

# Takashi Gojobori

## List of Publications by Year in descending order

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312  
papers

18,200  
citations

17440

63  
h-index

18130

120  
g-index

328  
all docs

328  
docs citations

328  
times ranked

21294  
citing authors

#	ARTICLE	IF	CITATIONS
1	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	27.8	743
2	The future of biocuration. Nature, 2008, 455, 47-50.	27.8	648
3	Metabolic efficiency and amino acid composition in the proteomes of <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3695-3700.	7.1	580
4	The genome of <i>Chenopodium quinoa</i> . Nature, 2017, 542, 307-312.	27.8	569
5	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	12.6	557
6	The genome sequence and structure of rice chromosome 1. Nature, 2002, 420, 312-316.	27.8	519
7	Pseudogenes as a paradigm of neutral evolution. Nature, 1981, 292, 237-239.	27.8	487
8	Biased biological functions of horizontally transferred genes in prokaryotic genomes. Nature Genetics, 2004, 36, 760-766.	21.4	459
9	Patterns of nucleotide substitution in pseudogenes and functional genes. Journal of Molecular Evolution, 1982, 18, 360-369.	1.8	438
10	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
11	Endogenous non-retroviral RNA virus elements in mammalian genomes. Nature, 2010, 463, 84-87.	27.8	404
12	Leptin and Obesity: Role and Clinical Implication. Frontiers in Endocrinology, 2021, 12, 585887.	3.5	363
13	A comparison of the molecular clock of hepatitis C virus in the United States and Japan predicts that hepatocellular carcinoma incidence in the United States will increase over the next two decades. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15584-15589.	7.1	307
14	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
15	Estimation of average number of nucleotide substitutions when the rate of substitution varies with nucleotide. Journal of Molecular Evolution, 1982, 18, 414-422.	1.8	282
16	FGFR-related gene <i>nou-darake</i> restricts brain tissues to the head region of planarians. Nature, 2002, 419, 620-624.	27.8	244
17	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . Genome Research, 2007, 17, 175-183.	5.5	218
18	Comparative Complete Genome Sequence Analysis of the Amino Acid Replacements Responsible for the Thermostability of <i>Corynebacterium efficiens</i> . Genome Research, 2003, 13, 1572-1579.	5.5	194

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19	A Large Variation in the Rates of Synonymous Substitution for RNA Viruses and Its Relationship to a Diversity of Viral Infection and Transmission Modes. <i>Molecular Biology and Evolution</i> , 2004, 21, 1074-1080.	8.9	192
20	Diversity of preferred nucleotide sequences around the translation initiation codon in eukaryote genomes. <i>Nucleic Acids Research</i> , 2007, 36, 861-871.	14.5	181
21	Long-range neural and gap junction protein-mediated cues control polarity during planarian regeneration. <i>Developmental Biology</i> , 2010, 339, 188-199.	2.0	176
22	Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7666-7671.	7.1	172
23	Sequence of a novel simian immunodeficiency virus from a wild-caught African mandrill. <i>Nature</i> , 1989, 341, 539-541.	27.8	166
24	The Origin and Evolution of Porcine Reproductive and Respiratory Syndrome Viruses. <i>Molecular Biology and Evolution</i> , 2005, 22, 1024-1031.	8.9	151
25	The First Symbiont-Free Genome Sequence of Marine Red Alga, <i>Susabi-nori</i> ( <i>Pyropia yezoensis</i> ). <i>PLoS ONE</i> , 2013, 8, e57122.	2.5	150
26	Constrained evolution with respect to gene overlap of hepatitis B virus. <i>Journal of Molecular Evolution</i> , 1997, 44, S83-S90.	1.8	148
27	CIBEX: Center for Information Biology gene EXpression database. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1079-1082.	0.2	138
28	Dynamic evolution of translation initiation mechanisms in prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6382-6387.	7.1	137
29	Evolutionary aspects of gobioid fishes based upon a phylogenetic analysis of mitochondrial cytochrome b genes. <i>Gene</i> , 2000, 259, 5-15.	2.2	124
30	Transcriptional Interferences in cis Natural Antisense Transcripts of Humans and Mice. <i>Genetics</i> , 2007, 176, 1299-1306.	2.9	124
31	Whole genome association study of rheumatoid arthritis using 27,039 microsatellites. <i>Human Molecular Genetics</i> , 2005, 14, 2305-2321.	2.9	122
32	Genome plasticity as a paradigm of eubacteria evolution. <i>Journal of Molecular Evolution</i> , 1997, 44, S57-S64.	1.8	120
33	Dissecting planarian central nervous system regeneration by the expression of neural-specific genes. <i>Development Growth and Differentiation</i> , 2002, 44, 135-146.	1.5	120
34	Evolution of complex structures: minicollagens shape the cnidarian nematocyst. <i>Trends in Genetics</i> , 2008, 24, 431-438.	6.7	117
35	SARS-CoV-2 infections and COVID-19 mortalities strongly correlate with ACE1 I/D genotype. <i>Gene</i> , 2020, 758, 144944.	2.2	116
36	The expression of neural-specific genes reveals the structural and molecular complexity of the planarian central nervous system. <i>Mechanisms of Development</i> , 2002, 116, 199-204.	1.7	113

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37	Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic divergence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7708-7713.	7.1	110
38	Theoretical Bases for Karyotype Evolution. 1. The Minimum-Interaction Hypothesis. <i>American Naturalist</i> , 1986, 128, 900-920.	2.1	106
39	Evolutionary changes of multiple visual pigment genes in the complete genome of Pacific bluefin tuna. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11061-11066.	7.1	106
40	Mitochondrial DNA polymorphism in Japanese. <i>Human Genetics</i> , 1984, 68, 324-332.	3.8	101
41	Rapid Evolution of Major Histocompatibility Complex Class I Genes in Primates Generates New Disease Alleles in Humans via Hitchhiking Diversity. <i>Genetics</i> , 2006, 173, 1555-1570.	2.9	100
42	SNP Profile within the Human Major Histocompatibility Complex Reveals an Extreme and Interrupted Level of Nucleotide Diversity. <i>Genome Research</i> , 2000, 10, 1579-1586.	5.5	99
43	Reevaluation of Amino Acid Variability of the Human Immunodeficiency Virus Type 1 gp120 Envelope Glycoprotein and Prediction of New Discontinuous Epitopes. <i>Journal of Virology</i> , 2000, 74, 4335-4350.	3.4	98
44	Challenges and Opportunities of Airborne Metagenomics. <i>Genome Biology and Evolution</i> , 2015, 7, 1216-1226.	2.5	97
45	Evolutionary relationship of hepatitis C, pesti-, flavi-, plantviruses, and newly discovered GB hepatitis agents. <i>FEBS Letters</i> , 1996, 378, 232-234.	2.8	93
46	Rate of Evolution in Brain-Expressed Genes in Humans and Other Primates. <i>PLoS Biology</i> , 2006, 5, e13.	5.6	93
47	Detection of apoptosis during planarian regeneration by the expression of apoptosis-related genes and TUNEL assay. <i>Gene</i> , 2004, 333, 15-25.	2.2	92
48	DDBJ launches a new archive database with analytical tools for next-generation sequence data. <i>Nucleic Acids Research</i> , 2010, 38, D33-D38.	14.5	86
49	Recombinational hotspot specific to female meiosis in the mouse major histocompatibility complex. <i>Immunogenetics</i> , 1990, 31, 79-88.	2.4	83
50	The evolutionary emergence of cell type-specific genes inferred from the gene expression analysis of <i>Hydra</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14735-14740.	7.1	83
51	Intragenic recombinations in rotaviruses. <i>FEBS Letters</i> , 1998, 427, 183-187.	2.8	81
52	The Temporal Sequence of the Mammalian Neocortical Neurogenetic Program Drives Mediolateral Pattern in the Chick Pallium. <i>Developmental Cell</i> , 2012, 22, 863-870.	7.0	81
53	Reduction of synonymous substitutions in the core protein gene of hepatitis C virus. <i>Journal of Molecular Evolution</i> , 1994, 38, 50-6.	1.8	78
54	Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye Between Octopus and Human. <i>Genome Research</i> , 2004, 14, 1555-1561.	5.5	78

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55	Evolution of gap junctions: the missing link?. <i>Current Biology</i> , 2004, 14, R879-R880.	3.9	76
56	Evolution of Vitamin B6 (Pyridoxine) Metabolism by Gain and Loss of Genes. <i>Molecular Biology and Evolution</i> , 2005, 22, 243-250.	8.9	76
57	Degeneration after sexual differentiation in hydra and its relevance to the evolution of aging. <i>Gene</i> , 2006, 385, 64-70.	2.2	76
58	An evolutionary origin and selection process of goldfish. <i>Gene</i> , 2009, 430, 5-11.	2.2	75
59	Eye-like ocelloids are built from different endosymbiotically acquired components. <i>Nature</i> , 2015, 523, 204-207.	27.8	74
60	Search for the Evolutionary Origin of a Brain: Planarian Brain Characterized by Microarray. <i>Molecular Biology and Evolution</i> , 2003, 20, 784-791.	8.9	73
61	Nematogalactin, a nematocyst protein with GlyXY and galectin domains, demonstrates nematocyte-specific alternative splicing in <i>Hydra</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18539-18544.	7.1	69
62	Machine learning and deep learning methods that use omics data for metastasis prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5008-5018.	4.1	69
63	Neural Network in Planarian Revealed by an Antibody against Planarian Synaptotagmin Homologue. <i>Biochemical and Biophysical Research Communications</i> , 1999, 260, 426-432.	2.1	68
64	Infectious Endogenous Retroviruses in Cats and Emergence of Recombinant Viruses. <i>Journal of Virology</i> , 2012, 86, 8634-8644.	3.4	68
65	The genome stability in <i>Corynebacterium</i> species due to lack of the recombinational repair system. <i>Gene</i> , 2003, 317, 149-155.	2.2	66
66	Low Concentrations of Vitamin C Reduce the Synthesis of Extracellular Polymers and Destabilize Bacterial Biofilms. <i>Frontiers in Microbiology</i> , 2017, 8, 2599.	3.5	66
67	Where is the origin of the Japanese gamecocks?. <i>Gene</i> , 2003, 317, 195-202.	2.2	65
68	Phylogenetic and virulence analysis of tick-borne encephalitis viruses from Japan and far-eastern Russia. <i>Journal of General Virology</i> , 1999, 80, 3127-3135.	2.9	65
69	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. <i>MBio</i> , 2012, 3, e00204-12.	4.1	64
70	Chinese spring wheat ( <i>Triticum aestivum</i> L.) chloroplast genome: Complete sequence and contig clones. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 243-253.	1.8	62
71	DTiGEMS+: drug target interaction prediction using graph embedding, graph mining, and similarity-based techniques. <i>Journal of Cheminformatics</i> , 2020, 12, 44.	6.1	62
72	Induction of a noggin-Like Gene by Ectopic DV Interaction during Planarian Regeneration. <i>Developmental Biology</i> , 2002, 250, 59-70.	2.0	61

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73	Molecular evolution and phylogeny of the human AIDS viruses LAV, HTLV-III, and ARV. <i>Journal of Molecular Evolution</i> , 1987, 24, 330-336.	1.8	60
74	Alternative splicing in human transcriptome: Functional and structural influence on proteins. <i>Gene</i> , 2006, 380, 63-71.	2.2	60
75	Evolutionary significance of intra-genome duplications on human chromosomes. <i>Gene</i> , 1997, 205, 19-27.	2.2	59
76	Strong Positive Selection and Recombination Drive the Antigenic Variation of the Pile Protein of the Human Pathogen <i>Neisseria meningitidis</i> . <i>Genetics</i> , 2004, 166, 25-32.	2.9	59
77	Comparative study of flux redistribution of metabolic pathway in glutamate production by two coryneform bacteria. <i>Metabolic Engineering</i> , 2005, 7, 59-69.	7.0	59
78	The Emerging Facets of Non-Cancerous Warburg Effect. <i>Frontiers in Endocrinology</i> , 2017, 8, 279.	3.5	59
79	CODON SUBSTITUTION IN EVOLUTION AND THE "SATURATION" OF SYNONYMOUS CHANGES. <i>Genetics</i> , 1983, 105, 1011-1027.	2.9	59
80	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
81	CovMT: an interactive SARS-CoV-2 mutation tracker, with a focus on critical variants. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 602.	9.1	57
82	Comparative genomics of bidirectional gene pairs and its implications for the evolution of a transcriptional regulation system. <i>Gene</i> , 2005, 353, 169-176.	2.2	56
83	Multiple Plastids Collected by the Dinoflagellate <i>Dinophysis mitra</i> through Kleptoplastidy. <i>Applied and Environmental Microbiology</i> , 2012, 78, 813-821.	3.1	56
84	Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish <i>Amphiprion percula</i> . <i>Molecular Ecology Resources</i> , 2019, 19, 570-585.	4.8	55
85	An alternative, zeaxanthin epoxidase-independent abscisic acid biosynthetic pathway in plants. <i>Molecular Plant</i> , 2022, 15, 151-166.	8.3	55
86	Molecular evolutionary analyses implicate injection treatment for schistosomiasis in the initial hepatitis C epidemics in Japan. <i>Journal of Hepatology</i> , 2005, 42, 47-53.	3.7	53
87	<i>Brachyury</i> downstream gene sets in a chordate, <i>Ciona intestinalis</i> : integrating notochord specification, morphogenesis and chordate evolution. <i>Evolution &amp; Development</i> , 2008, 10, 37-51.	2.0	53
88	The mitochondrial genome of the pufferfish, <i>Fugu rubripes</i> , and ordinal teleostean relationships. <i>Gene</i> , 2002, 295, 163-172.	2.2	52
89	Hepatitis C virus types 7, 8 and 9 should be classified as type 6 subtypes. <i>Journal of Hepatology</i> , 1996, 24, 622-624.	3.7	51
90	Marine metagenomics as a source for bioprospecting. <i>Marine Genomics</i> , 2015, 24, 21-30.	1.1	51

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91	Genetic polymorphism of the swine major histocompatibility complex (SLA) class II genes, SLA-1, -2 and -3. <i>Immunogenetics</i> , 2003, 55, 583-593.	2.4	48
92	Evolution of Bioluminescence in Marine Planktonic Copepods. <i>Molecular Biology and Evolution</i> , 2012, 29, 1669-1681.	8.9	48
93	Origins of Japanese flowering cherry ( <i>Prunus</i> subgenus <i>Cerasus</i> ) cultivars revealed using nuclear SSR markers. <i>Tree Genetics and Genomes</i> , 2014, 10, 477-487.	1.6	48
94	Molecular evolution of hemagglutinin genes of H1N1 swine and human influenza A viruses. <i>Journal of Molecular Evolution</i> , 1991, 32, 16-23.	1.8	47
95	Large-scale identification and characterization of alternative splicing variants of human gene transcripts using 56 419 completely sequenced and manually annotated full-length cDNAs. <i>Nucleic Acids Research</i> , 2006, 34, 3917-3928.	14.5	46
96	Gene organization of the quail major histocompatibility complex ( MhcCoja ) class I gene region. <i>Immunogenetics</i> , 1999, 49, 384-394.	2.4	45
97	Cloning and functional analysis of ascidian Mitf in vivo: insights into the origin of vertebrate pigment cells. <i>Mechanisms of Development</i> , 2003, 120, 1489-1504.	1.7	45
98	Frequent emergence and functional resurrection of processed pseudogenes in the human and mouse genomes. <i>Gene</i> , 2007, 389, 196-203.	2.2	44
99	Global Ramifications of Dust and Sandstorm Microbiota. <i>Genome Biology and Evolution</i> , 2018, 10, 1970-1987.	2.5	44
100	Atherosclerosis Linked to Aberrant Amino Acid Metabolism and Immunosuppressive Amino Acid Catabolizing Enzymes. <i>Frontiers in Immunology</i> , 2020, 11, 551758.	4.8	44
101	Molecular evolution of human T-cell leukemia virus. <i>Journal of Molecular Evolution</i> , 1990, 31, 493-499.	1.8	43
102	Classification of hepatitis C virus into major types and subtypes based on molecular evolutionary analysis. <i>Virus Research</i> , 1995, 36, 201-214.	2.2	43
103	The DNA Data Bank of Japan launches a new resource, the DDBJ Omics Archive of functional genomics experiments. <i>Nucleic Acids Research</i> , 2012, 40, D38-D42.	14.5	43
104	Innexin gap junctions in nerve cells coordinate spontaneous contractile behavior in Hydra polyps. <i>Scientific Reports</i> , 2014, 4, 3573.	3.3	43
105	Comparative genomic analysis of translation initiation mechanisms for genes lacking the Shine-Dalgarno sequence in prokaryotes. <i>Nucleic Acids Research</i> , 2017, 45, 3922-3931.	14.5	43
106	Early Detection of G + C Differences in Bacterial Species Inferred from the Comparative Analysis of the Two Completely Sequenced <i>Helicobacter pylori</i> Strains. <i>Journal of Molecular Evolution</i> , 2001, 53, 465-468.	1.8	41
107	Marine Metagenome as A Resource for Novel Enzymes. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 290-295.	6.9	41
108	Functional Pangenome Analysis Shows Key Features of E Protein Are Preserved in SARS and SARS-CoV-2. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 405.	3.9	40

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109	<i>In silico</i> chromosome staining: Reconstruction of Giemsa bands from the whole human genome sequence. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 797-802.	7.1	39
110	Evolution of Pacific Ocean and the Sea of Japan populations of the gobiid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> , based on molecular and morphological analyses. Gene, 2008, 427, 7-18.	2.2	38
111	Ascidian tyrosinase gene: Its unique structure and expression in the developing brain. , 1997, 208, 363-374.		37
112	Highly conserved upstream sequences for transcription factor genes and implications for the regulatory network. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17156-17161.	7.1	37
113	Tissue- and Stage-Dependent Dosage Compensation on the Neo-X Chromosome in <i>Drosophila pseudoobscura</i> . Molecular Biology and Evolution, 2014, 31, 614-624.	8.9	36
114	Metagenomic studies of the Red Sea. Gene, 2016, 576, 717-723.	2.2	36
115	Comparative analysis of the base biases at the gene terminal portions in seven eukaryote genomes. Nucleic Acids Research, 2003, 31, 5195-5201.	14.5	35
116	The evolutionary origin of long-crowing chicken: its evolutionary relationship with fighting cocks disclosed by the mtDNA sequence analysis. Gene, 2004, 333, 91-99.	2.2	35
117	Distribution and Effects of Nonsense Polymorphisms in Human Genes. PLoS ONE, 2008, 3, e3393.	2.5	35
118	A Non-sulfated Chondroitin Stabilizes Membrane Tubulation in Cnidarian Organelles. Journal of Biological Chemistry, 2010, 285, 25613-25623.	3.4	35
119	Relationships between serotypes and genotypes of hepatitis B virus: genetic classification of HBV by use of surface genes. Virus Research, 1995, 39, 25-34.	2.2	34
120	cimp1, A Novel Astacin Family Metalloproteinase Gene from East African Cichlids, Is Differentially Expressed Between Species During Growth. Molecular Biology and Evolution, 2005, 22, 1649-1660.	8.9	34
121	The evolutionary relationship between gene duplication and alternative splicing. Gene, 2008, 427, 19-31.	2.2	34
122	Evolutionary origin of a Kunitz-type trypsin inhibitor domain inserted in the amyloid $\beta$ precursor protein of Alzheimer's disease. Journal of Molecular Evolution, 1992, 34, 536-543.	1.8	33
123	Splice2Deep: An ensemble of deep convolutional neural networks for improved splice site prediction in genomic DNA. Gene: X, 2020, 763, 100035.	2.3	33
124	Mutation pattern of human immunodeficiency virus genes. Journal of Molecular Evolution, 1991, 32, 360-363.	1.8	32
125	The Evolutionary Rate of a Protein Is Influenced by Features of the Interacting Partners. Molecular Biology and Evolution, 2006, 23, 784-789.	8.9	32
126	Midline governs axon pathfinding by coordinating expression of two major guidance systems. Genes and Development, 2009, 23, 1165-1170.	5.9	32



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127	African origin of GB virus C/hepatitis G virus1. FEBS Letters, 1998, 423, 143-148.	2.8	31
128	Function and Evolutionary Origin of Unicellular Camera-Type Eye Structure. PLoS ONE, 2015, 10, e0118415.	2.5	31
129	Different evolutionary histories of kringle and protease domains in serine proteases: A typical example of domain evolution. Journal of Molecular Evolution, 1995, 40, 331-336.	1.8	30
130	Dynamic Evolution of Endogenous Retrovirus-Derived Genes Expressed in Bovine Conceptuses during the Period of Placentation. Genome Biology and Evolution, 2013, 5, 296-306.	2.5	30
131	Comparison of Gene Expression Profile of Epiretinal Membranes Obtained from Eyes with Proliferative Vitreoretinopathy to That of Secondary Epiretinal Membranes. PLoS ONE, 2013, 8, e54191.	2.5	30
132	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. Nucleic Acids Research, 2017, 45, gkw973.	14.5	30
133	Differential sensitivity of hepatitis C virus quasispecies to interferon- $\lambda$ therapy. Journal of Hepatology, 1994, 21, 884-886.	3.7	29
134	Structure and developmental expression of the ascidian TRP gene: Insights into the evolution of pigment cell-specific gene expression. Developmental Dynamics, 1999, 215, 225-237.	1.8	29
135	Microarray analysis of embryonic retinoic acid target genes in the ascidian <i>Ciona intestinalis</i> . Development Growth and Differentiation, 2003, 45, 249-259.	1.5	29
136	Regionalized nervous system in Hydra and the mechanism of its development. Gene Expression Patterns, 2019, 31, 42-59.	0.8	29
137	Molecular evolutionary rates of oncogenes. Journal of Molecular Evolution, 1987, 26, 148-156.	1.8	28
138	Evolution of pathogenic viruses with special reference to the rates of synonymous and nonsynonymous substitutions.. Japanese Journal of Genetics, 1994, 69, 481-488.	1.0	28
139	Gene Cluster Analysis Method Identifies Horizontally Transferred Genes with High Reliability and Indicates that They Provide the Main Mechanism of Operon Gain in 8 Species of $\beta$ -Proteobacteria. Molecular Biology and Evolution, 2007, 24, 805-813.	8.9	28
140	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. Functional and Integrative Genomics, 2010, 10, 307-319.	3.5	28
141	Genome and Transcriptome Analysis of the Food-Yeast <i>Candida utilis</i> . PLoS ONE, 2012, 7, e37226.	2.5	28
142	Angiotensin-Converting Enzyme (ACE) 1 Gene Polymorphism and Phenotypic Expression of COVID-19 Symptoms. Genes, 2021, 12, 1572.	2.4	28
143	NRSub: a non-redundant data base for the <i>Bacillus subtilis</i> genome. Nucleic Acids Research, 1994, 22, 5525-5529.	14.5	27
144	Cilium Evolution: Identification of a Novel Protein, Nematocilin, in the Mechanosensory Cilium of Hydra Nematocytes. Molecular Biology and Evolution, 2008, 25, 2009-2017.	8.9	27

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145	Low conservation and species-specific evolution of alternative splicing in humans and mice: comparative genomics analysis using well-annotated full-length cDNAs. <i>Nucleic Acids Research</i> , 2008, 36, 6386-6395.	14.5	27
146	DTi2Vec: Drug-target interaction prediction using network embedding and ensemble learning. <i>Journal of Cheminformatics</i> , 2021, 13, 71.	6.1	27
147	Evolutionary Process of Amino Acid Biosynthesis in <i>Corynebacterium</i> at the Whole Genome Level. <i>Molecular Biology and Evolution</i> , 2004, 21, 1683-1691.	8.9	26
148	Slow Evolutionary Rate of GB Virus C/Hepatitis G Virus. <i>Journal of Molecular Evolution</i> , 1999, 48, 383-389.	1.8	25
149	Multiple class I loci expressed by the quail Mhc. <i>Immunogenetics</i> , 1999, 49, 456-460.	2.4	25
150	Japanese domesticated chickens have been derived from Shamo traditional fighting cocks. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 16-21.	2.7	25
151	The X Files: The Mystery of X Chromosome Instability in Alzheimer's Disease. <i>Frontiers in Genetics</i> , 2019, 10, 1368.	2.3	25
152	Patterns of nucleotide substitutions inferred from the phylogenies of the class I major histocompatibility complex genes. <i>Journal of Molecular Evolution</i> , 1992, 35, 196-204.	1.8	24
153	Genetic Relationships among Japanese, Northern Han, Hui, Uygur, Kazakh, Greek, Saudi Arabian, and Italian Populations Based on Allelic Frequencies at Four VNTR (D1S80, D4S43, COL2A1, D17S5) and One STR (ACTBP2) Loci. <i>Human Heredity</i> , 1998, 48, 126-137.	0.8	24
154	Molecular hierarchy in neurons differentiated from mouse ES cells containing a single human chromosome 21. <i>Biochemical and Biophysical Research Communications</i> , 2004, 314, 335-350.	2.1	24
155	Genetic Stability of Human T Lymphotropic Virus Type I despite Antiviral Pressures by CTLs. <i>Journal of Immunology</i> , 2007, 178, 5966-5972.	0.8	24
156	Different Endosymbiotic Interactions in Two Hydra Species Reflect the Evolutionary History of Endosymbiosis. <i>Genome Biology and Evolution</i> , 2016, 8, 2155-2163.	2.5	24
157	Functional interrogation of Plasmodium genus metabolism identifies species- and stage-specific differences in nutrient essentiality and drug targeting. <i>PLoS Computational Biology</i> , 2018, 14, e1005895.	3.2	24
158	Monitoring of the toxic dinoflagellate <i>Alexandrium catenella</i> in Osaka Bay, Japan using a massively parallel sequencing (MPS)-based technique. <i>Harmful Algae</i> , 2019, 89, 101660.	4.8	24
159	magp4 gene may contribute to the diversification of cichlid morphs and their speciation. <i>Gene</i> , 2006, 373, 126-133.	2.2	23
160	Differential evolutionary rates of duplicated genes in protein interaction network. <i>Gene</i> , 2006, 385, 57-63.	2.2	23
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