

Naoki Osada

List of Publications by Year in descending order

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87
papers

2,701
citations

236925

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96
docs citations

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times ranked

4177
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#	ARTICLE	IF	CITATIONS
1	Predicting PRDM9 Binding Sites by a Convolutional Neural Network and Verification Using Genetic Recombination Map. <i>IPSI Transactions on Bioinformatics</i> , 2022, 15, 9-16.	0.2	0
2	Whole-Genome Sequencing of Vero E6 (VERO C1008) and Comparative Analysis of Four Vero Cell Sublines. <i>Frontiers in Genetics</i> , 2022, 13, 801382.	2.3	5
3	Insights into <i>Mus musculus</i> Population Structure across Eurasia Revealed by Whole-Genome Analysis. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	15
4	A New Approach to Drug Repurposing with Two-Stage Prediction, Machine Learning, and Unsupervised Clustering of Gene Expression. <i>OMICS A Journal of Integrative Biology</i> , 2022, 26, 339-347.	2.0	11
5	Testing sex-biased admixture origin of macaque species using autosomal and X-chromosomal genomic sequences. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	14
6	House mouse <i>Mus musculus</i> dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. <i>Heredity</i> , 2021, 126, 132-147.	2.6	26
7	Demographic History of the Brown Bear (<i>Ursus arctos</i>) on Hokkaido Island, Japan, Based on Whole-Genomic Sequence Analysis. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	10
8	Exploring models of human migration to the Japanese archipelago using genome-wide genetic data. <i>Anthropological Science</i> , 2021, 129, 45-58.	0.4	7
9	Phylogeographic study using nuclear genome sequences of <i>Mus musculus</i> to infer the origins of ventral fur color variation in the house mouse <i>Mus musculus</i> . <i>Genes and Genetic Systems</i> , 2021, 96, 271-284.	0.7	1
10	Dysfunctional missense variant of <i>OAT10/SLC22A13</i> decreases gout risk and serum uric acid levels. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 164-166.	0.9	26
11	Identification of Characteristic Genomic Markers in Human Hepatoma HuH-7 and Huh7.5.1-8 Cell Lines. <i>Frontiers in Genetics</i> , 2020, 11, 546106.	2.3	24
12	Comparative characterization of flavivirus production in two cell lines: Human hepatoma-derived Huh7.5.1-8 and African green monkey kidney-derived Vero. <i>PLoS ONE</i> , 2020, 15, e0232274.	2.5	13
13	Title is missing!. , 2020, 15, e0232274.		0
14	Title is missing!. , 2020, 15, e0232274.		0
15	Title is missing!. , 2020, 15, e0232274.		0
16	Title is missing!. , 2020, 15, e0232274.		0
17	Genetic diversity and population structure of <i>Glossina morsitans morsitans</i> in the active foci of human African trypanosomiasis in Zambia and Malawi. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007568.	3.0	3
18	Achiasmy and sex chromosome evolution. <i>Ecological Genetics and Genomics</i> , 2019, 13, 100046.	0.5	12

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19	A key metabolic gene for recurrent freshwater colonization and radiation in fishes. <i>Science</i> , 2019, 364, 886-889.	12.6	109
20	Novel endogenous simian retroviral integrations in Vero cells: implications for quality control of a human vaccine cell substrate. <i>Scientific Reports</i> , 2018, 8, 644.	3.3	21
21	Ancient hybridization and admixture in macaques (genus <i>Macaca</i>) inferred from whole genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 376-386.	2.7	38
22	Development of genotyping method for functionally relevant variants of cytochromes P450 in cynomolgus macaques. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2018, 41, e30-e34.	1.3	3
23	Comprehensive phylogenomic analysis reveals a novel cluster of simian endogenous retroviral sequences in Colobinae monkeys. <i>American Journal of Primatology</i> , 2018, 80, e22882.	1.7	3
24	Translational Repression of a Splice Variant of Cynomolgus Macaque CXCL11 by Its C-Terminal Sequence. <i>Journal of Interferon and Cytokine Research</i> , 2017, 37, 129-138.	1.2	0
25	<i>Cis</i> - and <i>Trans</i> -regulatory Effects on Gene Expression in a Natural Population of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2017, 206, 2139-2148.	2.9	57
26	A Generalized Linear Model for Decomposing <i>Cis</i> -regulatory, Parent-of-Origin, and Maternal Effects on Allele-Specific Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2227-2234.	1.8	11
27	Compensatory Evolution. , 2016, , 329-333.		1
28	Genetic diversity in humans and non-human primates and its evolutionary consequences. <i>Genes and Genetic Systems</i> , 2015, 90, 133-145.	0.7	27
29	Genome-scale approaches for studying human and non-human primate evolution. <i>Genes and Genetic Systems</i> , 2015, 90, 121-122.	0.7	0
30	Complex patterns of <i>cis</i> -regulatory polymorphisms in <i>ebony</i> underlie standing pigmentation variation in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2015, 24, 5829-5841.	3.9	32
31	An Individual-Based Diploid Model Predicts Limited Conditions Under Which Stochastic Gene Expression Becomes Advantageous. <i>Frontiers in Genetics</i> , 2015, 6, 336.	2.3	1
32	Model-Based Verification of Hypotheses on the Origin of Modern Japanese Revisited by Bayesian Inference Based on Genome-Wide SNP Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 1533-1543.	8.9	32
33	CYP2D44 polymorphisms in cynomolgus and rhesus macaques. <i>Molecular Biology Reports</i> , 2015, 42, 1149-1155.	2.3	10
34	Whole-Genome Sequencing of Six Mauritian Cynomolgus Macaques (<i>Macaca fascicularis</i>) Reveals a Genome-Wide Pattern of Polymorphisms under Extreme Population Bottleneck. <i>Genome Biology and Evolution</i> , 2015, 7, 821-830.	2.5	37
35	Ecological genomics in <i>Xanthomonas</i> : the nature of genetic adaptation with homologous recombination and host shifts. <i>BMC Genomics</i> , 2015, 16, 188.	2.8	23
36	Population genetics of non-genetic traits: Evolutionary roles of stochasticity in gene expression. <i>Gene</i> , 2015, 562, 16-21.	2.2	19

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37	Adaptive divergence with gene flow in incipient speciation of <i>Miscanthus floridulus</i> / <i>Miscanthus sinensis</i> complex (<i>Poaceae</i>). <i>Plant Journal</i> , 2014, 80, 834-847.	5.7	17
38	Whole-Genome Sequencing of Tibetan Macaque (<i>Macaca thibetana</i>) Provides New Insight into the Macaque Evolutionary History. <i>Molecular Biology and Evolution</i> , 2014, 31, 1475-1489.	8.9	49
39	Prdm9 Polymorphism Unveils Mouse Evolutionary Tracks. <i>DNA Research</i> , 2014, 21, 315-326.	3.4	54
40	The Genome Landscape of the African Green Monkey Kidney-Derived Vero Cell Line. <i>DNA Research</i> , 2014, 21, 673-683.	3.4	198
41	Dopamine Receptor Genes and Evolutionary Differentiation in the Domestication of Fighting Cocks and Long-Crowing Chickens. <i>PLoS ONE</i> , 2014, 9, e101778.	2.5	21
42	Systematic classification of vertebrate chemokines based on conserved synteny and evolutionary history. <i>Genes To Cells</i> , 2013, 18, 1-16.	1.2	107
43	Finding the Factors of Reduced Genetic Diversity on X Chromosomes of <i>Macaca fascicularis</i> : Male-Driven Evolution, Demography, and Natural Selection. <i>Genetics</i> , 2013, 195, 1027-1035.	2.9	16
44	Mitochondrial-Nuclear Interactions and Accelerated Compensatory Evolution: Evidence from the Primate Cytochrome c Oxidase Complex. <i>Molecular Biology and Evolution</i> , 2012, 29, 337-346.	8.9	203
45	Whole-genome sequencing and analysis of the Malaysian cynomolgus macaque (<i>Macaca fascicularis</i>) genome. <i>Genome Biology</i> , 2012, 13, R58.	9.6	72
46	Weak Selection and Protein Evolution. <i>Genetics</i> , 2012, 192, 15-31.	2.9	124
47	Evolutionary rates of commonly used nuclear and organelle markers of <i>Arabidopsis</i> relatives (<i>Brassicaceae</i>). <i>Gene</i> , 2012, 499, 194-201.	2.2	20
48	An Overview of Transcriptome Studies in Non-Human Primates. <i>Primate Monographs</i> , 2012, , 9-22.	0.8	0
49	Footprints of natural and artificial selection for photoperiod pathway genes in <i>Oryza</i> . <i>Plant Journal</i> , 2012, 70, 769-782.	5.7	40
50	Novel DNA sequence isolated from blood donors with high transaminase levels. <i>Hepatology Research</i> , 2011, 41, 971-981.	3.4	5
51	Phylogenetic Inconsistency Caused by Ancient Sex-Biased Gene Migration. <i>PLoS ONE</i> , 2011, 6, e25549.	2.5	4
52	CpG site degeneration triggered by the loss of functional constraint created a highly polymorphic macaque drug-metabolizing gene, CYP1A2. <i>BMC Evolutionary Biology</i> , 2011, 11, 283.	3.2	17
53	Characterization of MHC class I transcripts of a Malaysian cynomolgus macaque by high-throughput pyrosequencing and EST libraries. <i>Immunogenetics</i> , 2011, 63, 703-713.	2.4	9
54	A family tree of vertebrate chemokine receptors for a unified nomenclature. <i>Developmental and Comparative Immunology</i> , 2011, 35, 705-715.	2.3	107

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55	Population Genetics in Nonmodel Organisms: II. Natural Selection in Marginal Habitats Revealed by Deep Sequencing on Dual Platforms. <i>Molecular Biology and Evolution</i> , 2011, 28, 2833-2842.	8.9	23
56	Multilocus analysis of genetic divergence between outcrossing <i>Arabidopsis</i> species: evidence of genome-wide admixture. <i>New Phytologist</i> , 2010, 188, 488-500.	7.3	18
57	Ancient genome-wide admixture extends beyond the current hybrid zone between <i>Macaca fascicularis</i> and <i>M. mulatta</i> . <i>Molecular Ecology</i> , 2010, 19, 2884-2895.	3.9	53
58	Genetic Variants of <i>CYP3A4</i> and <i>CYP3A5</i> in <i>Cynomolgus</i> and Rhesus Macaques. <i>Drug Metabolism and Disposition</i> , 2010, 38, 209-214.	3.3	54
59	The evolution of mammalian chemokine genes. <i>Cytokine and Growth Factor Reviews</i> , 2010, 21, 253-262.	7.2	128
60	IL-10 Is a Negative Regulatory Factor of CAWS-Vasculitis in CBA/J Mice as Assessed by Comparison with Bruton's Tyrosine Kinase-Deficient CBA/N Mice. <i>Journal of Immunology</i> , 2009, 183, 3417-3424.	0.8	31
61	Quantifying dominance and deleterious effect on human disease genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 841-846.	7.1	13
62	Collection of <i>Macaca fascicularis</i> cDNAs derived from bone marrow, kidney, liver, pancreas, spleen, and thymus. <i>BMC Research Notes</i> , 2009, 2, 199.	1.4	11
63	Development of an integrative database with 499 novel microsatellite markers for <i>Macaca fascicularis</i> . <i>BMC Genetics</i> , 2009, 10, 24.	2.7	10
64	Multiple duplication of the bucentaur gene family, which recruits the APE-like domain of retrotransposon: Identification of a novel homolog and distinct cellular expression. <i>Gene</i> , 2009, 435, 88-95.	2.2	5
65	Extensive expansion and diversification of the chemokine gene family in zebrafish: Identification of a novel chemokine subfamily CX. <i>BMC Genomics</i> , 2008, 9, 222.	2.8	163
66	Large-scale analysis of <i>Macaca fascicularis</i> transcripts and inference of genetic divergence between <i>M. fascicularis</i> and <i>M. mulatta</i> . <i>BMC Genomics</i> , 2008, 9, 90.	2.8	40
67	Expressed sequence tags from cynomolgus monkey (<i>Macaca fascicularis</i>) liver: A systematic identification of drug-metabolizing enzymes. <i>FEBS Letters</i> , 2008, 582, 351-358.	2.8	21
68	Duplication and Gene Conversion in the <i>Drosophila melanogaster</i> Genome. <i>PLoS Genetics</i> , 2008, 4, e1000305.	3.5	60
69	Identification of a Novel CXCL1-Like Chemokine Gene in Macaques and Its Inactivation in Hominids. <i>Journal of Interferon and Cytokine Research</i> , 2007, 27, 32-37.	1.2	5
70	Inference of Expression-Dependent Negative Selection Based on Polymorphism and Divergence in the Human Genome. <i>Molecular Biology and Evolution</i> , 2007, 24, 1622-1626.	8.9	8
71	Aberrant termination of reproduction-related TMEM30C transcripts in the hominoids. <i>Gene</i> , 2007, 392, 151-156.	2.2	12
72	Positive and negative regulation of adenovirus infection by CAR-like soluble protein, CLSP. <i>Gene Therapy</i> , 2007, 14, 1199-1207.	4.5	8

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73	Genomic Inferences of the cis-Regulatory Nucleotide Polymorphisms Underlying Gene Expression Differences between <i>Drosophila melanogaster</i> Mating Races. <i>Molecular Biology and Evolution</i> , 2006, 23, 1585-1591.	8.9	25
74	Rate of Evolution in Brain-Expressed Genes in Humans and Other Primates. <i>PLoS Biology</i> , 2006, 5, e13.	5.6	93
75	A Tandem Gene Duplication Followed by Recruitment of a Retrotransposon Created the Paralogous Bucentaur Gene (bcntp97) in the Ancestral Ruminant. <i>Molecular Biology and Evolution</i> , 2006, 23, 798-806.	8.9	15
76	Evolution of Sexual Isolation during Secondary Contact: Genotypic versus Phenotypic Changes in Laboratory Populations. <i>American Naturalist</i> , 2005, 165, 420-428.	2.1	17
77	Inferring the Mode of Speciation From Genomic Data. <i>Genetics</i> , 2005, 169, 259-264.	2.9	75
78	Substitution Rate and Structural Divergence of 5'UTR Evolution: Comparative Analysis Between Human and <i>Cynomolgus</i> Monkey cDNAs. <i>Molecular Biology and Evolution</i> , 2005, 22, 1976-1982.	8.9	21
79	Molecular cloning, genomic characterization and over-expression of a novel gene, XRRA1, identified from human colorectal cancer cell HCT116Clone2_XRR and macaque testis. <i>BMC Genomics</i> , 2003, 4, 32.	2.8	14
80	A Transposable Element-Mediated Gene Divergence that Directly Produces a Novel Type Bovine Bcnt Protein Including the Endonuclease Domain of RTE-1. <i>Molecular Biology and Evolution</i> , 2003, 20, 1556-1563.	8.9	26
81	Analysis of 5'-End Sequences of Chimpanzee cDNAs. <i>Genome Research</i> , 2003, 13, 1022-1026.	5.5	17
82	Search for Genes Positively Selected during Primate Evolution by 5'-End-Sequence Screening of <i>Cynomolgus</i> Monkey cDNAs. <i>Genomics</i> , 2002, 79, 657-662.	2.9	19
83	<i>Cynomolgus</i> monkey testicular cDNAs for discovery of novel human genes in the human genome sequence. <i>BMC Genomics</i> , 2002, 3, 36.	2.8	16
84	Prediction of unidentified human genes on the basis of sequence similarity to novel cDNAs from <i>cynomolgus</i> monkey brain. <i>Genome Biology</i> , 2001, 3, research0006.1.	9.6	10
85	Assignment of 118 novel cDNAs of <i>cynomolgus</i> monkey brain to human chromosomes. <i>Gene</i> , 2001, 275, 31-37.	2.2	19
86	Sequence analysis, gene expression, and chromosomal assignment of mouse <i>Borg4</i> gene and its human orthologue. <i>Journal of Human Genetics</i> , 2000, 45, 374-377.	2.3	3
87	Extracting population genetics information from a diploid genome sequence. <i>Frontiers in Ecology and Evolution</i> , 0, 2, .	2.2	4