

Yoichiro Nakatani

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1246609/publications.pdf>

Version: 2024-02-01

20
papers

2,967
citations

516215

16
h-index

794141

19
g-index

23
all docs

23
docs citations

23
times ranked

4349
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Genomic Profiling of Neuroendocrine Carcinomas of the Gastrointestinal System. <i>Cancer Discovery</i> , 2022, 12, 692-711.	7.7	58
2	CTCF looping is established during gastrulation in medaka embryos. <i>Genome Research</i> , 2021, 31, 968-980.	2.4	37
3	Reconstruction of proto-vertebrate, proto-cyclostome and proto-gnathostome genomes provides new insights into early vertebrate evolution. <i>Nature Communications</i> , 2021, 12, 4489.	5.8	88
4	Macrosynteny analysis shows the absence of ancient whole-genome duplication in lepidopteran insects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1816-1818.	3.3	37
5	Genomes as documents of evolutionary history: a probabilistic macrosynteny model for the reconstruction of ancestral genomes. <i>Bioinformatics</i> , 2017, 33, i369-i378.	1.8	24
6	Associations between nucleosome phasing, sequence asymmetry, and tissue-specific expression in a set of inbred Medaka species. <i>BMC Genomics</i> , 2015, 16, 978.	1.2	3
7	Coordinated Changes in DNA Methylation in Antigen-Specific Memory CD4 T Cells. <i>Journal of Immunology</i> , 2013, 190, 4076-4091.	0.4	46
8	Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. <i>Genome Research</i> , 2012, 22, 1419-1425.	2.4	41
9	Genome-wide profiling of DNA methylation in human cancer cells. <i>Genomics</i> , 2011, 98, 280-287.	1.3	42
10	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. , 2011, , 39-47.		1
11	Reconstruction of the Vertebrate Ancestral Genome Reveals Dynamic Genome Reorganization in Early Vertebrates. , 2011, , 307-322.		1
12	Chromatin-Associated Periodicity in Genetic Variation Downstream of Transcriptional Start Sites. <i>Science</i> , 2009, 323, 401-404.	6.0	122
13	High-Resolution Analysis of the 5â€²-End Transcriptome Using a Next Generation DNA Sequencer. <i>PLoS ONE</i> , 2009, 4, e4108.	1.1	42
14	The genome of a lepidopteran model insect, the silkworm <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1036-1045.	1.2	592
15	Diversity of Ca ²⁺ -Induced Morphology Revealed by Morphological Phenotyping of Ca ²⁺ -Sensitive Mutants of <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2007, 6, 817-830.	3.4	24
16	Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. <i>Genome Research</i> , 2007, 17, 1254-1265.	2.4	444
17	UTGB/medaka: genomic resource database for medaka biology. <i>Nucleic Acids Research</i> , 2007, 36, D747-D752.	6.5	32
18	The medaka draft genome and insights into vertebrate genome evolution. <i>Nature</i> , 2007, 447, 714-719.	13.7	1,037

#	ARTICLE	IF	CITATIONS
19	High-dimensional and large-scale phenotyping of yeast mutants. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19015-19020.	3.3	276
20	Data mining tools for the <i>Saccharomyces cerevisiae</i> morphological database. Nucleic Acids Research, 2005, 33, W753-W757.	6.5	15