## Yasuhiro Go

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9374616/publications.pdf

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40 papers

1,481 citations

304743 22 h-index 345221 36 g-index

44 all docs

44 docs citations

times ranked

44

2127 citing authors

#	Article	IF	CITATIONS
1	Uterus-specific transcriptional regulation underlies eggshell pigment production in Japanese quail. PLoS ONE, 2022, 17, e0265008.	2.5	O
2	Population history and genomic admixture of sea snakes of the genus Laticauda in the West Pacific. Molecular Phylogenetics and Evolution, 2021, 155, 107005.	2.7	7
3	Redundant type II cadherins define neuroepithelial cell states for cytoarchitectonic robustness. Communications Biology, 2020, 3, 574.	4.4	9
4	Towards HCP-Style macaque connectomes: 24-Channel 3T multi-array coil, MRI sequences and preprocessing. Neurolmage, 2020, 215, 116800.	4.2	67
5	AUTS2 Regulation of Synapses for Proper Synaptic Inputs and Social Communication. IScience, 2020, 23, 101183.	4.1	38
6	MacaquePose: A Novel "In the Wild―Macaque Monkey Pose Dataset for Markerless Motion Capture. Frontiers in Behavioral Neuroscience, 2020, 14, 581154.	2.0	46
7	Transcriptome analysis revealed misregulated gene expression in blastoderms of interspecific chicken and Japanese quail F1 hybrids. PLoS ONE, 2020, 15, e0240183.	2.5	0
8	Considerable Synteny and Sequence Similarity of Primate Chromosomal Region VIIq31. Cytogenetic and Genome Research, 2019, 158, 88-97.	1.1	0
9	Loss of olfaction in sea snakes provides new perspectives on the aquatic adaptation of amniotes. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191828.	2.6	27
10	Digital gene atlas of neonate common marmoset brain. Neuroscience Research, 2018, 128, 1-13.	1.9	37
11	Nonsense mutation in PMEL is associated with yellowish plumage colour phenotype in Japanese quail. Scientific Reports, 2018, 8, 16732.	3.3	16
12	The neuropathological investigation of the brain in a monkey model of autism spectrum disorder with ABCA13 deletion. International Journal of Developmental Neuroscience, 2018, 71, 130-139.	1.6	16
13	Transcriptional activation of a chimeric retrogene PIPSL in a hominoid ancestor. Gene, 2018, 678, 318-323.	2.2	1
14	Human-specific features of spatial gene expression and regulation in eight brain regions. Genome Research, 2018, 28, 1097-1110.	5.5	66
15	Evolution of the sperm methylome of primates is associated with retrotransposon insertions and genome instability. Human Molecular Genetics, 2017, 26, 3508-3519.	2.9	16
16	Direct estimation of de novo mutation rates in a chimpanzee parent-offspring trio by ultra-deep whole genome sequencing. Scientific Reports, 2017, 7, 13561.	3.3	38
17	Single-neuron and genetic correlates of autistic behavior in macaque. Science Advances, 2016, 2, e1600558.	10.3	43
18	The life history of retrocopies illuminates the evolution of new mammalian genes. Genome Research, 2016, 26, 301-314.	5.5	104

#	Article	IF	Citations
19	Rapid Expansion of Phenylthiocarbamide Non-Tasters among Japanese Macaques. PLoS ONE, 2015, 10, e0132016.	2.5	11
20	Sporadic Premature Aging in a Japanese Monkey: A Primate Model for Progeria. PLoS ONE, 2014, 9, e111867.	2.5	8
21	Frequent Expansions of the Bitter Taste Receptor Gene Repertoire during Evolution of Mammals in the Euarchontoglires Clade. Molecular Biology and Evolution, 2014, 31, 2018-2031.	8.9	59
22	Bidirectional promoters are the major source of gene activation-associated non-coding RNAs in mammals. BMC Genomics, 2014, 15, 35.	2.8	106
23	From Genes to the Mind: Comparative Genomics and Cognitive Science Elucidating Aspects of the Apes That Make Us Human. SpringerBriefs in Biology, 2013, , 25-52.	0.5	0
24	Regional DNA methylation differences between humans and chimpanzees are associated with genetic changes, transcriptional divergence and disease genes. Journal of Human Genetics, 2013, 58, 446-454.	2.3	25
25	Expression of taste signal transduction molecules in the caecum of common marmosets. Biology Letters, 2013, 9, 20130409.	2.3	7
26	Monkeys, Apes, and Humans. SpringerBriefs in Biology, 2013, , .	0.5	3
27	Eco-Geographical Diversification of Bitter Taste Receptor Genes (TAS2Rs) among Subspecies of Chimpanzees (Pan troglodytes). PLoS ONE, 2012, 7, e43277.	2.5	24
28	Diversification of Bitter Taste Receptor Gene Family in Western Chimpanzees. Molecular Biology and Evolution, 2011, 28, 921-931.	8.9	36
29	Identification of non-taster Japanese macaques for a specific bitter taste. Primates, 2010, 51, 285-289.	1.1	34
30	Degeneration of Olfactory Receptor Gene Repertories in Primates: No Direct Link to Full Trichromatic Vision. Molecular Biology and Evolution, 2010, 27, 1192-1200.	8.9	166
31	Biological implication for loss of function at major histocompatibility complex loci. Immunogenetics, 2008, 60, 295-302.	2.4	7
32	Body mass of wild ring-tailed lemurs in Berenty Reserve, Madagascar, with reference to tick infestation: a preliminary analysis. Primates, 2008, 49, 9-15.	1.1	17
33	Similar Numbers but Different Repertoires of Olfactory Receptor Genes in Humans and Chimpanzees. Molecular Biology and Evolution, 2008, 25, 1897-1907.	8.9	96
34	Lineage-Specific Expansions and Contractions of the Bitter Taste Receptor Gene Repertoire in Vertebrates. Molecular Biology and Evolution, 2006, 23, 964-972.	8.9	78
35	Characterization and evolution of major histocompatibility complex class II genes in the aye-aye, Daubentonia madagascariensis. Primates, 2005, 46, 135-139.	1.1	6
36	Lineage-Specific Loss of Function of Bitter Taste Receptor Genes in Humans and Nonhuman PrimatesSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AB198983, AB199308 Genetics, 2005, 170, 313-326.	2.9	151

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#	Article	IF	CITATION
37	Frequent segmental sequence exchanges and rapid gene duplication characterize the MHC class I genes in lemurs. Immunogenetics, 2003, 55, 450-461.	2.4	23
38	Mhc-DRB genes evolution in lemurs. Immunogenetics, 2002, 54, 403-417.	2.4	31
39	Chromosomal localization of 18S rDNA and telomere sequence in the aye-aye, Daubentonia madagascariensis Genes and Genetic Systems, 2000, 75, 299-303.	0.7	10
40	PRINS analysis of the telomeric sequence in seven lemurs. Chromosome Research, 2000, 8, 57-65.	2.2	45