Shin-ichi Yokobori

List of Publications by Year in descending order

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98 papers 3,302 citations

126858 33 h-index 53 g-index

101 all docs

101 docs citations

times ranked

101

3127 citing authors

#	Article	IF	CITATIONS
1	Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein. Nature Communications, 2016, 7, 12808.	5.8	270
2	Transfer RNA editing in land snail mitochondria Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 10432-10435.	3.3	160
3	Experimental evidence for the thermophilicity of ancestral life. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11067-11072.	3.3	153
4	Evolution of Pulmonate Gastropod Mitochondrial Genomes: Comparisons of Gene Organizations of Euhadra, Cepaea and Albinaria and Implications of Unusual tRNA Secondary Structures. Genetics, 1997, 145, 749-758.	1.2	149
5	Long-Term Conservation of Six Duplicated Structural Genes in Cephalopod Mitochondrial Genomes. Molecular Biology and Evolution, 2004, 21, 2034-2046.	3.5	98
6	tRNA editing in metazoans. Nature, 1995, 377, 490-490.	13.7	95
7	Designing Thermostable Proteins: Ancestral Mutants of 3-Isopropylmalate Dehydrogenase Designed by using a Phylogenetic Tree. Journal of Molecular Biology, 2006, 355, 664-674.	2.0	93
8	The Mitochondrial Genome of the Hemichordate Balanoglossus carnosus and the Evolution of Deuterostome Mitochondria. Genetics, 1998, 150, 1115-1123.	1.2	90
9	Polyadenylation creates the discriminator nucleotide of chicken mitochondrial tRNATyr. Journal of Molecular Biology, 1997, 265, 95-99.	2.0	77
10	Complete DNA Sequence of the Mitochondrial Genome of the Ascidian Halocynthia roretzi (Chordata,) Tj ETQq0	0 0 0 rgBT	/Overlock 10 T
11	Genetic Code Variations in Mitochondria: tRNA as a Major Determinant of Genetic Code Plasticity. Journal of Molecular Evolution, 2001, 53, 314-326.	0.8	64
12	The Cephalopod Loligo bleekeri Mitochondrial Genome: Multiplied Noncoding Regions and Transposition of tRNA Genes. Journal of Molecular Evolution, 2002, 54, 486-500.	0.8	64
13	Complete nucleotide sequences of mitochondrial genomes of two solitary entoprocts, Loxocorone allax and Loxosomella aloxiata: Implications for lophotrochozoan phylogeny. Molecular Phylogenetics and Evolution, 2008, 47, 612-628.	1.2	60
14	Introns in protein-coding genes in Archaea. FEBS Letters, 2002, 510, 27-30.	1.3	59
15	Multiple origins of the ascidian-Prochloron symbiosis: Molecular phylogeny of photosymbiotic and non-symbiotic colonial ascidians inferred from 18S rDNA sequences. Molecular Phylogenetics and Evolution, 2006, 40, 8-19.	1.2	59
16	Codons AGA and AGG are read as glycine in ascidian mitochondria. Journal of Molecular Evolution, 1993, 36, 1-8.	0.8	53
17	STARLIFE—An International Campaign to Study the Role of Galactic Cosmic Radiation in Astrobiological Model Systems. Astrobiology, 2017, 17, 101-109.	1.5	53
18	Reconstructed ancestral enzymes suggest long-term cooling of Earth's photic zone since the Archean. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4619-4624.	3.3	53

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19	RNA editing in metazoan mitochondria: staying fit without sex. FEBS Letters, 1997, 409, 320-324.	1.3	52
20	Relationship among coelacanths, lungfishes, and tetrapods: A phylogenetic analysis based on mitochondrial cytochrome oxidase I gene sequences. Journal of Molecular Evolution, 1994, 38, 602-9.	0.8	51
21	Mitochondrial genome structure and evolution in the living fossil vampire squid, Vampyroteuthis infernalis, and extant cephalopods. Molecular Phylogenetics and Evolution, 2007, 44, 898-910.	1.2	51
22	Complete nucleotide sequence of the mitochondrial genome of Doliolum nationalis with implications for evolution of urochordates. Molecular Phylogenetics and Evolution, 2005, 34, 273-283.	1,2	49
23	tRNA Modification and Genetic Code Variations in Animal Mitochondria. Journal of Nucleic Acids, 2011, 2011, 1-12.	0.8	49
24	UV-resistant bacteria isolated from upper troposphere and lower stratosphere. Uchu Seibutsu Kagaku, 2008, 22, 18-25.	1.0	49
25	DNA Damage and Survival Time Course of Deinococcal Cell Pellets During 3 Years of Exposure to Outer Space. Frontiers in Microbiology, 2020, 11, 2050.	1.5	48
26	Investigation of the Interplanetary Transfer of Microbes in the Tanpopo Mission at the Exposed Facility of the International Space Station. Astrobiology, 2016, 16, 363-376.	1.5	47
27	Deinococcus aerius sp. nov., isolated from the high atmosphere. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 1862-1866.	0.8	46
28	Improvement of Bacillus circulans \hat{l}^2 -amylase activity attained using the ancestral mutation method. Protein Engineering, Design and Selection, 2010, 23, 519-528.	1.0	43
29	The Possible Interplanetary Transfer of Microbes: Assessing the Viability of Deinococcus spp. Under the ISS Environmental Conditions for Performing Exposure Experiments of Microbes in the Tanpopo Mission. Origins of Life and Evolution of Biospheres, 2013, 43, 411-428.	0.8	42
30	Deinococcus aetherius sp. nov., isolated from the stratosphere. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 776-779.	0.8	39
31	The substrate specificity of tRNA (m1G37) methyltransferase (TrmD) from Aquifex aeolicus. Genes To Cells, 2006, 11 , $1353-1365$.	0.5	38
32	An extra tRNAGly(U*CU) found in ascidian mitochondria responsible for decoding non-universal codons AGA/AGG as glycine. Nucleic Acids Research, 1999, 27, 2554-2559.	6.5	36
33	Mitochondrial Genome of Ciona savignyi (Urochordata, Ascidiacea, Enterogona): Comparison of Gene Arrangement and tRNA Genes with Halocynthia roretzi Mitochondrial Genome. Journal of Molecular Evolution, 2003, 57, 574-587.	0.8	36
34	Tolerance of Anhydrobiotic Eggs of the Tardigrade <i>Ramazzottius varieornatus</i> to Extreme Environments. Astrobiology, 2012, 12, 283-289.	1.5	35
35	Purification and characterization of pepsinogens from the gastric mucosa of African coelacanth, Latimeria chalumnae, and properties of the major pepsins. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2007, 146, 412-420.	0.7	33
36	Induction profile of HSP70-cognate genes by environmental pollutants in Chironomidae. Environmental Toxicology and Pharmacology, 2009, 28, 294-301.	2.0	33

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37	Robustness of predictions of extremely thermally stable proteins in ancient organisms. Evolution; International Journal of Organic Evolution, 2015, 69, 2954-2962.	1.1	33
38	Archaeal pre-mRNA splicing: A connection to hetero-oligomeric splicing endonuclease. Biochemical and Biophysical Research Communications, 2006, 346, 1024-1032.	1.0	30
39	Evolution of Eukaryotic DNA Polymerases via Interaction Between Cells and Large DNA Viruses. Journal of Molecular Evolution, 2015, 81, 24-33.	0.8	29
40	Gene Contents and Organization of a Mitochondrial DNA Segment of the Squid Loligo bleekeri. Journal of Molecular Evolution, 1999, 48, 692-702.	0.8	28
41	Ancestral amino acid substitution improves the thermal stability of recombinant lignin-peroxidase from white-rot fungi, Phanerochaete chrysosporium strain UAMH 3641. Protein Engineering, Design and Selection, 2015, 28, 221-230.	1.0	28
42	An Actin Homolog of the Archaeon Thermoplasma acidophilum That Retains the Ancient Characteristics of Eukaryotic Actin. Journal of Bacteriology, 2007, 189, 2039-2045.	1.0	27
43	Phylogeny-Based Design of a B-Subunit of DNA Gyrase and Its ATPase Domain Using a Small Set of Homologous Amino Acid Sequences. Journal of Molecular Biology, 2011, 412, 212-225.	2.0	27
44	Thermostability of ancestral mutants of Caldococcus noboribetusisocitrate dehydrogenase. FEMS Microbiology Letters, 2005, 243, 393-398.	0.7	26
45	The phylogenetic status of Paxillosida (Asteroidea) based on complete mitochondrial DNA sequences. Molecular Phylogenetics and Evolution, 2005, 36, 598-605.	1.2	25
46	Extremely Thermophilic Translation System in the Common Ancestor Commonote: Ancestral Mutants of Glycyl-tRNA Synthetase from the Extreme Thermophile Thermus thermophilus. Journal of Molecular Biology, 2007, 369, 1060-1069.	2.0	25
47	Gain and loss of an intron in a protein-coding gene in Archaea: the case of an archaeal RNA pseudouridine synthase gene. BMC Evolutionary Biology, 2009, 9, 198.	3.2	25
48	Potential speciation of morphotypes in the photosymbiotic ascidian Didemnum molle in the Ryukyu Archipelago, Japan. Coral Reefs, 2009, 28, 119-126.	0.9	24
49	A bacterial elongation factor G homologue exclusively functions in ribosome recycling in the spirochaete <i>Borrelia burgdorferi</i> i>Nolecular Microbiology, 2010, 75, 1445-1454.	1.2	24
50	Life without tRNAArg–adenosine deaminase TadA: evolutionary consequences of decoding the four CGN codons as arginine in Mycoplasmas and other Mollicutes. Nucleic Acids Research, 2013, 41, 6531-6543.	6.5	24
51	Establishment of mesophilic-like catalytic properties in a thermophilic enzyme without affecting its thermal stability. Scientific Reports, 2019, 9, 9346.	1.6	24
52	The complete mitochondrial genome of Caprella scaura (Crustacea, Amphipoda, Caprellidea), with emphasis on the unique gene order pattern and duplicated control region. Mitochondrial DNA, 2010, 21, 183-190.	0.6	23
53	Assessing Panspermia Hypothesis by Microorganisms Collected from The High Altitude Atmosphere. Uchu Seibutsu Kagaku, 2009, 23, 151-163.	1.0	21
54	Quest for Ancestors of Eukaryal Cells Based on Phylogenetic Analyses of Aminoacyl-tRNA Synthetases. Journal of Molecular Evolution, 2017, 84, 51-66.	0.8	21

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55	Taurine-containing Uridine Modifications in tRNA Anticodons Are Required to Decipher Non-universal Genetic Codes in Ascidian Mitochondria. Journal of Biological Chemistry, 2011, 286, 35494-35498.	1.6	20
56	Diversification of mitochondrial genome of Daphnia galeata (Cladocera, Crustacea): Comparison with phylogenetic consideration of the complete sequences of clones isolated from five lakes in Japan. Gene, 2017, 611, 38-46.	1.0	20
57	Updated mitochondrial phylogeny of Pteriomorph and Heterodont Bivalvia, including deep-sea chemosymbiotic Bathymodiolus mussels, vesicomyid clams and the thyasirid clam Conchocele cf. bisecta. Marine Genomics, 2017, 31, 43-52.	0.4	19
58	Hydroxylation of a conserved tRNA modification establishes non-universal genetic code in echinoderm mitochondria. Nature Structural and Molecular Biology, 2017, 24, 778-782.	3.6	18
59	Functional reconstitution of a crenarchaeal splicing endonuclease in vitro. Biochemical and Biophysical Research Communications, 2005, 334, 1254-1259.	1.0	16
60	Bacterial survival in response to desiccation and high humidity at above zero and subzero temperatures. Advances in Space Research, 2009, 43, 1285-1290.	1.2	16
61	Repetitive sequences in the lamprey mitochondrial DNA control region and speciation of Lethenteron. Gene, 2010, 465, 45-52.	1.0	16
62	Tanpopo Cosmic Dust Collector: Silica Aerogel Production and Bacterial DNA Contamination Analysis. Uchu Seibutsu Kagaku, 2011, 25, 7-12.	1.0	16
63	TANPOPO: Astrobiology Exposure and Micrometeoroid Capture Experiments. Uchu Seibutsu Kagaku, 2007, 21, 67-75.	1.0	15
64	Ultralow-density double-layer silica aerogel fabrication for the intact capture of cosmic dust in low-Earth orbits. Journal of Sol-Gel Science and Technology, 2016, 77, 325-334.	1.1	14
65	Birth of Archaeal Cells: Molecular Phylogenetic Analyses of G1P Dehydrogenase, G3P Dehydrogenases, and Glycerol Kinase Suggest Derived Features of Archaeal Membranes Having G1P Polar Lipids. Archaea, 2016, 2016, 1-16.	2.3	13
66	Japan Astrobiology Mars Project (JAMP): Search for Microbes on The Mars Surface with Special Interest in Methane-Oxidizing Bacteria. Uchu Seibutsu Kagaku, 2010, 24, 67-82.	1.0	12
67	Structural analysis of the plasmid pTA1 isolated from the thermoacidophilic archaeon Thermoplasma acidophilum. Extremophiles, 2006, 10, 327-335.	0.9	11
68	Tanpopo: Astrobiology Exposure and Micrometeoroid Capture Experiments. Transactions of the Japan Society for Aeronautical and Space Sciences Space Technology Japan, 2009, 7, Tk_49-Tk_55.	0.2	11
69	Tanpopo: Astrobiology Exposure and Micrometeoroid Capture Experiments— Proposed Experiments at the Exposure Facility of ISS-JEM. Transactions of the Japan Society for Aeronautical and Space Sciences Aerospace Technology Japan, 2014, 12, Tk_49-Tk_55.	0.1	11
70	Male death resulting from hybridization between subspecies of the gypsy moth, Lymantria dispar. Heredity, 2011, 106, 603-613.	1.2	10
71	Epistasis effects of multiple ancestral-consensus amino acid substitutions on the thermal stability of glycerol kinase from Cellulomonas sp. NT3060. Journal of Bioscience and Bioengineering, 2016, 121, 497-502.	1.1	10
72	Ascidian Mitochondrial tRNAMet Possessing Unique Structural Characteristics. Nucleosides, Nucleotides and Nucleic Acids, 1998, 17, 531-539.	0.4	10

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73	Design of a Silica-aerogel-based Cosmic Dust Collector for the Tanpopo Mission Aboard the International Space Station. Transactions of the Japan Society for Aeronautical and Space Sciences Aerospace Technology Japan, 2014, 12, Pk_29-Pk_34.	0.1	9
74	STXM-XANES analyses of Murchison meteorite samples captured by aerogel after hypervelocity impacts: A potential implication of organic matter degradation for micrometeoroid collection experiments. Geochemical Journal, 2019, 53, 53-67.	0.5	9
75	Decoding Mechanism of Non-universal Genetic Codes in Loligo bleekeri Mitochondria. Journal of Biological Chemistry, 2013, 288, 7645-7652.	1.6	8
76	Fluorescence imaging of microbe-containing particles shot from a two-stage Light-gas gun into an aerogel. Origins of Life and Evolution of Biospheres, 2014, 44, 43-60.	0.8	8
77	Evolution of Superoxide Dismutases and Catalases in Cyanobacteria: Occurrence of the Antioxidant Enzyme Genes before the Rise of Atmospheric Oxygen. Journal of Molecular Evolution, 2021, 89, 527-543.	0.8	8
78	Scientific Targets of Tanpopo: Astrobiology Exposure and Micrometeoroid Capture Experiments at the Japanese Experiment Module Exposed Facility of the International Space Station. Astrobiology, 2021, 21, 1451-1460.	1.5	7
79	Space Exposure of Amino Acids and Their Precursors during the Tanpopo Mission. Astrobiology, 2021, 21, 1479-1493.	1.5	6
80	How the Early Genetic Code Was Established?: Inference from the Analysis of Extant Animal Mitochondrial Decoding Systems. , 2014, , 25-40.		4
81	Planktonic adaptive evolution to the sea surface temperature in the Neoproterozoic inferred from ancestral NDK of marine cyanobacteria. Earth and Planetary Science Letters, 2019, 522, 98-106.	1.8	4
82	Mutation Analysis of the <i>rpoB </i> Gene in the Radiation-Resistant Bacterium <i>Deinococcus radiodurans </i> R1 Exposed to Space during the Tanpopo Experiment at the International Space Station. Astrobiology, 2021, 21, 1494-1504.	1.5	4
83	Space Exposure of Amino Acids and Their Precursors in the Tanpopo Mission Using the International Space Station. Transactions of the Japan Society for Aeronautical and Space Sciences Aerospace Technology Japan, 2014, 12, Pp_1-Pp_6.	0.1	3
84	Comparative Genomics of Thermophilic Bacteria and Archaea. , 2013, , 331-349.		2
85	Amino Acid Specificity of Ancestral Aminoacyl-tRNA Synthetase Prior to the Last Universal Common Ancestor Commonote commonote. Journal of Molecular Evolution, 2022, 90, 73-94.	0.8	2
86	Arabidopsis thaliana mitochondrial EF-G1 functions in two different translation steps. Journal of Biochemistry, 2014, 155, 107-114.	0.9	1
87	Development of mechanical space thermometer for the Tanpopo mission. Transactions of the JSME (in) Tj ETQq1	1	4 ₁ rgBT /Ove
88	Draft Genome Sequence of the Radioresistant Bacterium Deinococcus aerius TR0125, Isolated from the High Atmosphere above Japan. Genome Announcements, $2018, 6, .$	0.8	1
89	Characterization and phylogenetic position of two sympatric sister species of toxic flatworms Planocera multitentaculata and Planocera reticulata (Platyhelminthes: Acotylea). Mitochondrial DNA Part B: Resources, 2020, 5, 2352-2354.	0.2	1
90	Selection of Lichens Resistant to the Cosmic Environment ^ ^mdash;Thermal Cycle Treatment, UV Irradiation and Heavy Ion Beam Irradiation^ ^mdash;. Uchu Seibutsu Kagaku, 2013, 27, 9-18.	1.0	1

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91	Functional reconstitution of an archaeal splicing endonuclease in vitro. Nucleic Acids Symposium Series, 2005, 49, 103-104.	0.3	0
92	3P276 Hyperthermophilic translation system in the last common ancestor : ancestral mutants of Thermus thermophilus glycyl-tRNA synthetase(Proteins- protein engineering, and evolutionary) Tj ETQq0 0 0 rgBT	/ O værlock	100 Tf 50 691
93	Enzymatic and crystallographic characterization of archaeal tRNA splicing endonuclease. , 2009, , .		O
94	1P075 Elucidation of the protein sequence-stability relationship by comparing designed ancestral proteins with reduced neutral mutations(Protein:Property,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Ov	edaack 10	T 6 50 617 To
95	Eukaryotes Appearing. , 2019, , 105-121.		O
96	Mitogenome analysis of dwarf pufferfish (Carinotetraodon travancoricus) endemic to southwest India and its implications in the phylogeny of Tetraodontidae. Journal of Genetics, 2019, 98, 1.	0.4	0
97	1P144 Hyperthermophilic translation system in the common ancestor : Analysis of ancestral mutants of GlyRS of the Thermus thermophilus(4. Protein engineering, Poster Session, Abstract, Meeting) Tj ETQq1 1 0.7843	3 1:4: 0gBT /(Overlock 10
98	Temperature Measurement of Space Environment with Tanpopo Space Thermometer. The Proceedings of Mechanical Engineering Congress Japan, 2019, 2019, J19101.	0.0	0