Shigeharu Kinoshita

List of Publications by Year
in descending order

79	1,630	394421 19	330143 37
papers	citations	h-index	g-index

84	84	84	1865
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Draft Genome of the Pearl Oyster Pinctada fucata: A Platform for Understanding Bivalve Biology. DNA Research, 2012, 19, 117-130.	3.4	266
2	Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. Zoological Letters, 2016, 2, 3.	1.3	133
3	Deep Sequencing of ESTs from Nacreous and Prismatic Layer Producing Tissues and a Screen for Novel Shell Formation-Related Genes in the Pearl Oyster. PLoS ONE, 2011, 6, e21238.	2.5	124
4	Dual Roles of Notch in Regulation of Apically Restricted Mitosis and Apicobasal Polarity ofÂNeuroepithelial Cells. Neuron, 2011, 69, 215-230.	8.1	82
5	The Diversity of Shell Matrix Proteins: Genome-Wide Investigation of the Pearl Oyster, Pinctada fucata. Zoological Science, 2013, 30, 801.	0.7	71
6	Dietary supplementation of inosine monophosphate promotes cellular growth of muscle and upregulates growth-related gene expression in Nile tilapia Oreochromis niloticus. Aquaculture, 2017, 468, 297-306.	3.5	50
7	Quantitative expression analysis of nacreous shell matrix protein genes in the process of pearl biogenesis. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2009, 154, 346-350.	1.6	45
8	Novel Genes Participating in the Formation of Prismatic and Nacreous Layers in the Pearl Oyster as Revealed by Their Tissue Distribution and RNA Interference Knockdown. PLoS ONE, 2014, 9, e84706.	2.5	44
9	The occurrence of two types of hemopexin-like protein in medaka and differences in their affinity to heme. Journal of Experimental Biology, 2004, 207, 1387-1398.	1.7	43
10	Host gut-derived probiotic bacteria promote hypertrophic muscle progression and upregulate growth-related gene expression of slow-growing Malaysian Mahseer Tor tambroides. Aquaculture Reports, 2018, 9, 37-45.	1.7	40
11	Identification and characterization of a matrix protein (PPPâ€10) in the periostracum of the pearl oyster, Pinctada fucata. FEBS Open Bio, 2013, 3, 421-427.	2.3	37
12	Molecular Characterization of Mn-superoxide Dismutase and Gene Expression Studies in Dietary Restricted Brachionus plicatilis Rotifers. Hydrobiologia, 2005, 546, 117-123.	2.0	34
13	Structural and functional analyses of a TIMP and MMP in the ligament of Pinctada fucata. Journal of Structural Biology, 2017, 199, 216-224.	2.8	27
14	Gene expression profiles at different stages for formation of pearl sac and pearl in the pearl oyster Pinctada fucata. BMC Genomics, 2019, 20, 240.	2.8	26
15	Myocyte enhancer factor 2 regulates expression of medaka Oryzias latipes fast skeletal myosin heavy chain genes in a temperature-dependent manner. Gene, 2008, 407, 42-53.	2.2	24
16	Identification of genes differentially expressed by calorie restriction in the rotifer (Brachionus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 2010, 180, 105-116.	1.5	24
17	Evolution of the myosin heavy chain gene MYH14 and its intronic microRNA miR-499: muscle-specific miR-499 expression persists in the absence of the ancestral host gene. BMC Evolutionary Biology, 2013, 13, 142.	3.2	23
18	Dramatic improvement in genome assembly achieved using doubled-haploid genomes. Scientific Reports, 2014, 4, 6780.	3.3	21

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19	Deep sequencing, profiling and detailed annotation of microRNAs in Takifugu rubripes. BMC Genomics, 2015, 16, 457.	2.8	21
20	Global gene expression analysis of gill tissues from normal and thermally selected strains of rainbow trout. Fisheries Science, 2012, 78, 1041-1049.	1.6	20
21	Regulation of gene expression mediating indeterminate muscle growth in teleosts. Mechanisms of Development, 2015, 137, 53-65.	1.7	20
22	Different gene expression profiles between normal and thermally selected strains of rainbow trout, Oncorhynchus mykiss, as revealed by comprehensive transcriptome analysis. Gene, 2016, 576, 637-643.	2.2	20
23	The expression of multiple myosin heavy chain genes during skeletal muscle development of torafugu Takifugu rubripes embryos and larvae. Gene, 2013, 515, 144-154.	2.2	18
24	Piwi-interacting RNA (piRNA) expression patterns in pearl oyster (Pinctada fucata) somatic tissues. Scientific Reports, 2019, 9, 247.	3.3	18
25	The occurrence of eukaryotic type III glutamine synthetase in the marine diatom Chaetoceros compressum. Marine Genomics, 2009, 2, 103-111.	1.1	17
26	Multiple cis-elements in the 5â€²-flanking region of embryonic/larval fast-type of the myosin heavy chain gene of torafugu, MYHM743-2, function in the transcriptional regulation of its expression. Gene, 2011, 489, 41-54.	2.2	17
27	Comparison of Two Pearl Sacs Formed in the Same Recipient Oyster with Different Genetic Background Involved in Yellow Pigmentation in Pinctada fucata. Marine Biotechnology, 2018, 20, 594-602.	2.4	17
28	Pelagic eggs and larvae of Coelorinchus kishinouyei (Gadiformes: Macrouridae) collected from Suruga Bay, Japan. Ichthyological Research, 2010, 57, 169-179.	0.8	16
29	The Mining of Pearl Formation Genes in Pearl Oyster Pinctada fucata by cDNA Suppression Subtractive Hybridization. Marine Biotechnology, 2012, 14, 177-188.	2.4	15
30	A novel heat stress-responsive gene in the marine diatomChaetoceros compressumencoding two types of transcripts, a trypsin-like protease and its related protein, by alternative RNA splicing. FEBS Journal, 2001, 268, 4599-4609.	0.2	14
31	Molecular phylogenetic relationship of Tetraodon pufferfish based on mitochondrial DNA analysis. Fisheries Science, 2013, 79, 243-250.	1.6	14
32	Characterization of Pax3 and Pax7 genes and their expression patterns during different development and growth stages of Japanese pufferfish Takifugu rubripes. Gene, 2016, 575, 21-28.	2.2	14
33	Early development of medaka Oryzias latipes muscles as revealed by transgenic approaches using embryonic and larval types of myosin heavy chain genes. Developmental Dynamics, 2010, 239, 1807-1817.	1.8	13
34	Microsatellite and mitochondrial DNA analyses reveal no genetic difference between two pufferfish species torafugu Takifugu rubripes and karasu T. chinensis. Fisheries Science, 2011, 77, 59-67.	1.6	13
35	Whole-Genome Sequencing of 84 Japanese Eels Reveals Evidence against Panmixia and Support for Sympatric Speciation. Genes, 2018, 9, 474.	2.4	13
36	Thermal tolerance of a thermally selected strain of rainbow trout Oncorhynchus mykiss and the pedigrees of its F1 and F2 generations indicated by their critical thermal maxima. Fisheries Science, 2018, 84, 671-679.	1.6	13

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37	Identification and Characterization of microRNAs and Their Predicted Functions in Biomineralization in the Pearl Oyster (Pinctada fucata). Biology, 2019, 8, 47.	2.8	13
38	A Zebrafish Acromegaly Model Elevates DNA Damage and Impairs DNA Repair Pathways. Biology, 2018, 7, 47.	2.8	12
39	Increased Levels of Mitochondrial Gene Transcripts in the Thermally Selected Rainbow Trout (Oncorhynchus mykiss) Strain During Embryonic Development. Marine Biotechnology, 2006, 8, 178-188.	2.4	11
40	Differential expression of heat-shock proteins in F2 offspring from F1 hybrids produced between thermally selected and normal rainbow trout strains. Fisheries Science, 2012, 78, 1051-1057.	1.6	11
41	Draft Genome Sequence of Aeromonas hydrophila Strain Ae34, Isolated from a Septicemic and Moribund Koi Carp (Cyprinus carpio koi), a Freshwater Aquarium Fish. Genome Announcements, 2014, 2, .	0.8	10
42	DNA microarray analysis on gene candidates possibly related to tetrodotoxin accumulation in pufferfish. Toxicon, 2014, 77, 68-72.	1.6	10
43	Evolution and Distribution of Teleost myomiRNAs: Functionally Diversified myomiRs in Teleosts. Marine Biotechnology, 2016, 18, 436-447.	2.4	10
44	Ultrahigh-Density Linkage Map Construction Using Low-Coverage Whole-Genome Sequencing of a Doubled Haploid Population: Case Study of Torafugu (Takifugu rubripes). Genes, 2018, 9, 120.	2.4	10
45	Sodium alginate supplementation modulates gut microbiota, health parameters, growth performance and growthâ€related gene expression in Malaysian MahseerTor tambroides. Aquaculture Nutrition, 2019, 25, 1300-1317.	2.7	10
46	Species-specific expression variation of fish MYH14, an ancient vertebrate myosin heavy chain gene orthologue. Fisheries Science, 2011, 77, 847-853.	1.6	9
47	Cellular muscle growth and molecular cloning and expression of growth-related gene of Malaysian Mahseer Tor tambroides larvae fed with live and formulated feeds in indoor nursery rearing system. Aquaculture Reports, 2017, 5, 1-9.	1.7	9
48	Trivalent Iron Is Responsible for the Yellow Color Development in the Nacre of Akoya Pearl Oyster Shells. Marine Biotechnology, 2020, 22, 19-30.	2.4	8
49	A 5'-flanking region of embryonic-type myosin heavy chain gene, MYHM743-2, from torafugu Takifugu rubripes regulates developmental muscle-specific expression. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 76-81.	1.0	7
50	Stimulatory and inhibitory mechanisms of slow muscle-specific myosin heavy chain gene expression in fish: Transient and transgenic analysis of torafugu MYH promoter in zebrafish embryos. Experimental Cell Research, 2013, 319, 820-837.	2.6	7
51	Assessment of homozygosity levels in the mito-gynogenetic torafugu (Takifugu rubripes) by genome-wide SNP analyses. Aquaculture, 2013, 380-383, 114-119.	3.5	7
52	Initiating the Mollusk Genomics Annotation Community: Toward Creating the Complete Curated Gene-Set of the Japanese Pearl Oyster,Pinctada fucata. Zoological Science, 2013, 30, 794-796.	0.7	6
53	Evaluation of the thermal tolerances of different strains of rainbow trout Oncorhynchus mykiss by measuring the effective time required for loss of equilibrium at an approximate upper lethal temperature. Fisheries Science, 2019, 85, 839-845.	1.6	6
54	Discovery and functional understanding of MiRNAs in molluscs: a genome-wide profiling approach. RNA Biology, 2021, 18, 1702-1715.	3.1	6

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55	Novel Isoforms of N16 and N19 Families Implicated for the Nacreous Layer Formation in the Pearl Oyster Pinctada fucata. Marine Biotechnology, 2018, 20, 155-167.	2.4	5
56	Promoter analysis of the fish gene of slow/cardiac-type myosin heavy chain implicated in specification of muscle fiber types. Fish Physiology and Biochemistry, 2018, 44, 679-691.	2.3	5
57	Multiple transcription factors mediating the expressional regulation of myosin heavy chain gene involved in the indeterminate muscle growth of fish. Gene, 2019, 687, 308-318.	2.2	5
58	Differential Expression of mRNAs in the Marine Diatom Chaetoceros compressum Exposed to High Temperatures. Fisheries Science, 1998, 64, 831-835.	1.6	5
59	Metagenomic analysis provides functional insights into seasonal change of a non-cyanobacterial prokaryotic community in temperate coastal waters. PLoS ONE, 2021, 16, e0257862.	2.5	5
60	Artificially designed hybrids facilitate efficient generation of high-resolution linkage maps. Scientific Reports, 2018, 8, 16104.	3.3	4
61	Molecular and Functional Analyses of Aspolin, a Fish-Specific Protein Extremely Rich in Aspartic Acid. Marine Biotechnology, 2011, 13, 517-526.	2.4	3
62	Another polymorphic mitochondrial genome of Grampus griseus and phylogeny of family Delphinidae. Mitochondrial DNA Part B: Resources, 2021, 6, 2569-2571.	0.4	3
63	Regulation of the Expression of the Myosin Heavy Chain (MYH) Gene myh14 in Zebrafish Development. Marine Biotechnology, 2021, 23, 821-835.	2.4	3
64	Gene expression pattern during population growth of the rotifer Brachionus plicatilis. Fisheries Science, 2002, 68, 793-796.	1.6	3
65	Transcriptome Analysis of Yamame (Oncorhynchus masou) in Normal Conditions after Heat Stress. Biology, 2019, 8, 21.	2.8	2
66	An Acromegaly Disease Zebrafish Model Reveals Decline in Body Stem Cell Number along with Signs of Premature Aging. Biology, 2020, 9, 120.	2.8	2
67	Transcriptomic Insight into the Melon Morphology of Toothed Whales for Aquatic Molecular Developments. Sustainability, 2021, 13, 13997.	3.2	2
68	Exosome-derived small non-coding RNAs reveal immune response upon grafting transplantation in Pinctada fucata (Mollusca). Open Biology, 2022, 12, 210317.	3.6	2
69	Transcriptome analysis of tetrodotoxin sensing and tetrodotoxin action in the central nervous system of tiger puffer Takifugu rubripes juveniles. Fisheries Science, 2017, 83, 401-412.	1.6	1
70	Determination of thermal tolerance in rainbow trout Oncorhynchus mykiss based on effective time, and its reproducibility for a large number of fish. Fisheries Science, 2020, 86, 767-774.	1.6	1
71	Characterization and phylogenetic position of two sympatric sister species of toxic flatworms Planocera multitentaculata and Planocera reticulata (Platyhelminthes: Acotylea). Mitochondrial DNA Part B: Resources, 2020, 5, 2352-2354.	0.4	1
72	Conserved and Widespread Expression of piRNA-Like Molecules and PIWI-Like Genes Reveal Dual Functions of Transposon Silencing and Gene Regulation in Pinctada fucata (Mollusca). Frontiers in Marine Science, 2021, 8, .	2.5	1

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73	DNA cloning of peptide synthetase from cyanobacterium Aphanizomenon flos-aquae. Fisheries Science, 2002, 68, 621-622.	1.6	1
74	Implication of RNA splicing in heat stress responses and expression of a novel trypsin-like protease in the marine diatom <i>Chaetoceros compressum</i>. Fisheries Science, 2002, 68, 1052-1055.	1.6	1
75	Construction of a chromosome-level Japanese stickleback species genome using ultra-dense linkage analysis with single-cell sperm sequencing. NAR Genomics and Bioinformatics, 2022, 4, lqac026.	3.2	1
76	Draft Genome Sequence of Thermoanaerobacterium saccharolyticum Strain NTOU1, a Thermophilic Bacterium Isolated from Marine Shallow Hydrothermal Vents. Genome Announcements, 2014, 2, .	0.8	0
77	Transcriptome analysis of tetrodotoxin sensing and tetrodotoxin action in the central nervous system of tiger puffer Takifugu rubripes juveniles. Nippon Suisan Gakkaishi, 2018, 84, 586-586.	0.1	0
78	Primary structural analysis of medaka Wap 65 and Wap65-like protein and their gene expression. Fisheries Science, 2002, 68, 1293-1294.	1.6	0
79	Induction of endoplasmic reticulum stress markers in an acromegaly model. Journal of Cellular Biochemistry, 0, , .	2.6	0