp. nov., an endophytic actinomycete isolated from the roots of. <b>2019</b> , 71,	1
169	The evaluation of RNA-Seq de novo assembly by PacBio long read sequencing.	2
168	Short k-mer Abundance Profiles Yield Robust Machine Learning Features and Accurate Classifiers for RNA Viruses.	
167	De novo transcriptome analysis and gene expression profiling of fish scales isolated from Carassius auratus during space flight: Impact of melatonin on gene expression in response to space radiation. <b>2020</b> , 22, 2627-2636	2
166	Comparative RNA-Seq Analysis Reveals Potentially Resistance-Related Genes in Response to Bacterial Canker of Tomato. <b>2021</b> , 12,	3
165	NGScloud2: optimized bioinformatic analysis using Amazon Web Services.	
164	Comparative transcriptomics of spotted seatrout () populations to cold and heat stress. <b>2021</b> , 11, 1352-1367	3
163	Reference-free reconstruction and quantification of transcriptomes from Nanopore long-read sequencing.	2
162	The integrin-mediated adhesome complex, essential to multicellularity, is present in the most recent common ancestor of animals, fungi, and amoebae.	
161	Underwater CAM photosynthesis elucidated by Isoetes genome. <b>2021</b> , 12, 6348	3
160	Metagenomic Assembly: Overview, Challenges and Applications. <b>2016</b> , 89, 353-362	50
159	RNA-seq for revealing the function of the transcriptome. <b>2022</b> , 105-129	
158	A New Mitochondrial Genome of (Horvth) (Hemiptera: Delphacidae) and Mitogenome-Wide Investigation on Polymorphisms <b>2021</b> , 12,	3
157	Transcriptome Analysis Reveals Higher Levels of Mobile Element-Associated Abnormal Gene Transcripts in Temporal Lobe Epilepsy Patients. <b>2021</b> , 12, 767341	
156	Jumper enables discontinuous transcript assembly in coronaviruses. <b>2021</b> , 12, 6728	O

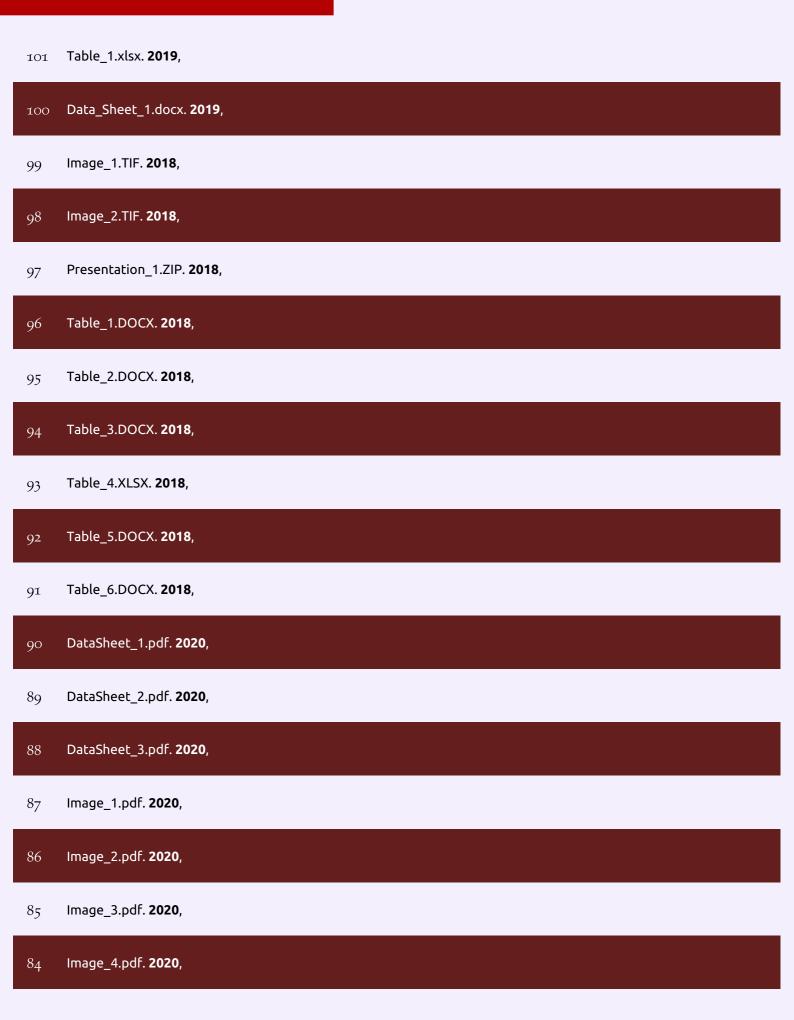
155	The Novel Nora Virus Confers Deleterious Effects to the Fitness of (Lepidoptera: Noctuidae). <b>2021</b> , 12, 727202		0
154	Comparative morphological, physiological, biochemical and genomic studies reveal novel genes of Dunaliella bioculata and D. quartolecta in response to salt stress. <b>2021</b> , 1		1
153	ClusTrast: a short read de novo transcript isoform assembler guided by clustered contigs.		О
152	A simple guide to de novo transcriptome assembly and annotation 2022,		4
151	Fecal microbiota transplantation as therapy for recurrent Clostridioides difficile infection is associated with amelioration of delirium and accompanied by changes in fecal microbiota and the metabolome <b>2021</b> , 73, 102502		1
150	Diet outweighs genetics in shaping gut microbiomes in Asian honeybee.		1
149	Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data <b>2022</b> ,		1
148	Transcriptome Profiles of Streptomyces sp Springer Protocols, <b>2022</b> , 339-346	0.3	
147	Comparative study of ten thogotovirus isolates and their distinct characteristics 2022, JVI0155621		1
146	Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins <b>2022</b> , 20, 4		O
145	ORTHOSKIM: in silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications <b>2022</b> ,		O
144	SLDMS: A Tool for Calculating the Overlapping Regions of Sequences <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 813036	6.2	
143	De novo and comparative transcriptomic analysis explain morphological differences in Panax notoginseng taproots <b>2022</b> , 23, 86		0
142	Amphioxus muscle transcriptomes reveal vertebrate-like myoblast fusion genes and a highly conserved role of insulin signalling in the metabolism of muscle <b>2022</b> , 23, 93		1
141	TransPi - a comprehensive TRanscriptome ANalysiS PIpeline for de novo transcriptome assembly <b>2022</b> ,		3
140	Gut Metagenome as a Potential Diagnostic and Predictive Biomarker in Slow Transit Constipation <b>2021</b> , 8, 777961		1
139	TahcoRoll: fast genomic signature profiling via thinned automaton and rolling hash. 2022,		0
138	Modern Approaches for Transcriptome Analyses in Plants <b>2021</b> , 1346, 11-50		

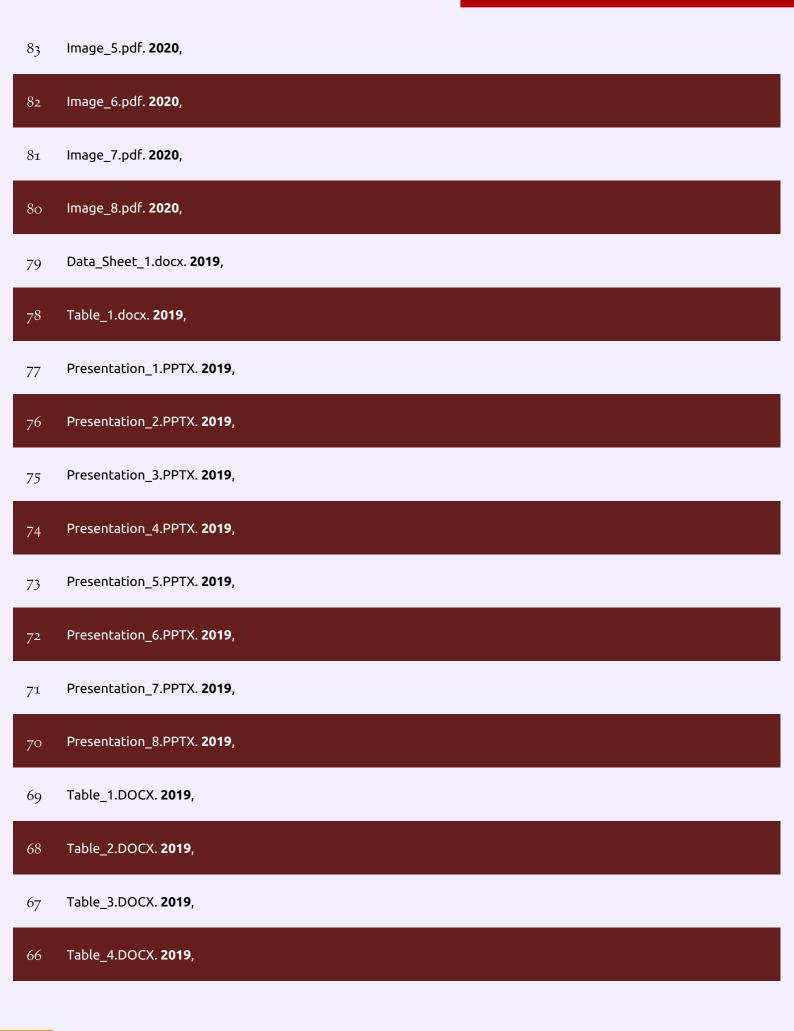
137	Pinus Sylvestris as a Reference Plant Species in Radiation Research: Transcriptomics of Trees from the Chernobyl Zone. <b>2022</b> , 219-232	
136	Using RNA-Seq for Transcriptome Profiling of Botrylloides sp. Regeneration <b>2022</b> , 2450, 599-615	O
135	Characterization and Comparative Analysis of Mitochondrial Genomes Among the Calliphoridae (Insecta: Diptera: Oestroidea) and Phylogenetic Implications <b>2022</b> , 13, 799203	
134	Alphaflexivirus Genomes in Stony Coral Tissue Loss Disease-Affected, Disease-Exposed, and Disease-Unexposed Coral Colonies in the U.S. Virgin Islands <b>2022</b> , 11, e0119921	O
133	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. 1	O
132	Discovery of 194 Unreported Conopeptides and Identification of a New Protein Disulfide Isomerase in Conus caracteristicus Using Integrated Transcriptomic and Proteomic Analysis. <b>2022</b> , 9,	
131	Dynamic molecular evolution of a supergene with suppressed recombination in white-throated sparrows.	
130	Transcriptome characterization of Larrea tridentata and identification of genes associated with phenylpropanoid metabolic pathways <b>2022</b> , 17, e0265231	
129	The first complete mitochondrial genome of Dufouriellini (Hemiptera: Anthocoridae) and implications for its phylogenetic position <b>2022</b> , e21885	1
128	Applications of de Bruijn graphs in microbiome research. <b>2022</b> , 1,	O
127	Tiglon enables accurate transcriptome assembly via integrating mappings of different aligners <b>2022</b> , 25, 104067	
127		
	<b>2022</b> , 25, 104067  Transcriptome alterations of radish shoots exposed to cadmium can be interpreted in the context	
126	<ul> <li>2022, 25, 104067</li> <li>Transcriptome alterations of radish shoots exposed to cadmium can be interpreted in the context of leaf senescence 2022, 1</li> <li>Complete chloroplast genome features of the model heavy metal hyperaccumulator Franch and its</li> </ul>	1
126	Transcriptome alterations of radish shoots exposed to cadmium can be interpreted in the context of leaf senescence 2022, 1  Complete chloroplast genome features of the model heavy metal hyperaccumulator Franch and its phylogenetic relationships with other Brassicaceae species 2022, 28, 775-789  Biogeography of culturable marine bacteria from both poles reveals that @verything is not	1
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126 125 124 123	Transcriptome alterations of radish shoots exposed to cadmium can be interpreted in the context of leaf senescence 2022, 1  Complete chloroplast genome features of the model heavy metal hyperaccumulator Franch and its phylogenetic relationships with other Brassicaceae species 2022, 28, 775-789  Biogeography of culturable marine bacteria from both poles reveals that @verything is not everywhereOat the genomic level 2021,  Phylogenomic and mitogenomic data can accelerate inventorying of tropical beetles during the current biodiversity crisis 2021, 10,  Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of	2

Cross-species transcriptomes reveal species-specific and shared molecular adaptations for plants 119 development on iron-rich rocky outcrops soils.. 2022, 23, 313 Analysis of Transcriptome Difference between Blood-Fed and Starved Tropical Bed Bug, (F.) 118 (Hemiptera: Cimicidae).. 2022, 13, DataSheet\_1.docx. 2020, 117 Table\_1.docx. 2020, 116 Data\_Sheet\_1.PDF. 2019, 115 Data\_Sheet\_1.PDF. 2019, 114 113 Data\_Sheet\_2.PDF. 2019, Image\_1.JPEG. **2019**, 112 Image\_2.JPEG. 2019, 111 Image\_3.JPEG. 2019, Image\_4.JPEG. 2019, 109 108 Image\_5.JPEG. 2019, Image\_6.JPEG. 2019, 107 Table\_1.XLSX. **2019**, 106 Table\_2.XLS. 2019, 105 104 Table\_3.XLSX. **2019**, Table\_4.XLSX. **2019**, 103

Table\_5.XLSX. 2019,

#### (2020-2019)





65 Computational approaches toward single-nucleotide polymorphism discovery and its applications in plant breeding. **2022**, 513-536

64	Genome informatics: present status and future prospects in agriculture. <b>2022</b> , 47-59		
63	Advancing Mitochondrial Metagenomics: A New Assembly Strategy and Validating the Power of Seed-Based Approach. <i>Diversity</i> , <b>2022</b> , 14, 317	2.5	
62	A Walk Through the Maze of Secondary Metabolism in Orchids: A Transcriptomic Approach <i>Frontiers in Plant Science</i> , <b>2022</b> , 13, 837563	6.2	
61	Genome Characterization and Phylogenetic Analysis of Bovine Hepacivirus in Inner Mongolia, Northeastern China. <i>Zoonoses</i> , <b>2022</b> , 2,		O
60	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence <i>Nature Plants</i> , <b>2022</b> ,	11.5	2
59	Bracovirus Sneaks Into Apoptotic Bodies Transmitting Immunosuppressive Signaling Driven by Integration-Mediated eIF5A Hypusination. <i>Frontiers in Immunology</i> , <b>2022</b> , 13,	8.4	1
58	Extensive diversity of RNA viruses in ticks revealed by metagenomics in northeastern China.		O
57	Genome assembly and analysis of the flavonoid and phenylpropanoid biosynthetic pathways in Fingerroot ginger (Boesenbergia rotunda).		
56	Understanding of the various aspects of gene regulatory networks related to crop improvement. <i>Gene</i> , <b>2022</b> , 833, 146556	3.8	O
55	Transcriptomics in Plant. <b>2022</b> , 99-127		
54	Genetic characterization of potential venom resistance proteins in California ground squirrels ( Otospermophilus beecheyi) using transcriptome analyses. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution,	1.8	
53	RNA Sequencing Unveils Very Small RNAs With Potential Regulatory Functions in Bacteria. <i>Frontiers in Molecular Biosciences</i> , <b>2022</b> , 9,	5.6	2
52	Transcriptome Data Analysis Using a De Novo Assembly Approach. <i>Springer Protocols</i> , <b>2022</b> , 195-209	0.3	
51	Improving the Annotation of the Venom Gland Transcriptome of Pamphobeteus verdolaga, Prospecting Novel Bioactive Peptides. <i>Toxins</i> , <b>2022</b> , 14, 408	4.9	
50	Proteotranscriptomics 🖪 facilitator in omics research. <i>Computational and Structural Biotechnology Journal</i> , <b>2022</b> , 20, 3667-3675	6.8	1
49	Genetic characterization of two G8P[8] rotavirus strains isolated in Guangzhou, China, in 2020/21: evidence of genome reassortment. <i>BMC Infectious Diseases</i> , <b>2022</b> , 22,	4	1
48	Genome Assembly and Analysis of the Flavonoid and Phenylpropanoid Biosynthetic Pathways in Fingerroot Ginger (Boesenbergia rotunda). <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23, 7269	6.3	

47	Phylotranscriptomics Illuminates the Placement of Whole Genome Duplications and Gene Retention in Ferns. <i>Frontiers in Plant Science</i> , 13,	6.2	2
46	RATTLE: reference-free reconstruction and quantification of transcriptomes from Nanopore sequencing. <i>Genome Biology</i> , <b>2022</b> , 23,	18.3	O
45	Multiomics analyses reveal the central role of nucleolus and nucleoid machinery during heat stress acclimation in Pinus radiata.		Ο
44	TransMeta simultaneously assembles multisample RNA-seq reads. <b>2022</b> , 32, 1398-1407		О
43	Complete chloroplast genome of Serrated Tussock, Nassella trichotoma (Poaceae: Stipeae). <b>2022</b> , 7, 1432-1434		
42	Mitochondrial genome sequencing, mapping, and assembly benchmarking for Culicoides species (Diptera: Ceratopogonidae). <b>2022</b> , 23,		
41	Genome sequencing and analysis uncover the regulatory elements involved in the development and oil biosynthesis of Pongamia pinnata (L.) [A potential biodiesel feedstock. 13,		
40	Gene Expression and Transcriptome Sequencing: Basics, Analysis, Advances.		
39	Streptomyces akebiae sp. nov., a novel actinomycete isolated from rhizosphere soil of Akebia trifoliate.		
38	Analysis of Crassostrea gasar transcriptome reveals candidate genes involved in metal metabolism. <b>2022</b> , 307, 136009		
37	The complete mitochondrial genome of Ahamus yushuensis Chu et Wang 1985 (Lepidoptera: Hepialidae) and phylogenetic analysis. <b>2022</b> , 7, 1611-1613		0
36	Significant compositional and functional variation reveals the patterns of gut microbiota evolution among the widespread Asian honeybee populations. 13,		1
35	Could foodomics hold the key to unlocking the role of prebiotics in gut microbiota and immunity?. <b>2022</b> , 48, 100920		1
34	De novo assembly and annotation of the transcriptome of the endangered seagrass Zostera capensis: Insights from differential gene expression under thermal stress. <b>2022</b> , 66, 100984		O
33	Dynamic molecular evolution of a supergene with suppressed recombination in white-throated sparrows. 11,		0
32	Genome survey and development of 13 SSR markers in Eucalyptus cloeziana by NGS. <b>2022</b> , 101,		O
31	Structure of a mitochondrial ribosome with fragmented rRNA in complex with membrane-targeting elements. <b>2022</b> , 13,		1
30	Deoxygenation lowers the thermal threshold of coral bleaching. <b>2022</b> , 12,		O

29	The reference genome and organelle genomes of wasabi (Eutrema japoniacum). 13,	О
28	Desert plant transcriptomics and adaptation to abiotic stress. <b>2023</b> , 199-256	O
27	Genome-scale signatures of adaptive gene expression changes in an invasive seaweed Gracilaria vermiculophylla.	1
26	De-novo transcriptome assembly for discovery of putative microsatellite markers and transcription factors in black pepper (Piper nigrum). <b>2019</b> , 89,	O
25	SaffronOMICS: Novel Approaches Toward Putting Saffron Data at Work. <b>2022</b> , 43-62	О
24	Phylogenomics and the flowering plant tree of life.	1
23	From Samples to Germline and Somatic Sequence Variation: A Focus on Next-Generation Sequencing in Melanoma Research. <b>2022</b> , 12, 1939	1
22	Upcoming progress of transcriptomics studies on plants: An overview. 13,	0
21	Unleashing the power within short-read RNA-seq for plant research: Beyond differential expression analysis and toward regulomics. 13,	O
20	Extensive diversity of RNA viruses in ticks revealed by metagenomics in northeastern China. <b>2022</b> , 16, e0011017	O
19	Nocardiopsis eucommiae sp. nov., a novel endophytic actinomycete isolated from leaves of Eucommia ulmoides Oliv <b>2022</b> , 72,	0
18	Complete Plastome of Physalis angulata var. villosa, Gene Organization, Comparative Genomics and Phylogenetic Relationships among Solanaceae. <b>2022</b> , 13, 2291	1
17	Genomic, Functional and Structural Analyses Reveal Mechanisms of Evolutionary Innovation within the Sea Anemone 8 Toxin Family.	1
16	Reduced effectiveness of purifying selection on new mutations in a parthenogenic terrestrial isopod (Trichoniscus pusillus).	O
15	Current Progress of Bioinformatics for Human Health. <b>2023</b> , 145-162	0
14	Optimization and application of non-native Phragmites australis transcriptome assemblies. <b>2023</b> , 18, e0280354	O
13	Beyond Transcript Concentrations: Quantifying Polyploid Expression Responses per Biomass, per Genome, and per Cell with RNA-Seq. <b>2023</b> , 227-250	1
12	Inference of Ancient Polyploidy Using Transcriptome Data. 2023, 47-76	O

11	An insight on the complete chloroplast genome of Gomphocarpus siniacus and Duvalia velutina, Asclepiadoideae (Apocynaceae). 84,	О
10	Genomics and Metabolomics: A Strategy for Elucidation of Metabolic Pathways in Medicinal Plants. <b>2022</b> , 343-360	O
9	Small population of the largest water strider after the late Pleistocene and the implications for its conservation. <b>2023</b> , 859, 147219	O
8	Insights into the convergent evolution of fructan biosynthesis in angiosperms from the highly characteristic chicory genome. <b>2023</b> , 238, 1245-1262	O
7	Genome, host genome integration, and gene expression in Diadegma fenestrale ichnovirus from the perspective of coevolutionary hosts. 14,	O
6	LSTrAP-denovo: Automated Generation of Transcriptome Atlases for Eukaryotic Species Without Genomes.	O
5	Two major chromosome evolution events with unrivaled conserved gene content in pomegranate. 14,	O
4	Global detection of human variants and isoforms by deep proteome sequencing.	O
3	A novel computational pipeline forvargene expression augments the discovery of changes in the Plasmodium falciparum transcriptome during transition from vivoto short-termin vitroculture.	O
2	Complete Mitochondrial Genome of Piophila casei (Diptera: Piophilidae): Genome Description and Phylogenetic Implications. <b>2023</b> , 14, 883	O
1	Transcriptomic analysis of cave, surface, and hybrid samples of the isopod Asellus aquaticus and identification of chromosomal location of candidate genes for cave phenotype evolution. <b>2023</b> , 14,	О