

Yoji Nakamura

List of Publications by Year in descending order

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11
papers

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1163117

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docs citations

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1334
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#	ARTICLE	IF	CITATIONS
1	Prediction of the Sex-Associated Genomic Region in Tunas (<i>Thunnus</i> Fishes). <i>International Journal of Genomics</i> , 2021, 2021, 1-14.	1.6	4
2	Draft Whole-Genome Sequence of <i>Triparma laevis</i> f. <i>inornata</i> (Parmales, Bolidophyceae), Isolated from the Oyashio Region, Western North Pacific Ocean. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
3	Targeted mutagenesis of the ryanodine receptor by Platinum TALENs causes slow swimming behaviour in Pacific bluefin tuna (<i>Thunnus orientalis</i>). <i>Scientific Reports</i> , 2019, 9, 13871.	3.3	14
4	Prediction of Horizontally and Widely Transferred Genes in Prokaryotes. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431881078.	1.2	3
5	Rhodopsin gene copies in Japanese eel originated in a teleost-specific genome duplication. <i>Zoological Letters</i> , 2017, 3, 18.	1.3	15
6	Effects of plankton net characteristics on metagenetic community analysis of metazoan zooplankton in a coastal marine ecosystem. <i>Journal of Experimental Marine Biology and Ecology</i> , 2015, 469, 36-43.	1.5	28
7	A ddRAD-based genetic map and its integration with the genome assembly of Japanese eel (<i>Anguilla</i>) Tj ETQq1 1 0.784314 rgBT /Overbo <i>Genomics</i> , 2014, 15, 233.	2.8	63
8	Evolutionary changes of multiple visual pigment genes in the complete genome of Pacific bluefin tuna. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11061-11066.	7.1	106
9	Comparative genomics reveals that a fish pathogenic bacterium <i>Edwardsiella tarda</i> has acquired the locus of enterocyte effacement (LEE) through horizontal gene transfer. <i>BMC Genomics</i> , 2013, 14, 642.	2.8	40
10	Biased biological functions of horizontally transferred genes in prokaryotic genomes. <i>Nature Genetics</i> , 2004, 36, 760-766.	21.4	459
11	The genome stability in <i>Corynebacterium</i> species due to lack of the recombinational repair system. <i>Gene</i> , 2003, 317, 149-155.	2.2	66