

# Masato Nikaido

## List of Publications by Year in descending order

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61  
papers

3,674  
citations

201674

27  
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138484

58  
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66  
docs citations

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times ranked

3806  
citing authors

#	ARTICLE	IF	CITATIONS
1	A transcriptomic reevaluation of the accessory olfactory organ in Bichir ( <i>Polypterus senegalus</i> ). <i>Zoological Letters</i> , 2022, 8, 5.	1.3	2
2	Remarkable diversity of vomeronasal type 2 receptor (OlfC) genes of basal ray-finned fish and its evolutionary trajectory in jawed vertebrates. <i>Scientific Reports</i> , 2022, 12, 6455.	3.3	3
3	New Sex Chromosomes in Lake Victoria Cichlid Fishes (Cichlidae: Haplochromini). <i>Genes</i> , 2022, 13, 804.	2.4	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. <i>Genes</i> , 2022, 13, 989.	2.4	3
5	Conserved keratin gene clusters in ancient fish: An evolutionary seed for terrestrial adaptation. <i>Genomics</i> , 2021, 113, 1120-1128.	2.9	7
6	Genomic Signatures for Species-Specific Adaptation in Lake Victoria Cichlids Derived from Large-Scale Standing Genetic Variation. <i>Molecular Biology and Evolution</i> , 2021, 38, 3111-3125.	8.9	9
7	Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. <i>DNA Research</i> , 2020, 27, .	3.4	10
8	Inactivation of ancV1R as a Predictive Signature for the Loss of Vomeronasal System in Mammals. <i>Genome Biology and Evolution</i> , 2020, 12, 766-778.	2.5	11
9	Evolution of &lt;i>V1R&/i> pheromone receptor genes in vertebrates: diversity and commonality. <i>Genes and Genetic Systems</i> , 2019, 94, 141-149.	0.7	11
10	Patterns of genomic differentiation between two Lake Victoria cichlid species, <i>Haplochromis pyrrhocephalus</i> and <i>H. sp. "maculata"</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 68.	3.2	4
11	Evolution of vomeronasal receptor 1 (V1R) genes in the common marmoset ( <i>Callithrix jacchus</i> ). <i>Gene</i> , 2018, 642, 343-353.	2.2	22
12	A single pheromone receptor gene conserved across 400 million years of vertebrate evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 2928-2939.	8.9	20
13	Distinct functions of two olfactory marker protein genes derived from teleost-specific whole genome duplication. <i>BMC Evolutionary Biology</i> , 2015, 15, 245.	3.2	16
14	A microsatellite-based genetic linkage map and putative sex-determining genomic regions in Lake Victoria cichlids. <i>Gene</i> , 2015, 560, 156-164.	2.2	12
15	Multiple Episodic Evolution Events in V1R Receptor Genes of East-African Cichlids. <i>Genome Biology and Evolution</i> , 2014, 6, 1135-1144.	2.5	22
16	The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 2014, 513, 375-381.	27.8	874
17	The complete mitochondrial genomes of deep-sea squid ( <i>Bathyteuthis abyssicola</i> ), bob-tail squid ( <i>Semirossia patagonica</i> ) and four giant cuttlefish ( <i>Sepia apama</i> , <i>S. latimanus</i> , <i>S. lycidas</i> and <i>S. pharansis</i> ), and their application to the phylogenetic analysis of Decapodiformes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 980-993.	2.7	29
18	Coelacanth genomes reveal signatures for evolutionary transition from water to land. <i>Genome Research</i> , 2013, 23, 1740-1748.	5.5	108

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19	Lineage-Specific Expansion of Vomeronasal Type 2 Receptor-Like (OlfC) Genes in Cichlids May Contribute to Diversification of Amino Acid Detection Systems. <i>Genome Biology and Evolution</i> , 2013, 5, 711-722.	2.5	26
20	Characterization of VIR receptor (ora) genes in Lake Victoria cichlids. <i>Gene</i> , 2012, 499, 273-279.	2.2	18
21	Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. <i>Gene</i> , 2012, 505, 324-332.	2.2	9
22	Genetically distinct coelacanth population off the northern Tanzanian coast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18009-18013.	7.1	20
23	Vertebrate Rhodopsin Adaptation to Dim Light via Rapid Meta-II Intermediate Formation. <i>Molecular Biology and Evolution</i> , 2010, 27, 506-519.	8.9	34
24	Genetic variation and demographic history of the <i>Haplochromis laparogramma</i> group of Lake Victoria—An analysis based on SINEs and mitochondrial DNA. <i>Gene</i> , 2010, 450, 39-47.	2.2	17
25	Characterization of a novel SINE superfamily from invertebrates: “Ceph-SINEs” from the genomes of squids and cuttlefish. <i>Gene</i> , 2010, 454, 8-19.	2.2	28
26	Conserved repertoire of orthologous vomeronasal type 1 receptor genes in ruminant species. <i>BMC Evolutionary Biology</i> , 2009, 9, 233.	3.2	32
27	Chronology of the extant African elephant species and case study of the species identification of the small African elephant with the molecular phylogenetic method. <i>Gene</i> , 2009, 441, 176-186.	2.2	11
28	Newly discovered young CORE-SINEs in marsupial genomes. <i>Gene</i> , 2008, 407, 176-185.	2.2	23
29	Molecular phylogenetic study on the origin and evolution of Mustelidae. <i>Gene</i> , 2007, 396, 1-12.	2.2	66
30	MyrSINEs: A novel SINE family in the anteater genomes. <i>Gene</i> , 2007, 400, 98-103.	2.2	11
31	Toothed whale monophyly reassessed by SINE insertion analysis: The absence of lineage sorting effects suggests a small population of a common ancestral species. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 216-224.	2.7	43
32	Genomic expansion of the Bov-A2 retroposon relating to phylogeny and breed management. <i>Mammalian Genome</i> , 2007, 18, 187-196.	2.2	11
33	The rise and fall of the CR1 subfamily in the lineage leading to penguins. <i>Gene</i> , 2006, 365, 57-66.	2.2	39
34	New candidate species most closely related to penguins. <i>Gene</i> , 2006, 378, 65-73.	2.2	29
35	Phylogenetic Analysis of Diprotodontian Marsupials Based on Complete Mitochondrial Genomes. <i>Genes and Genetic Systems</i> , 2006, 81, 181-191.	0.7	25
36	Extensive mitochondrial gene arrangements in coleoid Cephalopoda and their phylogenetic implications. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 648-658.	2.7	91

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37	Balaenoptera omurai is a newly discovered baleen whale that represents an ancient evolutionary lineage. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 40-52.	2.7	84
38	Baleen Whale Phylogeny and a Past Extensive Radiation Event Revealed by SINE Insertion Analysis. <i>Molecular Biology and Evolution</i> , 2006, 23, 866-873.	8.9	69
39	A Retroposon Analysis of Afrotherian Phylogeny. <i>Molecular Biology and Evolution</i> , 2005, 22, 1823-1833.	8.9	88
40	Mitochondrial Phylogenetics and Evolution of Mysticete Whales. <i>Systematic Biology</i> , 2005, 54, 77-90.	5.6	143
41	Retroposon Mapping in Molecular Systematics. , 2004, 260, 189-226.		47
42	First Application of the SINE (Short Interspersed Repetitive Element) Method to Infer Phylogenetic Relationships in Reptiles: An Example from the Turtle Superfamily Testudinoidea. <i>Molecular Biology and Evolution</i> , 2004, 21, 705-715.	8.9	46
43	Afrotherian phylogeny as inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 253-260.	2.7	49
44	Mitochondrial phylogeny of hedgehogs and monophyly of Eulipotyphla. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 276-284.	2.7	61
45	The status of the Japanese and East Asian bats of the genus <i>Myotis</i> (Vespertilionidae) based on mitochondrial sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 297-307.	2.7	74
46	Ancient SINEs from African Endemic Mammals. <i>Molecular Biology and Evolution</i> , 2003, 20, 522-527.	8.9	81
47	Unique Mammalian tRNA-Derived Repetitive Elements in Dermopterans: The t-SINE Family and Its Retrotransposition Through Multiple Sources. <i>Molecular Biology and Evolution</i> , 2003, 20, 1659-1668.	8.9	34
48	The phylogenetic relationships of insectivores with special reference to the lesser hedgehog tenrec as inferred from the complete sequence of their mitochondrial genome.. <i>Genes and Genetic Systems</i> , 2003, 78, 107-112.	0.7	12
49	Intra- and Interfamily Relationships of Vespertilionidae Inferred by Various Molecular Markers Including SINE Insertion Data. <i>Journal of Molecular Evolution</i> , 2002, 55, 284-301.	1.8	60
50	Éléments mobiles SINE en phylogénie. <i>Medecine/Sciences</i> , 2002, 18, 1276-1281.	0.2	1
51	Retroposon analysis of major cetacean lineages: The monophyly of toothed whales and the paraphyly of river dolphins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 7384-7389.	7.1	239
52	Maximum Likelihood Analysis of the Complete Mitochondrial Genomes of Eutherians and a Reevaluation of the Phylogeny of Bats and Insectivores. <i>Journal of Molecular Evolution</i> , 2001, 53, 508-516.	1.8	128
53	Evolution of CHR-2 SINEs in cetartiodactyl genomes: possible evidence for the monophyletic origin of toothed whales. <i>Mammalian Genome</i> , 2001, 12, 909-915.	2.2	34
54	Evolution of CHR-2 SINEs in cetartiodactyl genomes: possible evidence for the monophyletic origin of toothed whales. <i>Mammalian Genome</i> , 2001, 012, 0909-0915.	2.2	0

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55	CetSINEs and AREs are not SINEs but are parts of cetartiodactyl L1. <i>Mammalian Genome</i> , 2000, 11, 1123-1126.	2.2	7
56	Monophyletic Origin of the Order Chiroptera and Its Phylogenetic Position Among Mammalia, as Inferred from the Complete Sequence of the Mitochondrial DNA of a Japanese Megabat, the Ryukyu Flying Fox ( <i>Pteropus dasymallus</i> ). <i>Journal of Molecular Evolution</i> , 2000, 51, 318-328.	1.8	62
57	Consistency of SINE Insertion Topology and Flanking Sequence Tree: Quantifying Relationships Among Cetartiodactyls. <i>Molecular Biology and Evolution</i> , 2000, 17, 1417-1424.	8.9	35
58	Interordinal relationships and timescale of eutherian evolution as inferred from mitochondrial genome data. <i>Gene</i> , 2000, 259, 149-158.	2.2	107
59	Genealogy of families of SINEs in cetaceans and artiodactyls: the presence of a huge superfamily of tRNA(Glu)-derived families of SINEs. <i>Molecular Biology and Evolution</i> , 1999, 16, 1046-1060.	8.9	85
60	Phylogenetic relationships among cetartiodactyls based on insertions of short and long interspersed elements: Hippopotamuses are the closest extant relatives of whales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10261-10266.	7.1	402
61	A SINE that acquired a role in signal transduction during evolution. <i>Molecular Biology and Evolution</i> , 1998, 15, 923-925.	8.9	24