

Yangzhen Li

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Insights into the genetic covariation between harvest survival and growth rate in olive flounder (<i>Paralichthys olivaceus</i>) under commercial production environment. <i>Aquaculture and Fisheries</i> , 2023, 8, 135-140.	2.2	1
2	Genetic parameter estimates for female proportion in tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture</i> , 2022, 548, 737652.	3.5	2
3	Comprehensive Analysis of Circular RNAs to Decipher the Potential Roles in Blind-Side Hypermelanosis in Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	2
4	Transcriptomic analysis reveals the gene expression profiles in the spleen of spotted knifejaw (<i>Oplegnathus punctatus</i>) infected by <i>Vibrio harveyi</i> . <i>Developmental and Comparative Immunology</i> , 2022, 133, 104432.	2.3	2
5	Weighted gene co-expression network analysis reveals the mechanisms of evolutionary adaptation and selection behind blind-side hypermelanosis in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture</i> , 2022, 558, 738394.	3.5	0
6	Selective breeding for juvenile survival in Chinese tongue sole (<i>Cynoglossus semilaevis</i>): Heritability and selection response. <i>Aquaculture</i> , 2021, 531, 735901.	3.5	7
7	Effects of dietary supplementation of <i>Lactobacillus plantarum</i> and <i>Bacillus subtilis</i> on growth performance, survival, immune response, antioxidant capacity and digestive enzyme activity in olive flounder (<i>Paralichthys olivaceus</i>). <i>Aquaculture and Fisheries</i> , 2021, 6, 283-288.	2.2	21
8	Transcriptome analysis and candidate gene identification reveals insights into the molecular mechanisms of hypermelanosis in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture and Fisheries</i> , 2021, , .	2.2	4
9	Insights into the heritable variation of hypermelanosis in Chinese tongue sole (<i>Cynoglossus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.5	6
10	Development of a 38â€K single nucleotide polymorphism array and application in genomic selection for resistance against <i>Vibrio harveyi</i> in Chinese tongue sole, <i>Cynoglossus semilaevis</i> . <i>Genomics</i> , 2021, 113, 1838-1844.	2.9	5
11	Dietary bile acid supplementation reveals beneficial effects on intestinal healthy status of tongue sole (<i>Cynoglossus semilaevis</i>). <i>Fish and Shellfish Immunology</i> , 2021, 116, 52-60.	3.6	18
12	Identification and functional analysis of the perforin-1 like gene in disease resistance in half smooth tongue sole (<i>Cynoglossus semilaevis</i>). <i>Developmental and Comparative Immunology</i> , 2021, 122, 104135.	2.3	3
13	Identification of Potential Blind-Side Hypermelanosis-Related lncRNAâ€miRNAâ€mRNA Regulatory Network in a Flatfish Species, Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>Frontiers in Genetics</i> , 2021, 12, 817117.	2.3	6
14	Heritability of disease resistance to <i>Edwardsiella tarda</i> in olive flounder (<i>Paralichthys olivaceus</i>). <i>Aquaculture</i> , 2020, 519, 734750.	3.5	7
15	Out-of-season artificial reproduction techniques of cultured female tongue sole (<i>Cynoglossus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 fertilization. <i>Aquaculture</i> , 2020, 518, 734866.	3.5	11
16	Prediction of genomic breeding values based on pre-selected SNPs using ssGBLUP, WssGBLUP and BayesB for <i>Edwardsiellosis</i> resistance in Japanese flounder. <i>Genetics Selection Evolution</i> , 2020, 52, 49.	3.0	22
17	Novel insights into the selective breeding for disease resistance to vibriosis by using natural outbreak survival data in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture</i> , 2020, 529, 735670.	3.5	7
18	Estimation of heritabilities of disease resistance to <i>Edwardsiella tarda</i> and genetic correlations between resistance and growth traits in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture and Fisheries</i> , 2020, 5, 289-293.	2.2	7

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19	Differences in DNA Methylation Between Disease-Resistant and Disease-Susceptible Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>) Families. <i>Frontiers in Genetics</i> , 2019, 10, 847.	2.3	21
20	Genetic analysis of disease resistance to <i>Vibrio harveyi</i> by challenge test in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Aquaculture</i> , 2019, 503, 430-435.	3.5	32
21	Estimation of genetic parameters for juvenile growth performance traits in olive flounder (<i>Paralichthys olivaceus</i>). <i>Aquaculture and Fisheries</i> , 2019, 4, 48-52.	2.2	10
22	Expression analysis and characterization of <i>dmrt2</i> in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Theriogenology</i> , 2019, 138, 1-8.	2.1	35
23	Genetic parameters and genotype by environment interactions for growth traits and survival of olive flounder (<i>Paralichthys olivaceus</i>) in recirculating aquaculture system and flow-through system. <i>Aquaculture</i> , 2019, 510, 56-60.	3.5	13
24	iTRAQ-based analysis of 17 β -estradiol induced proteome in Chinese tongue sole <i>Cynoglossus semilaevis</i> . <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1659-1668.	1.3	2
25	Genome-Wide Association Mapping and Gene Expression Analyses Reveal Genetic Mechanisms of Disease Resistance Variations in <i>Cynoglossus semilaevis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1167.	2.3	21
26	Genetic parameters estimates for growth performance traits at harvest in Japanese flounder (<i>Paralichthys olivaceus</i>). <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1659-1668.	3.5	22
27	Genomic Selection Using BayesC π and GBLUP for Resistance Against <i>Edwardsiella tarda</i> in Japanese Flounder (<i>Paralichthys olivaceus</i>). <i>Marine Biotechnology</i> , 2018, 20, 559-565.	2.4	34
28	Genome editing reveals <i>dmrt1</i> as an essential male sex-determining gene in Chinese tongue sole (<i>Cynoglossus semilaevis</i>). <i>Scientific Reports</i> , 2017, 7, 42213.	3.3	144
29	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. <i>Nature Genetics</i> , 2017, 49, 119-124.	21.4	178
30	Characterization and expression pattern of <i>respon din1</i> in <i>Cynoglossus semilaevis</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 772-780.	1.3	4
31	Locus Mapping, Molecular Cloning, and Expression Analysis of <i>rps6kb2</i> , a Novel Metamorphosis-Related Gene in Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>Marine Biotechnology</i> , 2017, 19, 497-516.	2.4	5
32	Ubiquitin ligase gene <i>neurl3</i> plays a role in spermatogenesis of half-smooth tongue sole (<i>Cynoglossus semilaevis</i>). <i>Journal of Oceanology and Limnology</i> , 2017, 35, 163-169.	2.2	21
33	Phenotypic and genetic parameter estimation of juvenile growth and bottom color traits in half-smooth tongue sole, <i>Cynoglossus semilaevis</i> . <i>Acta Oceanologica Sinica</i> , 2016, 35, 83-87.	1.0	4
34	Analysis of phenotypic and genetic parameters for growth related traits in the half smooth tongue sole, <i>Cynoglossus semilaevis</i> . <i>Chinese Journal of Oceanology and Limnology</i> , 2016, 34, 163-169.	0.7	10
35	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014, 46, 253-260.	21.4	685
36	Differences in sex reversion and growth between normal and neomale stock in half-smooth tongue sole, <i>Cynoglossus semilaevis</i> . <i>Aquaculture International</i> , 2014, 22, 1437-1449.	2.2	15

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37	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615.	5.5	356
38	Construction of a High-Density Microsatellite Genetic Linkage Map and Mapping of Sexual and Growth-Related Traits in Half-Smooth Tongue Sole (<i>Cynoglossus semilaevis</i>). <i>PLoS ONE</i> , 2012, 7, e52097.	2.5	78