Gene Discovery through Transcriptome Sequencing for fortunei

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Citation Report

#	Article	IF	CITATIONS
1	Applications of next-generation sequencing to the study of biological invasions. Environmental Epigenetics, 2015, 61, 488-504.	0.9	66
2	The Genetics of the Golden Mussel (Limnoperna fortunei): Are Genes Related to Invasiveness?. , 2015, , 67-75.		8
3	De novo assembly of the transcriptome of <i>Acanthaster planci</i> testes. Molecular Ecology Resources, 2015, 15, 953-966.	2.2	17
4	What are we missing about marine invasions? Filling in the gaps with evolutionary genomics. Marine Biology, $2016, 163, 1.$	0.7	39
5	Hsp70 gene expansions in the scallop Patinopecten yessoensis and their expression regulation after exposure to the toxic dinoflagellate Alexandrium catenella. Fish and Shellfish Immunology, 2016, 58, 266-273.	1.6	49
6	Allatostatin-type A, kisspeptin and galanin GPCRs and putative ligands as candidate regulatory factors of mantle function. Marine Genomics, 2016, 27, 25-35.	0.4	21
7	The complete mitochondrial genome of the golden mussel Limnoperna fortunei and comparative mitogenomics of Mytilidae. Gene, 2016, 577, 202-208.	1.0	25
8	De novo assembly and characterization of foot transcriptome and microsatellite marker development for Paphia textile. Gene, 2016, 576, 537-543.	1.0	26
9	Annotation of nerve cord transcriptome in earthworm Eisenia fetida. Genomics Data, 2017, 14, 91-105.	1.3	17
10	Sequencing and de novo assembly of visceral mass transcriptome of the critically endangered land snail Satsuma myomphala: Annotation and SSR discovery. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 77-89.	0.4	10
11	The purplish bifurcate mussel Mytilisepta virgata gene expression atlas reveals a remarkable tissue functional specialization. BMC Genomics, 2017, 18, 590.	1.2	32
12	Physiological response of invasive mussel Limnoperna fortunei (Dunker, 1857) (Bivalvia: Mytilidae) submitted to transport and experimental conditions. Brazilian Journal of Biology, 2017, 77, 191-198.	0.4	10
13	De novo transcriptome of the pallial gland of the date mussel (Lithophaga lithophaga). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 26, 1-9.	0.4	4
14	A hybrid-hierarchical genome assembly strategy to sequence the invasive golden mussel, Limnoperna fortunei. GigaScience, 2018, 7, .	3.3	60
15	RNA Sequencing, <i>De novo</i> assembly, functional annotation and SSR analysis of the endangered diving beetle <scp><i>Cybister chinensis</i></scp> (= <scp><i>Cybister japonicus</i></scp>) using the Illumina platform. Entomological Research, 2018, 48, 60-72.	0.6	3
16	De novo assembly, gene annotation, and marker development using Illumina paired-end transcriptome sequencing in the Crassadoma gigantea. Gene, 2018, 658, 54-62.	1.0	9
17	<scp>eS</scp> nail: A transcriptomeâ€based molecular resource of the central nervous system for terrestrial gastropods. Molecular Ecology Resources, 2018, 18, 147-158.	2.2	3
18	Transcriptome analysis of the threatened snail Ellobium chinense reveals candidate genes for adaptation and identifies SSRs for conservation genetics. Genes and Genomics, 2018, 40, 333-347.	0.5	6

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19	Byssus Structure and Protein Composition in the Highly Invasive Fouling Mussel Limnoperna fortunei. Frontiers in Physiology, 2018, 9, 418.	1.3	28
20	Chemical oxidants affect byssus adhesion in the highly invasive fouling mussel Limnoperna fortunei. Science of the Total Environment, 2019, 646, 1367-1375.	3.9	20
21	RNAi based transcriptome suggests genes potentially regulated by HSF1 in the Pacific oyster Crassostrea gigas under thermal stress. BMC Genomics, 2019, 20, 639.	1.2	18
22	Diverse expression regulation of Hsp70 genes in scallops after exposure to toxic Alexandrium dinoflagellates. Chemosphere, 2019, 234, 62-69.	4.2	31
23	Golden mussel (Limnoperna fortunei) as a bioindicator in aquatic environments contaminated with mercury: Cytotoxic and genotoxic aspects. Science of the Total Environment, 2019, 675, 343-353.	3.9	16
24	Integrated transcriptomic and functional immunological approach for assessing the invasiveness of bivalve alien species. Scientific Reports, 2019, 9, 19879.	1.6	5
25	Genetic and functional repertoires of Limnoperna fortunei (Dunker, 1857) (Mollusca, Mytilidae): a review on the use of molecular techniques for the detection and control of the golden mussel. Hydrobiologia, 2020, 847, 2193-2202.	1.0	12
26	The golden mussel proteome and its response to niclosamide: Uncovering rational targets for control or elimination. Journal of Proteomics, 2020, 217, 103651.	1.2	5
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28	Omicsâ€based molecular analyses of adhesion by aquatic invertebrates. Biological Reviews, 2021, 96, 1051-1075.	4.7	30
29	Resilience in Greenland intertidal Mytilus: The hidden stress defense. Science of the Total Environment, 2021, 767, 144366.	3.9	25
31	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. PLoS ONE, 2016, 11, e0148622.	1.1	61
32	De novo transcriptome analysis and microsatellite marker development for population genetic study of a serious insect pest, Rhopalosiphum padi (L.) (Hemiptera: Aphididae). PLoS ONE, 2017, 12, e0172513.	1.1	41
34	Ultrastructure of the gill ciliary epithelium of Limnoperna fortunei (Dunker 1857), the invasive golden mussel. BMC Zoology, 2022, 7, .	0.3	8
35	Stress response gene family expansions correlate with invasive potential in teleost fish. Journal of Experimental Biology, 2022, 225, .	0.8	2
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Article IF Citations