

# Changwei Shao

## List of Publications by Year in descending order

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108  
papers

3,980  
citations

201385

27  
h-index

133063

59  
g-index

114  
all docs

114  
docs citations

114  
times ranked

3910  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-level genome and population genomic analysis provide insights into the evolution and environmental adaptation of Jinjiang oyster ( <i>Crassostrea ariakensis</i> ). <i>Molecular Ecology Resources</i> , 2022, 22, 1529-1544.	2.2	16
2	Understanding asymmetrical malpigmentation in flatfishes and improvement measures for aquaculture. <i>Reviews in Aquaculture</i> , 2022, 14, 1333-1344.	4.6	3
3	Identification of global alternative splicing and sex-specific splicing via comparative transcriptome analysis of gonads of Chinese tongue sole (&lt;i>Cynoglossus semilaevis&lt;/i>). <i>Zoological Research</i> , 2022, 43, 319-330.	0.9	5
4	Single-Cell Atlas of the Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ) Ovary Reveals Transcriptional Programs of Oogenesis in Fish. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 828124.	1.8	5
5	Gdnf Acts as a Germ Cell-Derived Growth Factor and Regulates the Zebrafish Germ Stem Cell Niche in Autocrine- and Paracrine-Dependent Manners. <i>Cells</i> , 2022, 11, 1295.	1.8	7
6	The identification of miRNAs that regulate ovarian maturation in <i>Cynoglossus semilaevis</i> . <i>Aquaculture</i> , 2022, 555, 738250.	1.7	5
7	Transcriptome Analysis Indicates Immune Responses against <i>Vibrio harveyi</i> in Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Animals</i> , 2022, 12, 1144.	1.0	4
8	Genome-wide DNA methylation and gene expression patterns of androgenetic haploid tiger pufferfish ( <i>Takifugu rubripes</i> ) provide insights into haploid syndrome. <i>Scientific Reports</i> , 2022, 12, 8252.	1.6	1
9	A Potential Role of the Translation Elongation Factor <i>eef1a1</i> in Gonadal High-Temperature Perception in Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Animals</i> , 2022, 12, 1603.	1.0	1
10	Cloning and functional analysis of <i>c/ebp1</i> as negative regulator of <i>dmrt1</i> in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Gene</i> , 2021, 768, 145321.	1.0	6
11	lncRNA DMRT2-AS acts as a transcriptional regulator of <i>dmrt2</i> involving in sex differentiation in the Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2021, 253, 110542.	0.7	13
12	Cloning, expression and functional analysis of the desert hedgehog ( <i>dhh</i> ) gene in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Gene Expression Patterns</i> , 2021, 39, 119163.	0.3	3
13	<i>Oryzias curvinotus</i> in Sanya Does Not Contain the Male Sex-Determining Gene <i>dmy</i> . <i>Animals</i> , 2021, 11, 1327.	1.0	7
14	Comprehensive CircRNA Profiling and Selection of Key CircRNAs Reveal the Potential Regulatory Roles of CircRNAs throughout Ovarian Development and Maturation in <i>Cynoglossus semilaevis</i> . <i>Biology</i> , 2021, 10, 830.	1.3	5
15	Temporal Transcriptome Analysis Reveals Dynamic Expression Profiles of Gametes and Embryonic Development in Japanese Flounder ( <i>Paralichthys olivaceus</i> ). <i>Genes</i> , 2021, 12, 1561.	1.0	2
16	Footprints of global change in marine life: Inferring past environment based on DNA methylation and gene expression marks. <i>Molecular Ecology</i> , 2021, 30, 747-760.	2.0	22
17	MicroRNA <i>ssa-mir-196a-4</i> decreases <i>lgr8</i> expression in testis development of Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2021, 258, 110695.	0.7	1
18	A Chromosome-Level Genome Assembly of Yellowtail Kingfish ( <i>Seriola lalandi</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 825742.	1.1	1

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19	Early response to heat stress in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ): performance of different sexes, candidate genes and networks. <i>BMC Genomics</i> , 2020, 21, 745.	1.2	7
20	A Chromosome-Level Genome Assembly of the Anglerfish <i>Lophius litulon</i> . <i>Frontiers in Genetics</i> , 2020, 11, 581161.	1.1	2
21	Chromosome-Level Clam Genome Helps Elucidate the Molecular Basis of Adaptation to a Buried Lifestyle. <i>IScience</i> , 2020, 23, 101148.	1.9	33
22	Chromosome-level genome assembly of the greenfin horse-faced filefish ( <i>Thamnaconus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Ecology Resources, 2020, 20, 1069-1079.	2.2	27
23	Draft genomes of female and male turbot <i>Scophthalmus maximus</i> . <i>Scientific Data</i> , 2020, 7, 90.	2.4	15
24	Chromosome-level genome assembly of the East Asian common octopus ( <i>Octopus sinensis</i> ) using PacBio sequencing and Hi-C technology. <i>Molecular Ecology Resources</i> , 2020, 20, 1572-1582.	2.2	28
25	Androgenetic haploid Japanese pufferfish ( <i>Takifugu rubripes</i> ) induced by cold shock. <i>Aquaculture Research</i> , 2019, 50, 3802-3811.	0.9	5
26	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.	1.1	21
27	Changes in DNA methylation during epigenetic-associated sex reversal under low temperature in <i>Takifugu rubripes</i> . <i>PLoS ONE</i> , 2019, 14, e0221641.	1.1	34
28	Expression analysis and characterization of <i>dmrt2</i> in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Theriogenology</i> , 2019, 138, 1-8.	0.9	35
29	iTRAQ-based analysis of 17 $\beta$ -estradiol induced proteome in Chinese tongue sole <i>Cynoglossus semilaevis</i> . <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1659-1668.	0.6	2
30	Transcriptome of Gonads From High Temperature Induced Sex Reversal During Sex Determination and Differentiation in Chinese Tongue Sole, <i>Cynoglossus semilaevis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1128.	1.1	38
31	Cloning, tissue distribution and methylation analyses of <i>Lhx9</i> in Chinese tongue sole ( <i>Cynoglossus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1.0 6	1.0	6
32	Expression analysis and characterization of <i>zglp1</i> in the Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Gene</i> , 2019, 683, 72-79.	1.0	8
33	Genome-wide identification and characterization of heat shock protein family 70 provides insight into its divergent functions on immune response and development of <i>Paralichthys olivaceus</i> . <i>PeerJ</i> , 2019, 7, e7781.	0.9	11
34	The Augmented R-Loop Is a Unifying Mechanism for Myelodysplastic Syndromes Induced by High-Risk Splicing Factor Mutations. <i>Molecular Cell</i> , 2018, 69, 412-425.e6.	4.5	203
35	Capturing the interactome of newly transcribed RNA. <i>Nature Methods</i> , 2018, 15, 213-220.	9.0	170
36	QTL Detection for Albinism-Related Loci in Chinese Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Journal of Ocean University of China</i> , 2018, 17, 1404-1410.	0.6	4

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37	The autosomal Gsdf gene plays a role in male gonad development in Chinese tongue sole ( <i>Cynoglossus</i> ) Tj ETQq1 1.0.784314 rgBT /Overlock 10 Tf 50	1.6	30
38	Chromosome-level genome assembly of the spotted sea bass, <i>Lateolabrax maculatus</i> . <i>GigaScience</i> , 2018, 7, .	3.3	39
39	Molecular Characterization and Expression and DNA Methylation Analyses of a Galectin-Related Protein Gene from <i>Cynoglossus semilaevis</i> . <i>Journal of Ocean University of China</i> , 2018, 17, 1189-1196.	0.6	2
40	Genomic Selection Using BayesC and GBLUP for Resistance Against <i>Edwardsiella tarda</i> in Japanese Flounder ( <i>Paralichthys olivaceus</i> ). <i>Marine Biotechnology</i> , 2018, 20, 559-565.	1.1	34
41	DNA methylation levels and expression patterns of <i>Smyd1a</i> and <i>Smyd1b</i> genes during Metamorphosis of the Japanese Flounder ( <i>Paralichthys olivaceus</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2018, 223, 16-22.	0.7	12
42	Molecular characterization and expression analysis of <i>strbp</i> in Chinese tongue sole ( <i>Cynoglossus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	7
43	Genome editing reveals <i>dmt1</i> as an essential male sex-determining gene in Chinese tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Scientific Reports</i> , 2017, 7, 42213.	1.6	144
44	Proteome profiling reveals immune responses in Japanese flounder ( <i>Paralichthys olivaceus</i> ) infected with <i>Edwardsiella tarda</i> by iTRAQ analysis. <i>Fish and Shellfish Immunology</i> , 2017, 66, 325-333.	1.6	34
45	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. <i>Nature Genetics</i> , 2017, 49, 119-124.	9.4	178
46	Identification, characterization and functional analysis of regulatory region of <i>nanos</i> gene from half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Gene</i> , 2017, 617, 8-16.	1.0	6
47	Characterization and expression pattern of <i>respondin1</i> in <i>Cynoglossus semilaevis</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 772-780.	0.6	4
48	NEAT1 scaffolds RNA-binding proteins and the Microprocessor to globally enhance pri-miRNA processing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 816-824.	3.6	165
49	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.	1.1	5
50	Molecular characterization of <i>Pod1</i> during sex development in Chinese tongue sole ( <i>Cynoglossus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	3
51	The integrated analysis of RNA-seq and microRNA-seq depicts miRNA-mRNA networks involved in Japanese flounder ( <i>Paralichthys olivaceus</i> ) albinism. <i>PLoS ONE</i> , 2017, 12, e0181761.	1.1	13
52	Molecular cloning and expression analysis of the <i>aqp1aa</i> gene in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>PLoS ONE</i> , 2017, 12, e0175033.	1.1	7
53	Identification and analysis of the $\beta$ -catenin1 gene in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>PLoS ONE</i> , 2017, 12, e0176122.	1.1	9
54	Discovery and identification of candidate sex-related genes based on transcriptome sequencing of Russian sturgeon ( <i>Acipenser gueldenstaedtii</i> ) gonads. <i>Physiological Genomics</i> , 2016, 48, 464-476.	1.0	23

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55	Two Figla homologues have disparate functions during sex differentiation in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Scientific Reports</i> , 2016, 6, 28219.	1.6	33
56	Distinct splicing signatures affect converged pathways in myelodysplastic syndrome patients carrying mutations in different splicing regulators. <i>Rna</i> , 2016, 22, 1535-1549.	1.6	40
57	Molecular characterization and expression analysis of Patched 1 gene in the half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Acta Oceanologica Sinica</i> , 2016, 35, 19-28.	0.4	4
58	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.	0.4	4
59	Location of <i>Vibrio anguillarum</i> resistance-associated trait loci in half-smooth tongue sole <i>Cynoglossus semilaevis</i> at its microsatellite linkage map. <i>Chinese Journal of Oceanology and Limnology</i> , 2016, 34, 1309-1319.	0.7	11
60	Expression analysis and characterization of an autosome-localized <i>tesk1</i> gene in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Gene</i> , 2016, 582, 161-167.	1.0	4
61	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
62	Transcriptome analysis revealed changes of multiple genes involved in immunity in <i>Cynoglossus semilaevis</i> during <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2015, 43, 209-218.	1.6	108
63	Genome-wide SNP identification for the construction of a high-resolution genetic map of Japanese flounder ( <i>Paralichthys olivaceus</i> ): applications to QTL mapping of <i>Vibrio anguillarum</i> disease resistance and comparative genomic analysis. <i>DNA Research</i> , 2015, 22, 161-170.	1.5	134
64	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015, 6, 6986.	5.8	222
65	Cloning and Characterization of <i>tesk1</i> , a Novel Spermatogenesis-Related Gene, in the Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>PLoS ONE</i> , 2014, 9, e107922.	1.1	18
66	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.	9.4	685
67	Cloning, expression and methylation analysis of <i>piwil2</i> in half-smooth tongue sole ( <i>Cynoglossus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	0.4	23
68	Molecular characterization, sexually dimorphic expression, and functional analysis of 3'UTR-untranslated region of <i>vasa</i> gene in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Theriogenology</i> , 2014, 82, 213-224.	0.9	12
69	Gene cloning and expression analysis of IRF1 in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Molecular Biology Reports</i> , 2014, 41, 4093-4101.	1.0	9
70	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615.	2.4	356
71	Expression and purification of half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ) CSDAZL protein. <i>Protein Expression and Purification</i> , 2014, 102, 8-12.	0.6	11
72	A first generation BAC-based physical map of the half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ) genome. <i>BMC Genomics</i> , 2014, 15, 215.	1.2	12

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73	Molecular characterization and functional divergence of two Gadd45g homologs in sex determination in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014, 177-178, 56-64.	0.7	15
74	Characterization of the <i>cyp19a1a</i> gene from a BAC sequence in half-smooth tongue sole ( <i>Cynoglossus</i> ) Tj ETQq0 0.0,rgBT /Oyerlock 10	0.4	0
75	Construction of a microsatellite-based genetic linkage map for half-smooth tongue sole <i>Cynoglossus semilaevis</i> . <i>Environmental Epigenetics</i> , 2013, 59, 99-108.	0.9	5
76	Selection of the families with high growth rate and high female proportion in half-smooth tongue sole( <i>Cynoglossus semilaevis</i> ). <i>Journal of Fisheries of China</i> , 2013, 37, 481.	0.1	1
77	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.	1.1	78
78	Induction of Mitogynogenetic Diploids and Identification of WW Super-female Using Sex-Specific SSR Markers in Half-Smooth Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Marine Biotechnology</i> , 2012, 14, 120-128.	1.1	87
79	Construction of High-Density Genetic Linkage Maps and Mapping of Growth-Related Quantitative Trait Loci in the Japanese Flounder ( <i>Paralichthys olivaceus</i> ). <i>PLoS ONE</i> , 2012, 7, e50404.	1.1	71
80	Chromosome mapping of 5S rDNA in olive flounder ( <i>Paralichthys olivaceus</i> ) and half-smooth tongue-sole ( <i>Cynoglossus semilaevis</i> ) and molecular systematics analysis of five flatfishes. <i>Journal of Fisheries of China</i> , 2012, 36, 1159.	0.1	2
81	Molecular cloning, characterization and expression analysis of <i>Sox9a</i> and <i>Foxl2</i> genes in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Acta Oceanologica Sinica</i> , 2011, 30, 68-77.	0.4	49
82	Construction and application of a built-in dual luciferase reporter for microRNA functional analysis. <i>Electronic Journal of Biotechnology</i> , 2011, 14, .	1.2	2
83	Comparison of chromosome preparation methods for the different developmental stages of the half-smooth tongue sole, <i>Cynoglossus semilaevis</i> . <i>Micron</i> , 2010, 41, 47-50.	1.1	22
84	Construction of Two BAC Libraries from Half-Smooth Tongue Sole <i>Cynoglossus semilaevis</i> and Identification of Clones Containing Candidate Sex-Determination Genes. <i>Marine Biotechnology</i> , 2010, 12, 558-568.	1.1	51
85	Artificial Gynogenesis and Sex Determination in Half-Smooth Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Marine Biotechnology</i> , 2009, 11, 243-251.	1.1	116
86	Construction of a Genetic Linkage Map and Mapping of a Female-Specific DNA Marker in Half-Smooth Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Marine Biotechnology</i> , 2009, 11, 699-709.	1.1	63
87	Isolation and characterization of polymorphic microsatellite DNA markers in the rock bream ( <i>Oplegnathus fasciatus</i> ). <i>Conservation Genetics</i> , 2009, 10, 527-529.	0.8	11
88	Ten polymorphic microsatellite loci for the Atlantic halibut ( <i>Hippoglossus hippoglossus</i> ) and cross-species application in related species. <i>Conservation Genetics</i> , 2009, 10, 611-614.	0.8	2
89	Eighteen novel microsatellite markers for the Chinese sea perch, <i>Lateolabrax maculatus</i> . <i>Conservation Genetics</i> , 2009, 10, 623-625.	0.8	18
90	Isolation and characterization of polymorphic microsatellite loci from a dinucleotide-enriched genomic library of seven-band grouper ( <i>Epinephelus septemfasciatus</i> ) and cross-species amplification. <i>Conservation Genetics</i> , 2009, 10, 627-629.	0.8	9

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91	Isolation and characterization of polymorphic microsatellite loci from a dinucleotide-enriched genomic library of starry flounder ( <i>Platichthys stellatus</i> ) and cross-species amplification. <i>Conservation Genetics</i> , 2009, 10, 631-633.	0.8	6
92	Isolation and characterization of polymorphic microsatellite loci from so-iuy mullet ( <i>Mugil soiuy</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	0.8	8
93	Development of polymorphic microsatellite markers from barfin flounder ( <i>Verasper moseri</i> ) and their cross-species amplification. <i>Conservation Genetics</i> , 2009, 10, 701-703.	0.8	4
94	New polymorphic microsatellite markers for the summer flounder, <i>Paralichthys dentatus</i> . <i>Conservation Genetics</i> , 2009, 10, 717-719.	0.8	1
95	Twelve novel polymorphic microsatellite loci for the Yellow grouper ( <i>Epinephelus awoara</i> ) and cross-species amplifications. <i>Conservation Genetics</i> , 2009, 10, 743-745.	0.8	15
96	Isolation and characterization of polymorphic microsatellite loci from a dinucleotide-enriched genomic library of spotted maigre ( <i>Nibeaaalbiflora</i> ). <i>Conservation Genetics</i> , 2009, 10, 789-791.	0.8	10
97	Isolation and characterization of 12 dinucleotide microsatellite loci from Belengerâ€™s jewfish ( <i>Johnius</i> ) Tj ETQq1 1 0.784314 rgBT /Over	0.8	3
98	Isolation and characterization of polymorphic microsatellite loci from a repeat-enriched genomic library of stone flounder ( <i>KareiusAbicoloratus</i> ) and cross-species amplification. <i>Conservation Genetics</i> , 2009, 10, 1041-1043.	0.8	0
99	Isolation and characterization of polymorphic microsatellite loci from black sea bass ( <i>Centropristis</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	0.8	0
100	Isolation and characterization of 12 microsatellite loci from cutlassfish ( <i>Trichiurus haumela</i> ). <i>Conservation Genetics</i> , 2009, 10, 1171-1173.	0.8	5
101	Isolation and characterization of polymorphic microsatellite loci from fat greenling ( <i>Hexagrammos</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	5
102	Isolation and characterization of polymorphic microsatellite loci from black snapper <i>Sebastes fuscescens</i> (Houttuyn). <i>Conservation Genetics</i> , 2009, 10, 1541-1543.	0.8	1
103	Isolation and characterization of 12 polymorphic microsatellite markers from ladyfish ( <i>Elops saurus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	0.8	2
104	Development of 40 microsatellite markers in spotted halibut ( <i>Verasper variegatus</i> ) and the crossâ€™species amplification in barfin flounder ( <i>Verasper moseri</i> â€™). <i>Animal Genetics</i> , 2009, 40, 576-578.	0.6	13
105	PERMANENT GENETIC RESOURCES: Isolation and characterization of microsatellite DNA loci from the southern flounder, <i>Paralichthys lethostigma</i> . <i>Molecular Ecology Resources</i> , 2008, 8, 381-383.	2.2	8
106	Development of 15 novel dinucleotide microsatellite markers in the Senegalese sole <i>Solea senegalensis</i> . <i>Fisheries Science</i> , 2008, 74, 1357-1359.	0.7	5
107	Molecular marker-assisted sex control in half-smooth tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Aquaculture</i> , 2008, 283, 7-12.	1.7	59
108	Polymorphic dinucleotide microsatellites in tongue sole ( <i>Cynoglossus semilaevis</i> ). <i>Molecular Ecology Notes</i> , 2007, 7, 1147-1149.	1.7	52