

Ruijia Wang

List of Publications by Citations

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45
papers

1,570
citations

23
h-index

39
g-index

49
ext. papers

2,153
ext. citations

6.3
avg, IF

4.38
L-index

#	Paper	IF	Citations
45	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017 , 1, 120	12.3	202
44	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016 , 7, 11757	17.4	173
43	RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following <i>Edwardsiella ictaluri</i> infection in channel catfish, <i>Ictalurus punctatus</i> . <i>Fish and Shellfish Immunology</i> , 2012 , 32, 816-27	4.3	164
42	PolyA_DB 3 catalogs cleavage and polyadenylation sites identified by deep sequencing in multiple genomes. <i>Nucleic Acids Research</i> , 2018 , 46, D315-D319	20.1	88
41	A genome-wide association study in catfish reveals the presence of functional hubs of related genes within QTLs for columnaris disease resistance. <i>BMC Genomics</i> , 2015 , 16, 196	4.5	82
40	Evasion of mucosal defenses during <i>Aeromonas hydrophila</i> infection of channel catfish (<i>Ictalurus punctatus</i>) skin. <i>Developmental and Comparative Immunology</i> , 2013 , 39, 447-55	3.2	67
39	Construction of a high-density, high-resolution genetic map and its integration with BAC-based physical map in channel catfish. <i>DNA Research</i> , 2015 , 22, 39-52	4.5	64
38	Bulk segregant RNA-seq reveals expression and positional candidate genes and allele-specific expression for disease resistance against enteric septicemia of catfish. <i>BMC Genomics</i> , 2013 , 14, 929	4.5	60
37	Cellular stress alters 3WTR landscape through alternative polyadenylation and isoform-specific degradation. <i>Nature Communications</i> , 2018 , 9, 2268	17.4	52
36	A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3389-3398	3.2	40
35	A compendium of conserved cleavage and polyadenylation events in mammalian genes. <i>Genome Research</i> , 2018 , 28, 1427-1441	9.7	39
34	Sea cucumber genome provides insights into saponin biosynthesis and aestivation regulation. <i>Cell Discovery</i> , 2018 , 4, 29	22.3	38
33	Regulation of Intronic Polyadenylation by PCF11 Impacts mRNA Expression of Long Genes. <i>Cell Reports</i> , 2019 , 26, 2766-2778.e6	10.6	37
32	Construction of a High-Density Genetic Map and Quantitative Trait Locus Mapping in the Sea Cucumber <i>Apostichopus japonicus</i> . <i>Scientific Reports</i> , 2015 , 5, 14852	4.9	35
31	Expression of nitric oxide synthase (NOS) genes in channel catfish is highly regulated and time dependent after bacterial challenges. <i>Developmental and Comparative Immunology</i> , 2014 , 45, 74-86	3.2	34
30	Genome-wide identification and characterization of five MyD88 duplication genes in Yesso scallop (<i>Patinopecten yessoensis</i>) and expression changes in response to bacterial challenge. <i>Fish and Shellfish Immunology</i> , 2015 , 46, 181-91	4.3	33
29	Four lysozymes (one c-type and three g-type) in catfish are drastically but differentially induced after bacterial infection. <i>Fish and Shellfish Immunology</i> , 2013 , 35, 136-45	4.3	32

28	Identification and analysis of genome-wide SNPs provide insight into signatures of selection and domestication in channel catfish (<i>Ictalurus punctatus</i>). <i>PLoS ONE</i> , 2014 , 9, e109666	3.7	32
27	Characterizations and expression analyses of NF- κ B and Rel genes in the Yesso scallop (<i>Patinopecten yessoensis</i>) suggest specific response patterns against Gram-negative infection in bivalves. <i>Fish and Shellfish Immunology</i> , 2015 , 44, 611-21	4.3	30
26	Pathogen recognition receptors in channel catfish: IV. Identification, phylogeny and expression analysis of peptidoglycan recognition proteins. <i>Developmental and Comparative Immunology</i> , 2014 , 46, 291-9	3.2	26
25	The cytochrome P450 genes of channel catfish: their involvement in disease defense responses as revealed by meta-analysis of RNA-Seq data sets. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 2813-28	4	25
24	The genome-wide identification of mitogen-activated protein kinase kinase (MKK) genes in Yesso scallop <i>Patinopecten yessoensis</i> and their expression responses to bacteria challenges. <i>Fish and Shellfish Immunology</i> , 2015 , 45, 901-11	4.3	24
23	Genome-wide identification and characterization of TRAF genes in the Yesso scallop (<i>Patinopecten yessoensis</i>) and their distinct expression patterns in response to bacterial challenge. <i>Fish and Shellfish Immunology</i> , 2015 , 47, 545-55	4.3	23
22	The mRNA Export Receptor NXF1 Coordinates Transcriptional Dynamics, Alternative Polyadenylation, and mRNA Export. <i>Molecular Cell</i> , 2019 , 74, 118-131.e7	17.6	22
21	Rapid development of molecular resources for a freshwater mussel, <i>Villosa lienosa</i> (Bivalvia:Unionidae), using an RNA-seq-based approach. <i>Freshwater Science</i> , 2012 , 31, 695-708	2	22
20	Analysis of 52 Rab GTPases from channel catfish and their involvement in immune responses after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2014 , 45, 21-34	3.2	20
19	Genome-wide identification, characterization and expression analyses of two TNFRs in Yesso scallop (<i>Patinopecten yessoensis</i>) provide insight into the disparity of responses to bacterial infections and heat stress in bivalves. <i>Fish and Shellfish Immunology</i> , 2016 , 52, 44-56	4.3	19
18	Long Non-Coding RNAs (lncRNAs) of Sea Cucumber: Large-Scale Prediction, Expression Profiling, Non-Coding Network Construction, and lncRNA-microRNA-Gene Interaction Analysis of lncRNAs in <i>Apostichopus japonicus</i> and <i>Holothuria glaberrima</i> During LPS Challenge and Radial Organ Complex Regeneration. <i>Marine Biotechnology</i> , 2016 , 18, 485-99	3.4	18
17	Identification, characterization and expression profiling of the Tollip gene in Yesso scallop (<i>Patinopecten yessoensis</i>). <i>Genes and Genetic Systems</i> , 2015 , 90, 99-108	1.4	16
16	APALyzer: a bioinformatics package for analysis of alternative polyadenylation isoforms. <i>Bioinformatics</i> , 2020 , 36, 3907-3909	7.2	15
15	Channel catfish hemoglobin genes: identification, phylogenetic and syntenic analysis, and specific induction in response to heat stress. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014 , 9, 11-22	2	9
14	Ribosomal protein genes are highly enriched among genes with allele-specific expression in the interspecific F1 hybrid catfish. <i>Molecular Genetics and Genomics</i> , 2016 , 291, 1083-93	3.1	5
13	Molecular characterization, phylogenetic analysis and expression profiling of myoglobin and cytoglobin genes in response to heat stress in channel catfish <i>Ictalurus punctatus</i> . <i>Journal of Fish Biology</i> , 2015 , 86, 592-604	1.9	4
12	The Rho GTPase Family Genes in Bivalvia Genomes: Sequence, Evolution and Expression Analysis. <i>PLoS ONE</i> , 2015 , 10, e0143932	3.7	4
11	HD-Marker: a highly multiplexed and flexible approach for targeted genotyping of more than 10,000 genes in a single-tube assay. <i>Genome Research</i> , 2018 , 28, 1919-1930	9.7	4

10	Genetic Analysis Using RNA-Seq: Bulk Segregant RNA-Seq 2017 , 169-178		2
9	Bioinformatics Considerations and Approaches for High-Density Linkage Mapping in Aquaculture 2017 , 356-379		2
8	Genomic Resources for Functional Genomics in Aquaculture Species 2012 , 41-77		2
7	Modulation of alternative cleavage and polyadenylation events by dCas9-mediated CRISPRpas. <i>Methods in Enzymology</i> , 2021 , 655, 459-482	1.7	2
6	Functional Genomics Research in Aquaculture: Principles and General Approaches 2012 , 1-40		1
5	FIP1L1 Regulates Alternative Polyadenylation of Leukemia-Associated Genes in Acute Myeloid Leukemia. <i>Blood</i> , 2018 , 132, 3882-3882	2.2	1
4	MAAPER: model-based analysis of alternative polyadenylation using 3Vend-linked reads. <i>Genome Biology</i> , 2021 , 22, 222	18.3	1
3	Analysis of Duplicated Genes and Multi-Gene Families 2017 , 98-109		
2	Analysis of Long Non-coding RNAs 2017 , 179-199		
1	Genome Annotation: Determination of the Coding Potential of the Genome 2017 , 74-85		