Hidenori Nishihara

List of Publications by Year
in descending order

49 papers	2,960 citations	236912 25 h-index	197805 49 g-index
50 all docs	50 docs citations	50 times ranked	3936 citing authors

#	Article	IF	Citations
1	Placental Mammals Acquired Functional Sequences in NRK for Regulating the CK2â€“PTENâ€“AKT Pathway and Placental Cell Proliferation. Molecular Biology and Evolution, 2022, 39, .	8.9	9
2	Maelstrom functions in the production of Siwi-piRISC capable of regulating transposons in Bombyx germ cells. IScience, 2022, 25, 103914.	4.1	5
3	Paleogenomics reveals independent and hybrid origins of two morphologically distinct wolf lineages endemic to Japan. Current Biology, 2022, 32, 2494-2504.e5.	3.9	5
4	SINEs as Credible Signs to Prove Common Ancestry in the Tree of Life: A Brief Review of Pioneering Case Studies in Retroposon Systematics. Genes, 2022, 13, 989.	2.4	3
5	Hamster PIWI proteins bind to piRNAs with stage-specific size variations during oocyte maturation. Nucleic Acids Research, 2021, 49, 2700-2720.	14.5	26
6	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. Royal Society Open Science, 2021, 8, 210518.	2.4	8
7	Replacement of owl monkey centromere satellite by a newly evolved variant was a recent and rapid process. Genes To Cells, 2021, 26, 979-986.	1.2	2
8	Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. DNA Research, 2020, 27, .	3.4	10
9	Hadean Primordial Metabolism Pathway Driven by a Nuclear Geyser. Journal of Geography (Chigaku) Tj ETQq1 1 0.784314 rgBT /Overl	0.3	2
10	Evolutionary Gain of Dbx1 Expression Drives Subplate Identity in the Cerebral Cortex. Cell Reports, 2019, 29, 645-658.e5.	6.4	11
11	Retrotransposons spread potential cis-regulatory elements during mammary gland evolution. Nucleic Acids Research, 2019, 47, 11551-11562.	14.5	17
12	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	7.0	26
13	Transposable elements as genetic accelerators of evolution: contribution to genome size, gene regulatory network rewiring and morphological innovation. Genes and Genetic Systems, 2019, 94, 269-281.	0.7	34
14	Evolution of transposable elements and evolution of eukaryote genomes mediated by transposable elements. Genes and Genetic Systems, 2019, 94, 231-231.	0.7	2
15	The CENP-B box, a nucleotide motif involved in centromere formation, has multiple origins in New World monkeys. Genes and Genetic Systems, 2019, 94, 301-306.	0.7	7
16	Evolutionary Origin of OwlRep, a Megasatellite DNA Associated with Adaptation of Owl Monkeys to Nocturnal Lifestyle. Genome Biology and Evolution, 2018, 10, 157-165.	2.5	5
17	Phylogenetic analysis of proteins involved in the stringent response in plant cells. Journal of Plant Research, 2017, 130, 625-634.	2.4	31
18	Support for Lungfish as the Closest Relative of Tetrapods by Using Slowly Evolving Ray-finned fish as the Outgroup. Genome Biology and Evolution, 2017, 9, evw288.	2.5	11

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19	Coordinately Co-opted Multiple Transposable Elements Constitute an Enhancer for wnt5a Expression in the Mammalian Secondary Palate. PLoS Genetics, 2016, 12, e1006380.	3.5	47
20	Resolving the Phylogenetic Position of Coelacanth: The Closest Relative Is Not Always the Most Appropriate Outgroup. Genome Biology and Evolution, 2016, 8, 1208-1221.	2.5	29
21	MetaSINEs: Broad Distribution of a Novel SINE Superfamily in Animals. Genome Biology and Evolution, 2016, 8, 528-539.	2.5	22
22	Determining the Position of Storks on the Phylogenetic Tree of Waterbirds by Retroposon Insertion Analysis. Genome Biology and Evolution, 2015, 7, 3180-3189.	2.5	16
23	The genomic substrate for adaptive radiation in African cichlid fish. Nature, 2014, 513, 375-381.	27.8	874
24	The complete mitochondrial genomes of deep-sea squid (Bathyteuthis abyssicola), bob-tail squid (Semirossia patagonica) and four giant cuttlefish (Sepia apama, S. latimanus, S. lycidas and S. pharanis), and their application to the phylogenetic analysis of Decapodiformes. Molecular Phylogenetics and Evolution, 2013, 69, 980-993.	2.7	29
25	Coelacanth genomes reveal signatures for evolutionary transition from water to land. Genome Research, 2013, 23, 1740-1748.	5.5	108
26	Phylogeny of Galactolipid Synthase Homologs Together with their Enzymatic Analyses Revealed a Possible Origin and Divergence Time for Photosynthetic Membrane Biogenesis. DNA Research, 2012, 19, 91-102.	3.4	37
27	Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. Gene, 2012, 505, 324-332.	2.2	9
28	A SINE-Derived Element Constitutes a Unique Modular Enhancer for Mammalian Diencephalic Fgf8. PLoS ONE, 2012, 7, e43785.	2.5	33
29	Reverse Evolution in RH1 for Adaptation of Cichlids to Water Depth in Lake Tanganyika. Molecular Biology and Evolution, 2011, 28, 1769-1776.	8.9	33
30	B Chromosomes Have a Functional Effect on Female Sex Determination in Lake Victoria Cichlid Fishes. PLoS Genetics, 2011, 7, e1002203.	3.5	134
31	A Mammalian Conserved Element Derived from SINE Displays Enhancer Properties Recapitulating Satb2 Expression in Early-Born Callosal Projection Neurons. PLoS ONE, 2011, 6, e28497.	2.5	49
32	Emergence of mammals by emergency: exaptation. Genes To Cells, 2010, 15, 801-812.	1.2	27
33	Characterization of a novel SINE superfamily from invertebrates: â€œCeph-SINEsâ€•from the genomes of squids and cuttlefish. Gene, 2010, 454, 8-19.	2.2	28
34	The evolution of two partner LINE/SINE families and a full-length chromodomain-containing Ty3/Gypsy LTR element in the first reptilian genome of Anolis carolinensis. Gene, 2009, 441, 111-118.	2.2	41
35	Characterization and evolutionary landscape of AmnSINE1 in Amniota genomes. Gene, 2009, 441, 100-110.	2.2	24
36	Retroposon analysis and recent geological data suggest near-simultaneous divergence of the three superorders of mammals. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5235-5240.	7.1	162

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37	Identification of four Engrailed genes in the Japanese lamprey, Lethenteron japonicum. Developmental Dynamics, 2008, 237, 1581-1589.	1.8	33
38	Newly discovered young CORE-SINEs in marsupial genomes. Gene, 2008, 407, 176-185.	2.2	23
39	Possible involvement of SINEs in mammalian-specific brain formation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4220-4225.	7.1	177
40	Retroposons: Genetic Footprints on the Evolutionary Paths of Life. Methods in Molecular Biology, 2008, 422, 201-225.	0.9	20
41	Acquisition of Endonuclease Specificity during Evolution of L1 Retrotransposon. Molecular Biology and Evolution, 2007, 24, 2009-2015.	8.9	12
42	Novel SINE Families from Salmons Validate Parahucho (Salmonidae) as a Distinct Genus and Give Evidence that SINEs Can Incorporate LINE-related 3â€²-Tails of Other SINEs. Molecular Biology and Evolution, 2007, 24, 1656-1666.	8.9	27
43	MyrSINEs: A novel SINE family in the anteater genomes. Gene, 2007, 400, 98-103.	2.2	11
44	Rooting the eutherian tree: the power and pitfalls of phylogenomics. Genome Biology, 2007, 8, R199.	9.6	82
45	Pegasoferae, an unexpected mammalian clade revealed by tracking ancient retroposon insertions. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9929-9934.	7.1	207
46	Functional noncoding sequences derived from SINEs in the mammalian genome. Genome Research, 2006, 16, 864-874.	5.5	207
47	A Retroposon Analysis of Afrotherian Phylogeny. Molecular Biology and Evolution, 2005, 22, 1823-1833.	8.9	88
48	Ancient SINEs from African Endemic Mammals. Molecular Biology and Evolution, 2003, 20, 522-527.	8.9	81
49	Characterization of Novel Alu- and tRNA-Related SINEs from the Tree Shrew and Evolutionary Implications of Their Origins. Molecular Biology and Evolution, 2002, 19, 1964-1972.	8.9	76