

Takashi Gojobori

List of Publications by Year in descending order

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Version: 2024-02-01

312
papers

18,200
citations

17405

63
h-index

18075

120
g-index

328
all docs

328
docs citations

328
times ranked

21294
citing authors

#	ARTICLE	IF	CITATIONS
1	An alternative, zeaxanthin epoxidase-independent abscisic acid biosynthetic pathway in plants. <i>Molecular Plant</i> , 2022, 15, 151-166.	3.9	55
2	Seawater desalination based drinking water: Microbial characterization during distribution with and without residual chlorine. <i>Water Research</i> , 2022, 210, 117975.	5.3	13
3	An open chat with Takashi Gojobori. <i>FEBS Open Bio</i> , 2022, 12, 338-339.	1.0	0
4	From shallow to deep: some lessons learned from application of machine learning for recognition of functional genomic elements in human genome. <i>Human Genomics</i> , 2022, 16, 7.	1.4	3
5	Affinity2Vec: drug-target binding affinity prediction through representation learning, graph mining, and machine learning. <i>Scientific Reports</i> , 2022, 12, 4751.	1.6	23
6	A cautionary signal from the Red Sea on the impact of increased dust activity on marine microbiota. <i>BMC Genomics</i> , 2022, 23, 277.	1.2	8
7	DeepSVP: integration of genotype and phenotype for structural variant prioritization using deep learning. <i>Bioinformatics</i> , 2022, 38, 1677-1684.	1.8	7
8	Role of C-Reactive Protein in Diabetic Inflammation. <i>Mediators of Inflammation</i> , 2022, 2022, 1-15.	1.4	22
9	Identification of lipolytic enzymes using high-throughput single-cell screening and sorting of a metagenomic library. <i>New Biotechnology</i> , 2022, 70, 102-108.	2.4	6
10	Population structure of indigenous inhabitants of Arabia. <i>PLoS Genetics</i> , 2021, 17, e1009210.	1.5	14
11	MetaCancer: A deep learning-based pan-cancer metastasis prediction model developed using multi-omics data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4404-4411.	1.9	19
12	IBDDDB: a manually curated and text-mining-enhanced database of genes involved in inflammatory bowel disease. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	8
13	Characterization of microbiologically influenced corrosion by comprehensive metagenomic analysis of an inland oil field. <i>Gene</i> , 2021, 774, 145425.	1.0	10
14	Biomedical computing in the Arab world. <i>Communications of the ACM</i> , 2021, 64, 108-113.	3.3	0
15	Significant variants of type 2 diabetes in the Arabian Region through an Integration of exome databases. <i>PLoS ONE</i> , 2021, 16, e0249226.	1.1	0
16	Rise and fall of the global conversation and shifting sentiments during the COVID-19 pandemic. <i>Humanities and Social Sciences Communications</i> , 2021, 8, .	1.3	12
17	Leptin and Obesity: Role and Clinical Implication. <i>Frontiers in Endocrinology</i> , 2021, 12, 585887.	1.5	363
18	A single neuron subset governs a single coactive neuron circuit in <i>Hydra vulgaris</i> , representing a possible ancestral feature of neural evolution. <i>Scientific Reports</i> , 2021, 11, 10828.	1.6	5

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19	Transmission dynamics of SARS-CoV-2 on the Diamond Princess uncovered using viral genome sequence analysis. <i>Gene</i> , 2021, 779, 145496.	1.0	7
20	CovMT: an interactive SARS-CoV-2 mutation tracker, with a focus on critical variants. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 602.	4.6	57
21	Evolution of memory system-related genes. <i>FEBS Open Bio</i> , 2021, 11, 3201-3210.	1.0	4
22	Development of a time-series shotgun metagenomics database for monitoring microbial communities at the Pacific coast of Japan. <i>Scientific Reports</i> , 2021, 11, 12222.	1.6	6
23	DES-Tcell is a knowledgebase for exploring immunology-related literature. <i>Scientific Reports</i> , 2021, 11, 14344.	1.6	1
24	Detection of SARS-CoV-2 variants requires urgent global coordination. <i>International Journal of Infectious Diseases</i> , 2021, 109, 50-53.	1.5	4
25	Seasonal and annual changes in the microbial communities of Ofunato Bay, Japan, based on metagenomics. <i>Scientific Reports</i> , 2021, 11, 17277.	1.6	4
26	Genome sequencing and identification of cellulase genes in <i>Bacillus paralicheniformis</i> strains from the Red Sea. <i>BMC Microbiology</i> , 2021, 21, 254.	1.3	10
27	DTi2Vec: Drug-target interaction prediction using network embedding and ensemble learning. <i>Journal of Cheminformatics</i> , 2021, 13, 71.	2.8	27
28	Re-infection with a different SARS-CoV-2 clade and prolonged viral shedding in a hematopoietic stem cell transplantation patient. <i>International Journal of Infectious Diseases</i> , 2021, 110, 267-271.	1.5	9
29	Angiotensin-Converting Enzyme (ACE) 1 Gene Polymorphism and Phenotypic Expression of COVID-19 Symptoms. <i>Genes</i> , 2021, 12, 1572.	1.0	28
30	Machine learning and deep learning methods that use omics data for metastasis prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5008-5018.	1.9	69
31	Metagenomic analysis provides functional insights into seasonal change of a non-cyanobacterial prokaryotic community in temperate coastal waters. <i>PLoS ONE</i> , 2021, 16, e0257862.	1.1	5
32	Levothyroxine Treatment and the Risk of Cardiac Arrhythmias – Focus on the Patient Submitted to Thyroid Surgery. <i>Frontiers in Endocrinology</i> , 2021, 12, 758043.	1.5	9
33	Predicting Bone Metastasis Using Gene Expression-Based Machine Learning Models. <i>Frontiers in Genetics</i> , 2021, 12, 771092.	1.1	10
34	Integration of Droplet Microfluidic Tools for Single-cell Functional Metagenomics: An Engineering Head Start. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 504-518.	3.0	4
35	What is the right sequencing approach? Solo VS extended family analysis in consanguineous populations. <i>BMC Medical Genomics</i> , 2020, 13, 103.	0.7	10
36	PATH: A Tool That Facilitates the Searching for Heterologous Biosynthetic Routes. <i>ACS Synthetic Biology</i> , 2020, 9, 3217-3227.	1.9	7

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37	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.	1.8	40
38	Sequencing effort dictates gene discovery in marine microbial metagenomes. <i>Environmental Microbiology</i> , 2020, 22, 4589-4603.	1.8	13
39	Atherosclerosis Linked to Aberrant Amino Acid Metabolism and Immunosuppressive Amino Acid Catabolizing Enzymes. <i>Frontiers in Immunology</i> , 2020, 11, 551758.	2.2	44
40	Splice2Deep: An ensemble of deep convolutional neural networks for improved splice site prediction in genomic DNA. <i>Gene: X</i> , 2020, 763, 100035.	2.3	33
41	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> . <i>PLoS Genetics</i> , 2020, 16, e1008831.	1.5	22
42	DTiGEMS+: drug-target interaction prediction using graph embedding, graph mining, and similarity-based techniques. <i>Journal of Cheminformatics</i> , 2020, 12, 44.	2.8	62
43	SARS-CoV-2 infections and COVID-19 mortalities strongly correlate with ACE1 I/D genotype. <i>Gene</i> , 2020, 758, 144944.	1.0	116
44	DES-ROD: Exploring Literature to Develop New Links between RNA Oxidation and Human Diseases. <i>Oxidative Medicine and Cellular Longevity</i> , 2020, 2020, 1-13.	1.9	3
45	Marine Metagenomic Sequence Counts of Reads Assigned to Taxa Consistently Proportionate to Read Counts Obtained for per g of Seawater Sample. , 2019, , 183-188.		1
46	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.	2.2	24
47	Construction of complete <i>Tupaia belangeri</i> transcriptome database by whole-genome and comprehensive RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 12372.	1.6	16
48	Mining biosynthetic gene clusters in <i>Virgibacillus</i> genomes. <i>BMC Genomics</i> , 2019, 20, 696.	1.2	7
49	Regionalized nervous system in <i>Hydra</i> and the mechanism of its development. <i>Gene Expression Patterns</i> , 2019, 31, 42-59.	0.3	29
50	A Preliminary Metagenome Analysis Based on a Combination of Protein Domains. <i>Proteomes</i> , 2019, 7, 19.	1.7	0
51	Finding <i>Nemo</i> '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.	2.2	55
52	The X Files: The Mystery of X Chromosome Instability in Alzheimer's Disease. <i>Frontiers in Genetics</i> , 2019, 10, 1368.	1.1	25
53	Metagenomic Methods: From Seawater to the Database. , 2019, , 3-16.		1
54	In Memory of Vladimir B. Bajic (1952-2019). <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 473-474.	3.0	1

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55	Metagenome-based diversity analyses suggest a strong locality signal for bacterial communities associated with oyster aquaculture farms in Ofunato Bay. <i>Gene</i> , 2018, 665, 149-154.	1.0	14
56	Seasonal changes in the communities of photosynthetic picoeukaryotes in Ofunato Bay as revealed by shotgun metagenomic sequencing. <i>Gene</i> , 2018, 665, 127-132.	1.0	6
57	Seasonal changes in the abundance of bacterial genes related to dimethylsulfoniopropionate catabolism in seawater from Ofunato Bay revealed by metagenomic analysis. <i>Gene</i> , 2018, 665, 174-184.	1.0	17
58	Taxonomic profiles in metagenomic analyses of free-living microbial communities in the Ofunato Bay. <i>Gene</i> , 2018, 665, 192-200.	1.0	15
59	Basin-scale seasonal changes in marine free-living bacterioplankton community in the Ofunato Bay. <i>Gene</i> , 2018, 665, 185-191.	1.0	10
60	Whole-Genome Sequencing of 84 Japanese Eels Reveals Evidence against Panmixia and Support for Sympatric Speciation. <i>Genes</i> , 2018, 9, 474.	1.0	13
61	Global Ramifications of Dust and Sandstorm Microbiota. <i>Genome Biology and Evolution</i> , 2018, 10, 1970-1987.	1.1	44
62	Gene-by-gene or localized dosage compensation on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1875-1881.	1.1	8
63	In silico exploration of Red Sea <i>Bacillus</i> genomes for natural product biosynthetic gene clusters. <i>BMC Genomics</i> , 2018, 19, 382.	1.2	17
64	Functional interrogation of <i>Plasmodium</i> genus metabolism identifies species- and stage-specific differences in nutrient essentiality and drug targeting. <i>PLoS Computational Biology</i> , 2018, 14, e1005895.	1.5	24
65	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. <i>Nucleic Acids Research</i> , 2017, 45, gkw973.	6.5	30
66	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	13.7	569
67	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	1.2	11
68	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.	6.5	43
69	Building a bio-based industry in the Middle East through harnessing the potential of the Red Sea biodiversity. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4837-4851.	1.7	10
70	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017, 2, e006.	0.7	6
71	The Emerging Facets of Non-Cancerous Warburg Effect. <i>Frontiers in Endocrinology</i> , 2017, 8, 279.	1.5	59
72	Low Concentrations of Vitamin C Reduce the Synthesis of Extracellular Polymers and Destabilize Bacterial Biofilms. <i>Frontiers in Microbiology</i> , 2017, 8, 2599.	1.5	66

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73	Accelerated pseudogenization on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Nature Communications</i> , 2016, 7, 13659.	5.8	15
74	V-GAP: Viral genome assembly pipeline. <i>Gene</i> , 2016, 576, 676-680.	1.0	9
75	Editorial. <i>Gene</i> , 2016, 576, 592.	1.0	0
76	Two-step evolution of endosymbiosis between hydra and algae. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 19-25.	1.2	9
77	VaProS: a database-integration approach for protein/genome information retrieval. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 69-81.	1.2	9
78	Structural adaption of extremophile proteins to the environments with special reference to hydrophobic networks. <i>Ecological Genetics and Genomics</i> , 2016, 1, 1-5.	0.3	7
79	Selection pressure on human STR loci and its relevance in repeat expansion disease. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1851-1869.	1.0	15
80	Evolutionary Transitions of MicroRNA-Target Pairs. <i>Genome Biology and Evolution</i> , 2016, 8, 1621-1633.	1.1	23
81	Different Endosymbiotic Interactions in Two Hydra Species Reflect the Evolutionary History of Endosymbiosis. <i>Genome Biology and Evolution</i> , 2016, 8, 2155-2163.	1.1	24
82	DESM: portal for microbial knowledge exploration systems. <i>Nucleic Acids Research</i> , 2016, 44, D624-D633.	6.5	12
83	Databases of the marine metagenomics. <i>Gene</i> , 2016, 576, 724-728.	1.0	20
84	Speciation of two gobioid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> revealed by multi-locus nuclear and mitochondrial DNA analyses. <i>Gene</i> , 2016, 576, 593-602.	1.0	8
85	Single-cell technologies in environmental omics. <i>Gene</i> , 2016, 576, 701-707.	1.0	20
86	Metagenomic studies of the Red Sea. <i>Gene</i> , 2016, 576, 717-723.	1.0	36
87	Influences of diurnal sampling bias on fixed-point monitoring of plankton biodiversity determined using a massively parallel sequencing-based technique. <i>Gene</i> , 2016, 576, 667-675.	1.0	11
88	Comparative miRNAs analysis of Two contrasting broccoli inbred lines with divergent head-forming capacity under temperature stress. <i>BMC Genomics</i> , 2015, 16, 1026.	1.2	22
89	Function and Evolutionary Origin of Unicellular Camera-Type Eye Structure. <i>PLoS ONE</i> , 2015, 10, e0118415.	1.1	31
90	Challenges and Opportunities of Airborne Metagenomics. <i>Genome Biology and Evolution</i> , 2015, 7, 1216-1226.	1.1	97

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91	Eye-like ocelloids are built from different endosymbiotically acquired components. <i>Nature</i> , 2015, 523, 204-207.	13.7	74
92	Ecological genomics in <i>Xanthomonas</i> : the nature of genetic adaptation with homologous recombination and host shifts. <i>BMC Genomics</i> , 2015, 16, 188.	1.2	23
93	Marine Metagenome as A Resource for Novel Enzymes. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 290-295.	3.0	41
94	Marine metagenomics as a source for bioprospecting. <i>Marine Genomics</i> , 2015, 24, 21-30.	0.4	51
95	Coevolution of Axon Guidance Molecule Slit and Its Receptor Robo. <i>PLoS ONE</i> , 2014, 9, e94970.	1.1	7
96	Tissue- and Stage-Dependent Dosage Compensation on the Neo-X Chromosome in <i>Drosophila pseudoobscura</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 614-624.	3.5	36
97	Adaptive divergence with gene flow in incipient speciation of <i>Miscanthus floridulus</i> / <i>M. sinensis</i> complex (<i>Poaceae</i>). <i>Plant Journal</i> , 2014, 80, 834-847.	2.8	17
98	Evolutionarily conserved transcription factor Apontic controls the G1/S progression by inducing cyclin E during eye development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9497-9502.	3.3	18
99	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.	0.6	48
100	Innexin gap junctions in nerve cells coordinate spontaneous contractile behavior in <i>Hydra</i> polyps. <i>Scientific Reports</i> , 2014, 4, 3573.	1.6	43
101	Dopamine Receptor Genes and Evolutionary Differentiation in the Domestication of Fighting Cocks and Long-Crowing Chickens. <i>PLoS ONE</i> , 2014, 9, e101778.	1.1	21
102	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.	3.3	106
103	Computational analysis and functional expression of ancestral copepod luciferase. <i>Gene</i> , 2013, 528, 201-205.	1.0	20
104	Dynamic Evolution of Endogenous Retrovirus-Derived Genes Expressed in Bovine Conceptuses during the Period of Placentation. <i>Genome Biology and Evolution</i> , 2013, 5, 296-306.	1.1	30
105	H-InvDB in 2013: an omics study platform for human functional gene and transcript discovery. <i>Nucleic Acids Research</i> , 2013, 41, D915-D919.	6.5	22
106	Comparison of Gene Expression Profile of Epiretinal Membranes Obtained from Eyes with Proliferative Vitreoretinopathy to That of Secondary Epiretinal Membranes. <i>PLoS ONE</i> , 2013, 8, e54191.	1.1	30
107	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.	1.1	150
108	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.	6.5	43

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109	Evolution of Bioluminescence in Marine Planktonic Copepods. <i>Molecular Biology and Evolution</i> , 2012, 29, 1669-1681.	3.5	48
110	A New Database (GCD) on Genome Composition for Eukaryote and Prokaryote Genome Sequences and Their Initial Analyses. <i>Genome Biology and Evolution</i> , 2012, 4, 501-512.	1.1	16
111	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.	1.8	64
112	Infectious Endogenous Retroviruses in Cats and Emergence of Recombinant Viruses. <i>Journal of Virology</i> , 2012, 86, 8634-8644.	1.5	68
113	TP Atlas: integration and dissemination of advances in Targeted Proteins Research Program (TPRP) structural biology project phase II in Japan. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 145-154.	1.2	2
114	Multiple Plastids Collected by the Dinoflagellate <i>Dinophysis mitra</i> through Kleptoplastidy. <i>Applied and Environmental Microbiology</i> , 2012, 78, 813-821.	1.4	56
115	A prioritization analysis of disease association by data-mining of functional annotation of human genes. <i>Genomics</i> , 2012, 99, 1-9.	1.3	11
116	The Temporal Sequence of the Mammalian Neocortical Neurogenetic Program Drives Mediolateral Pattern in the Chick Pallium. <i>Developmental Cell</i> , 2012, 22, 863-870.	3.1	81
117	Genome and Transcriptome Analysis of the Food-Yeast <i>Candida utilis</i> . <i>PLoS ONE</i> , 2012, 7, e37226.	1.1	28
118	Prediction of Protein-Destabilizing Polymorphisms by Manual Curation with Protein Structure. <i>PLoS ONE</i> , 2012, 7, e50445.	1.1	4
119	Gene dosage imbalance of human chromosome 21 in mouse embryonic stem cells differentiating to neurons. <i>Gene</i> , 2011, 481, 93-101.	1.0	6
120	Evolutionary Patterns of Recently Emerged Animal Duplogs. <i>Genome Biology and Evolution</i> , 2011, 3, 1119-1135.	1.1	18
121	Evolutionary history of dog rabies in Brazil. <i>Journal of General Virology</i> , 2011, 92, 85-90.	1.3	13
122	Welcome to <i>Genome Biology and Evolution</i> . <i>Genome Biology and Evolution</i> , 2010, 1, 1-1.	1.1	1
123	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. <i>Functional and Integrative Genomics</i> , 2010, 10, 307-319.	1.4	28
124	Low genetic diversities of rabies virus populations within different hosts in Brazil. <i>Infection, Genetics and Evolution</i> , 2010, 10, 278-283.	1.0	5
125	Endogenous non-retroviral RNA virus elements in mammalian genomes. <i>Nature</i> , 2010, 463, 84-87.	13.7	404
126	The dynamic genome of <i>Hydra</i> . <i>Nature</i> , 2010, 464, 592-596.	13.7	743

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127	Dynamic evolution of translation initiation mechanisms in prokaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6382-6387.	3.3	137
128	Evolutionary Pattern of Gene Homogenization between Primate-Specific Paralogs after Human and Macaque Speciation Using the 4-2-4 Method. Molecular Biology and Evolution, 2010, 27, 2152-2171.	3.5	19
129	DDBJ launches a new archive database with analytical tools for next-generation sequence data. Nucleic Acids Research, 2010, 38, D33-D38.	6.5	86
130	Nematogalectin, a nematocyst protein with GlyXY and galectin domains, demonstrates nematocyte-specific alternative splicing in <i>Hydra</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18539-18544.	3.3	69
131	A Non-sulfated Chondroitin Stabilizes Membrane Tubulation in Cnidarian Organelles. Journal of Biological Chemistry, 2010, 285, 25613-25623.	1.6	35
132	Gene expression profile of fibrovascular membranes from patients with proliferative diabetic retinopathy. British Journal of Ophthalmology, 2010, 94, 795-801.	2.1	19
133	Long-range neural and gap junction protein-mediated cues control polarity during planarian regeneration. Developmental Biology, 2010, 339, 188-199.	0.9	176
134	Genome Network Project: An Integrated Genomic Platform. Nature Precedings, 2009, , .	0.1	0
135	DDBJ Activities: Contribution to the Research in Information Biology. Nature Precedings, 2009, , .	0.1	0
136	Methods for Incorporating the Hypermutability of CpG Dinucleotides in Detecting Natural Selection Operating at the Amino Acid Sequence Level. Molecular Biology and Evolution, 2009, 26, 2275-2284.	3.5	18
137	VarySysDB: a human genetic polymorphism database based on all H-InvDB transcripts. Nucleic Acids Research, 2009, 37, D810-D815.	6.5	14
138	Midline governs axon pathfinding by coordinating expression of two major guidance systems. Genes and Development, 2009, 23, 1165-1170.	2.7	32
139	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
140	An evolutionary origin and selection process of goldfish. Gene, 2009, 430, 5-11.	1.0	75
141	The evolutionary study of small RNA-directed gene silencing pathways by investigating RNase III enzymes. Gene, 2009, 435, 1-8.	1.0	5
142	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557
143	Detecting Linkage between a Trait and a Marker in a Random Mating Population without Pedigree Record. PLoS ONE, 2009, 4, e4956.	1.1	0
144	The Promoter Signatures in Rice LEA Genes Can Be Used to Build a Co-expressing LEA Gene Network. Rice, 2008, 1, 177-187.	1.7	14

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145	The future of biocuration. <i>Nature</i> , 2008, 455, 47-50.	13.7	648
146	<i>Brachyury</i> downstream gene sets in a chordate, <i>Ciona intestinalis</i> : integrating notochord specification, morphogenesis and chordate evolution. <i>Evolution & Development</i> , 2008, 10, 37-51.	1.1	53
147	Evolution of complex structures: minicollagens shape the cnidarian nematocyst. <i>Trends in Genetics</i> , 2008, 24, 431-438.	2.9	117
148	Eukaryotic nuclear structure explains the evolutionary rate difference of ribosome export factors. <i>Gene</i> , 2008, 421, 7-13.	1.0	1
149	The origin of nucleus: Rebuild from the prokaryotic ancestors of ribosome export factors. <i>Gene</i> , 2008, 423, 149-152.	1.0	7
150	The evolutionary relationship between gene duplication and alternative splicing. <i>Gene</i> , 2008, 427, 19-31.	1.0	34
151	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. <i>Gene</i> , 2008, 427, 7-18.	1.0	38
152	Cilium Evolution: Identification of a Novel Protein, Nematocilin, in the Mechanosensory Cilium of <i>Hydra</i> Nematocytes. <i>Molecular Biology and Evolution</i> , 2008, 25, 2009-2017.	3.5	27
153	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.	6.5	27
154	Distribution and Effects of Nonsense Polymorphisms in Human Genes. <i>PLoS ONE</i> , 2008, 3, e3393.	1.1	35
155	Transcriptional Interferences in cis Natural Antisense Transcripts of Humans and Mice. <i>Genetics</i> , 2007, 176, 1299-1306.	1.2	124
156	Compensatory Change of Interacting Amino Acids in the Coevolution of Transcriptional Coactivator MBF1 and TATA-Box Binding Protein. <i>Molecular Biology and Evolution</i> , 2007, 24, 1458-1463.	3.5	20
157	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 β -Proteobacteria. <i>Molecular Biology and Evolution</i> , 2007, 24, 805-813.	3.5	28
158	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
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