

# Yoji Nakamura

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8449824/publications.pdf>

Version: 2024-02-01

11  
papers

806  
citations

1163117

8  
h-index

1125743

13  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1334  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biased biological functions of horizontally transferred genes in prokaryotic genomes. <i>Nature Genetics</i> , 2004, 36, 760-766.	21.4	459
2	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
3	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
4	A ddRAD-based genetic map and its integration with the genome assembly of Japanese eel ( <i>Anguilla japonica</i> ). <i>BMC Genomics</i> , 2014, 15, 233.	2.8	63
5	Comparative genomics reveals that a fish pathogenic bacterium <i>Edwardsiella ictaluri</i> has acquired the locus of enterocyte effacement (LEE) through horizontal gene transfer. <i>BMC Genomics</i> , 2013, 14, 642.	2.8	40
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	Rhodopsin gene copies in Japanese eel originated in a teleost-specific genome duplication. <i>Zoological Letters</i> , 2017, 3, 18.	1.3	15
8	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
9	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
10	Prediction of Horizontally and Widely Transferred Genes in Prokaryotes. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431881078.	1.2	3
11	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