Wen-Hsiung Li

List of Publications by Year
in descending order

353 papers	35,129 citations	4584 88 h-index	5244 171 g-index
364 all docs	364 docs citations	364 times ranked	34847 citing authors

#	Article	IF	Citations
1	The codon adaptation index-a measure of directional synonymous codon usage bias, and its potential applications. Nucleic Acids Research, 1987, 15, 1281-1295.	6.5	3,290
2	Unbiased estimation of the rates of synonymous and nonsynonymous substitution. Journal of Molecular Evolution, 1993, 36, 96-99.	0.8	1,049
3	Comparative Analysis of the Receptor-Like Kinase Family in Arabidopsis and Rice[W]. Plant Cell, 2004, 16, 1220-1234.	3.1	980
4	An evolutionary perspective on synonymous codon usage in unicellular organisms. Journal of Molecular Evolution, 1986, 24, 28-38.	0.8	801
5	Role of duplicate genes in genetic robustness against null mutations. Nature, 2003, 421, 63-66.	13.7	790
6	Genomic Divergences between Humans and Other Hominoids and the Effective Population Size of the Common Ancestor of Humans and Chimpanzees. American Journal of Human Genetics, 2001, 68, 444-456.	2.6	662
7	Uncovering Small RNA-Mediated Responses to Phosphate Deficiency in Arabidopsis by Deep Sequencing. Plant Physiology, 2009, 151, 2120-2132.	2.3	631
8	Human polymorphism at microRNAs and microRNA target sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3300-3305.	3.3	616
9	Mutation rates differ among regions of the mammalian genome. Nature, 1989, 337, 283-285.	13.7	599
10	Codon usage in regulatory genes inEscherichia colidoes not reflect selection for â€˜rareâ€™ codons. Nucleic Acids Research, 1986, 14, 7737-7749.	6.5	530
11	Pseudogenes as a paradigm of neutral evolution. Nature, 1981, 292, 237-239.	13.7	487
12	An evaluation of the molecular clock hypothesis using mammalian DNA sequences. Journal of Molecular Evolution, 1987, 25, 330-342.	0.8	456
13	Evolutionary analyses of the human genome. Nature, 2001, 409, 847-849.	13.7	442
14	Patterns of nucleotide substitution in pseudogenes and functional genes. Journal of Molecular Evolution, 1982, 18, 360-369.	0.8	438
15	Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100. Nature, 1986, 323, 738-742.	13.7	431
16	Extent of Gene Duplication in the Genomes of Drosophila, Nematode, and Yeast. Molecular Biology and Evolution, 2002, 19, 256-262.	3.5	422
17	The molecular clock runs more slowly in man than in apes and monkeys. Nature, 1987, 326, 93-96.	13.7	396
18	Dating the Monocot?Dicot Divergence and the Origin of Core Eudicots Using Whole Chloroplast Genomes. Journal of Molecular Evolution, 2004, 58, 424-441.	0.8	389

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19	Transposable elements are found in a large number of human protein-coding genes. Trends in Genetics, 2001, 17, 619-621.	2.9	383
20	Nonrandomness of point mutation as reflected in nucleotide substitutions in pseudogenes and its evolutionary implications. Journal of Molecular Evolution, 1984, 21, 58-71.	0.8	362
21	Rates of Nucleotide Substitution in Angiosperm Mitochondrial DNA Sequences and Dates of Divergence Between Brassica and Other Angiosperm Lineages. Journal of Molecular Evolution, 1999, 48, 597-604.	0.8	343
22	On the rate of DNA sequence evolution inDrosophila. Journal of Molecular Evolution, 1989, 28, 398-402.	0.8	321
23	Expression divergence between duplicate genes. Trends in Genetics, 2005, 21, 602-607.	2.9	321
24	Is the guinea-pig a rodent?. Nature, 1991, 351, 649-652.	13.7	318
25	Mammalian Housekeeping Genes Evolve More Slowly than Tissue-Specific Genes. Molecular Biology and Evolution, 2004, 21, 236-239.	3.5	318
26	Rates of Nucleotide Substitution in Primates and Rodents and the Generationâ€“Time Effect Hypothesis. Molecular Phylogenetics and Evolution, 1996, 5, 182-187.	1.2	316
27	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6496-505.	3.3	313
28	LINKAGE DISEQUILIBRIUM IN SUBDIVIDED POPULATIONS. Genetics, 1973, 75, 213-219.	1.2	288
29	Rapid divergence in expression between duplicate genes inferred from microarray data. Trends in Genetics, 2002, 18, 609-613.	2.9	286
30	High Polymorphism at the Human Melanocortin 1 Receptor Locus. Genetics, 1999, 151, 1547-1557.	1.2	258
31	Models of nearly neutral mutations with particular implications for nonrandom usage of synonymous codons. Journal of Molecular Evolution, 1987, 24, 337-345.	0.8	251
32	The KA/KS Ratio Test for Assessing the Protein-Coding Potential of Genomic Regions: An Empirical and Simulation Study. Genome Research, 2002, 12, 198-202.	2.4	233
33	Male-driven evolution of DNA sequences. Nature, 1993, 362, 745-747.	13.7	230
34	Strong male-driven evolution of DNA sequences in humans and apes. Nature, 2002, 416, 624-626.	13.7	226
35	Transcription Factor Families Have Much Higher Expansion Rates in Plants than in Animals. Plant Physiology, 2005, 139, 18-26.	2.3	218
36	Divergence in the Spatial Pattern of Gene Expression Between Human Duplicate Genes. Genome Research, 2003, 13, 1638-1645.	2.4	212

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37	Structure and evolution of the apolipoprotein multigene family. Journal of Molecular Biology, 1986, 187, 325-340.	2.0	210
38	Simultaneous amino acid substitutions at antigenic sites drive influenza A hemagglutinin evolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6283-6288.	3.3	210
39	Male-driven evolution. Current Opinion in Genetics and Development, 2002, 12, 650-656.	1.5	206
40	Rates of synonymous substitution in plant nuclear genes. Journal of Molecular Evolution, 1989, 29, 208-211.	0.8	179
41	Larger Genetic Differences Within Africans Than Between Africans and Eurasians. Genetics, 2002, 161, 269-274.	1.2	178
42	Signalling pathway for RKIP and Let-7 regulates and predicts metastatic breast cancer. EMBO Journal, 2011, 30, 4500-4514.	3.5	175
43	Duplicate genes increase gene expression diversity within and between species. Nature Genetics, 2004, 36, 577-579.	9.4	170
44	Estimation of Confidence in Phylogeny: The Complete-and-Partial Bootstrap Technique. Molecular Phylogenetics and Evolution, 1995, 4, 44-63.	1.2	168
45	Trichromatic vision in prosimians. Nature, 1999, 402, 36-36.	13.7	167
46	RATE OF GENE SILENCING AT DUPLICATE LOCI: A THEORETICAL STUDY AND INTERPRETATION OF DATA FROM TETRAPLOID FISHES. Genetics, 1980, 95, 237-258.	1.2	162
47	A large number of novel coding small open reading frames in the intergenic regions of the Arabidopsis thaliana genome are transcribed and/or under purifying selection. Genome Research, 2007, 17, 632-640.	2.4	157
48	Natural selection on cis and trans regulation in yeasts. Genome Research, 2010, 20, 826-836.	2.4	156
49	Characterizing Regulatory and Functional Differentiation between Maize Mesophyll and Bundle Sheath Cells by Transcriptomic Analysis Â Â. Plant Physiology, 2012, 160, 165-177.	2.3	156
50	Accumulation of mutations in sexual and asexual populations. Genetical Research, 1987, 49, 135-146.	0.3	153
51	Evolutionary Diversification of DNA Methyltransferases in Eukaryotic Genomes. Molecular Biology and Evolution, 2005, 22, 1119-1128.	3.5	153
52	MicroRNA regulation of human proteinâ€“protein interaction network. Rna, 2007, 13, 1402-1408.	1.6	153
53	Molecular evolution of trichromacy in primates. Vision Research, 1998, 38, 3299-3306.	0.7	151
54	The size distribution of insertions and deletions in human and rodent pseudogenes suggests the logarithmic gap penalty for sequence alignment. Journal of Molecular Evolution, 1995, 40, 464-473.	0.8	145

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55	Selective Constraints, Amino Acid Composition, and the Rate of Protein Evolution. Molecular Biology and Evolution, 2000, 17, 656-664.	3.5	144
56	Chromosome-wide SNPs reveal an ancient origin for Plasmodium falciparum. Nature, 2002, 418, 323-324.	13.7	141
57	Coordinated histone modifications are associated with gene expression variation within and between species. Genome Research, 2011, 21, 590-598.	2.4	140
58	Evidence from opsin genes rejects nocturnality in ancestral primates. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14712-14716.	3.3	139
59	DISTRIBUTION OF NUCLEOTIDE DIFFERENCES BETWEEN TWO RANDOMLY CHOSEN CISTRONS IN A FINITE POPULATION. Genetics, 1977, 85, 331-337.	1.2	138
60	Deletions in processed pseudogenes accumulate faster in rodents than in humans. Journal of Molecular Evolution, 1989, 28, 279-285.	0.8	133
61	Low Nucleotide Diversity in Chimpanzees and Bonobos. Genetics, 2003, 164, 1511-1518.	1.2	133
62	Coalescing into the 21st Century: An Overview and Prospects of Coalescent Theory. Theoretical Population Biology, 1999, 56, 1-10.	0.5	132
63	Slow Molecular Clocks in Old World Monkeys, Apes, and Humans. Molecular Biology and Evolution, 2002, 19, 2191-2198.	3.5	129
64	Different evolutionary patterns between young duplicate genes in the human genome. Genome Biology, 2003, 4, R56.	13.9	128
65	Patterns of expansion and expression divergence in the plant polygalacturonase gene family. Genome Biology, 2006, 7, R87.	13.9	124
66	Down-Regulation of Cytokinin Oxidase 2 Expression Increases Tiller Number and Improves Rice Yield. Rice, 2015, 8, 36.	1.7	123
67	Molecular evolution meets the genomics revolution. Nature Genetics, 2003, 33, 255-265.	9.4	120
68	DNA replication timing and selection shape the landscape of nucleotide variation in cancer genomes. Nature Communications, 2012, 3, 1004.	5.8	120
69	Opsin gene and photopigment polymorphism in a prosimian primate. Vision Research, 2002, 42, 11-18.	0.7	119
70	Inheritance of Gene Expression Level and Selective Constraints on Trans- and Cis-Regulatory Changes in Yeast. Molecular Biology and Evolution, 2013, 30, 2121-2133.	3.5	113
71	Stable linkage disequilibrium without epistasis in subdivided populations. Theoretical Population Biology, 1974, 6, 173-183.	0.5	111
72	Evolution of DNA Sequences. , 1985, , 1-94.		108

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73	Patterns of Segmental Duplication in the Human Genome. Molecular Biology and Evolution, 2004, 22, 135-141.	3.5	107
74	Gene essentiality, gene duplicability and protein connectivity in human and mouse. Trends in Genetics, 2007, 23, 375-378.	2.9	107
75	CpG island density and its correlations with genomic features in mammalian genomes. Genome Biology, 2008, 9, R79.	13.9	107
76	Drift variances of heterozygosity and genetic distance in transient states. Genetical Research, 1975, 25, 229-247.	0.3	106
77	Origins and antiquity of X-linked triallelic color vision systems in New World monkeys. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 13749-13754.	3.3	101
78	Organismal complexity, protein complexity, and gene duplicability. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15661-15665.	3.3	100
79	RNA landscape of evolution for optimal exon and intron discrimination. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5797-5802.	3.3	99
80	What Amino Acid Properties Affect Protein Evolution?. Journal of Molecular Evolution, 1998, 47, 557-564.	0.8	98
81	Molecular Systematics of Pikas (Genus Ochotona) Inferred from Mitochondrial DNA Sequences. Molecular Phylogenetics and Evolution, 2000, 16, 85-95.	1.2	98
82	Phylogenetic analysis based on rRNA sequences supports the archaebacterial rather than the eocyte tree. Nature, 1989, 339, 145-147.	13.7	97
83	Inconsistency of the Maximum-parsimony Method: the Case of Five Taxa With a Molecular Clock. Systematic Biology, 1993, 42, 113-125.	2.7	97
84	Historical contingency in the evolution of primate color vision. Journal of Human Evolution, 2003, 44, 25-45.	1.3	96
85	Ubiquitin genes as a paradigm of concerted evolution of tandem repeats. Journal of Molecular Evolution, 1987, 25, 58-64.	0.8	95
86	Mouse Very-Low-Density-Lipoprotein Receptor (VLDLR) cDNA Cloning, Tissue-specific Expression and Evolutionary Relationship with the Low-density-lipoprotein Receptor. FEBS Journal, 1994, 224, 975-982.	0.2	95
87	Statistical methods for identifying yeast cell cycle transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13532-13537.	3.3	94
88	Quantitative characterization of the transcriptional regulatory network in the yeast cell cycle. Bioinformatics, 2004, 20, 1914-1927.	1.8	93
89	Densities, length proportions, and other distributional features of repetitive sequences in the human genome estimated from 430 megabases of genomic sequence. Gene, 2000, 259, 81-88.	1.0	91
90	Signatures of Domain Shuffling in the Human Genome. Genome Research, 2002, 12, 1642-1650.	2.4	91

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91	Multidimensional scaling for large genomic data sets. BMC Bioinformatics, 2008, 9, 179.	1.2	91
92	Rate of Protein Evolution Versus Fitness Effect of Gene Deletion. Molecular Biology and Evolution, 2003, 20, 772-774.	3.5	89
93	Antroquinonol from ethanolic extract of mycelium of Antrodia cinnamomea protects hepatic cells from ethanol-induced oxidative stress through Nrf-2 activation. Journal of Ethnopharmacology, 2011, 136, 168-177.	2.0	89
94	Positional distribution of transcription factor binding sites in Arabidopsis thaliana. Scientific Reports, 2016, 6, 25164.	1.6	89
95	Alternative mRNA Splicing and Differential Promoter Utilization Determine Tissue-specific Expression of the Apolipoprotein B mRNA-editing Protein (Apobec1) Gene in Mice.. Journal of Biological Chemistry, 1995, 270, 13042-13056.	1.6	88
96	Intragenic Spatial Patterns of Codon Usage Bias in Prokaryotic and Eukaryotic Genomes. Genetics, 2004, 168, 2245-2260.	1.2	88
97	Proportion of Solvent-Exposed Amino Acids in a Protein and Rate of Protein Evolution. Molecular Biology and Evolution, 2007, 24, 1005-1011.	3.5	88
98	The Chicken Frizzle Feather Is Due to an Î±-Keratin (KRT75) Mutation That Causes a Defective Rachis. PLoS Genetics, 2012, 8, e1002748.	1.5	88
99	MAINTENANCE OF GENETIC VARIABILITY UNDER THE JOINT EFFECT OF MUTATION, SELECTION AND RANDOM DRIFT. Genetics, 1978, 90, 349-382.	1.2	87
100	Molecular Evolution of Bat Color Vision Genes. Molecular Biology and Evolution, 2003, 21, 295-302.	3.5	86
101	Lowly Expressed Human MicroRNA Genes Evolve Rapidly. Molecular Biology and Evolution, 2009, 26, 1195-1198.	3.5	86
102	Non-random association between electromorphs and inversion chromosomes in finite populations. Genetical Research, 1980, 35, 65-83.	0.3	85
103	Molecular Phylogenetic Studies of Brassica,Rorippa,Arabidopsis and Allied Genera Based on the Internal Transcribed Spacer Region of 18Sâ€“25S rDNA. Molecular Phylogenetics and Evolution, 1999, 13, 455-462.	1.2	85
104	Nucleotide Diversity in Gorillas. Genetics, 2004, 166, 1375-1383.	1.2	85
105	Expansion of Hexose Transporter Genes Was Associated with the Evolution of Aerobic Fermentation in Yeasts. Molecular Biology and Evolution, 2011, 28, 131-142.	3.5	82
106	The molecular clock ticks regularly in muroid rodents and hamsters. Journal of Molecular Evolution, 1992, 35, 377-84.	0.8	81
107	Evolutionary Persistence of Functional Compensation by Duplicate Genes in Arabidopsis. Genome Biology and Evolution, 2009, 1, 409-414.	1.1	81
108	Higher rates of amino acid substitution in rodents than in humans. Molecular Phylogenetics and Evolution, 1992, 1, 211-214.	1.2	80

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109	Gene admixture in the Silk Road region of China: Evidence from mtDNA and melanocortin 1 receptor polymorphism.. Genes and Genetic Systems, 2000, 75, 173-178.	0.2	79
110	Role of positive selection in the retention of duplicate genes in mammalian genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2232-2236.	3.3	79
111	Human TRIM71 and Its Nematode Homologue Are Targets of let-7 MicroRNA and Its Zebrafish Orthologue Is Essential for Development. Molecular Biology and Evolution, 2007, 24, 2525-2534.	3.5	79
112	Genomic and transcriptomic analyses of the medicinal fungus Antrodia cinnamomea for its metabolite biosynthesis and sexual development. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4743-52.	3.3	79
113	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	3.5	79
114	The Nonsynonymous/Synonymous Substitution Rate Ratio versus the Radical/Conservative Replacement Rate Ratio in the Evolution of Mammalian Genes. Molecular Biology and Evolution, 2007, 24, 2235-2241.	3.5	77
115	Evolution of paired domains: Isolation and sequencing of jellyfish and hydra Pax genes related to Pax-5 and Pax-6. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 5156-5161.	3.3	76
116	Functional Compensation of Primary and Secondary Metabolites by Duplicate Genes in Arabidopsis thaliana. Molecular Biology and Evolution, 2011, 28, 377-382.	3.5	76
117	The rises and falls of opsin genes in 59 ray-finned fish genomes and their implications for environmental adaptation. Scientific Reports, 2017, 7, 15568.	1.6	76
118	Protein Function, Connectivity, and Duplicability in Yeast. Molecular Biology and Evolution, 2006, 23, 30-39.	3.5	74
119	Functional characterization of cellulases identified from the cow rumen fungus Neocallimastix patriciarum W5 by transcriptomic and secretomic analyses. Biotechnology for Biofuels, 2011, 4, 24.	6.2	74
120	Anatomical and transcriptional dynamics of maize embryonic leaves during seed germination. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3979-3984.	3.3	74
121	Topographical mapping of Î±- and Î²-keratins on developing chicken skin integuments: Functional interaction and evolutionary perspectives. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6770-9.	3.3	74
122	Evolution of the Hominoid Semenogelin Genes, the Major Proteins of Ejaculated Semen. Journal of Molecular Evolution, 2003, 57, 261-270.	0.8	73
123	Origins, Lineage-Specific Expansions, and Multiple Losses of Tyrosine Kinases in Eukaryotes. Molecular Biology and Evolution, 2004, 21, 828-840.	3.5	73
124	Comparison of Three Methods for Estimating Rates of Synonymous and Nonsynonymous Nucleotide Substitutions. Molecular Biology and Evolution, 2004, 21, 2290-2298.	3.5	73
125	Transcriptome dynamics of developing maize leaves and genomewide prediction of cis elements and their cognate transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2477-86.	3.3	73
126	So, what about the molecular clock hypothesis?. Current Opinion in Genetics and Development, 1993, 3, 896-901.	1.5	72

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127	Evolution of the yeast protein interaction network. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12820-12824.	3.3	72
128	Prediction of splice sites with dependency graphs and their expanded bayesian networks. Bioinformatics, 2005, 21, 471-482.	1.8	72
129	Assembling a cellulase cocktail and a cellodextrin transporter into a yeast host for CBP ethanol production. Biotechnology for Biofuels, 2013, 6, 19.	6.2	72
130	A new measure of the robustness of biochemical networks. Bioinformatics, 2005, 21, 2698-2705.	1.8	71
131	Human SNPs Reveal No Evidence of Frequent Positive Selection. Molecular Biology and Evolution, 2005, 22, 2504-2507.	3.5	71
132	Estimation of evolutionary distances under stationary and nonstationary models of nucleotide substitution. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5899-5905.	3.3	69
133	Comparative transcriptomics method to infer gene coexpression networks and its applications to maize and rice leaf transcriptomes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3091-3099.	3.3	69
134	A study of the phylogeny of Brassica rapa, B. nigra, Raphanus sativus, and their related genera using noncoding regions of chloroplast DNA. Molecular Phylogenetics and Evolution, 2002, 23, 268-275.	1.2	68
135	Gene Expression Evolves Faster in Narrowly Than in Broadly Expressed Mammalian Genes. Molecular Biology and Evolution, 2005, 22, 2113-2118.	3.5	68
136	Comparative Methods for the Analysis of Gene-Expression Evolution: An Example Using Yeast Functional Genomic Data. Molecular Biology and Evolution, 2005, 22, 40-50.	3.5	68
137	The genetic basis of evolutionary change in gene expression levels. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 2581-2590.	1.8	68
138	Title is missing!. Genetica, 1998, 102/103, 383-391.	0.5	67
139	Isolation and expression of a Pax-6 gene in the regenerating and intact Planarian Dugesia(G)tigrina. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 558-563.	3.3	67
140	Genomic Organization, Transcriptomic Analysis, and Functional Characterization of Avian Î±- and Î²-Keratins in Diverse Feather Forms. Genome Biology and Evolution, 2014, 6, 2258-2273.	1.1	67
141	Understanding the origins of AIDS viruses. Nature, 1988, 336, 315-315.	13.7	66
142	Episodic Evolution of Growth Hormone in Primates and Emergence of the Species Specificity of Human Growth Hormone Receptor. Molecular Biology and Evolution, 2001, 18, 945-953.	3.5	66
143	A general additive distance with time-reversibility and rate variation among nucleotide sites.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 4671-4676.	3.3	65
144	Apobec-1 and apolipoprotein B mRNA editing. Lipids and Lipid Metabolism, 1997, 1345, 11-26.	2.6	65

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145	A highly efficient Î²-glucosidase from the buffalo rumen fungus Neocallimastix patriciarum W5. Biotechnology for Biofuels, 2012, 5, 24.	6.2	65
146	Genome-Wide Patterns of Genetic Variation in Two Domestic Chickens. Genome Biology and Evolution, 2013, 5, 1376-1392.	1.1	65
147	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. PLoS Computational Biology, 2015, 11, e1004497.	1.5	65
148	Molecular Genetics of Spectral Tuning in New World Monkey Color Vision. Journal of Molecular Evolution, 1998, 46, 697-702.	0.8	64
149	NJML: A Hybrid Algorithm for the Neighbor-Joining and Maximum-Likelihood Methods. Molecular Biology and Evolution, 2000, 17, 1401-1409.	3.5	61
150	Experimental Evolution of Yeast for High-Temperature Tolerance. Molecular Biology and Evolution, 2018, 35, 1823-1839.	3.5	61
151	Distribution of nucleotide differences between two randomly chosen cistrons in a subdivided population: The finite island model. Theoretical Population Biology, 1976, 10, 303-308.	0.5	60
152	Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. BMC Bioinformatics, 2006, 7, 421.	1.2	59
153	The chimpanzee and us. Nature, 2005, 437, 50-51.	13.7	58
154	Human-specific insertions and deletions inferred from mammalian genome sequences. Genome Research, 2006, 17, 16-22.	2.4	58
155	External factors accelerate expression divergence between duplicate genes. Trends in Genetics, 2007, 23, 162-166.	2.9	58
156	The transient distribution of allele frequencies under mutation pressure. Genetical Research, 1976, 28, 205-214.	0.3	57
157	Metabolic engineering a yeast to produce astaxanthin. Bioresource Technology, 2017, 245, 899-905.	4.8	56
158	Alternatively and Constitutively Spliced Exons Are Subject to Different Evolutionary Forces. Molecular Biology and Evolution, 2006, 23, 675-682.	3.5	55
159	Overlapping genes in the human and mouse genomes. BMC Genomics, 2008, 9, 169.	1.2	55
160	Mixed culture fermentation from lignocellulosic materials using thermophilic lignocellulose-degrading anaerobes. Process Biochemistry, 2011, 46, 489-493.	1.8	55
161	Sex Differences in Mutation Rate in Higher Primates Estimated from AMG Intron Sequences. Journal of Molecular Evolution, 1997, 44, 463-465.	0.8	53
162	Protein Under-Wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. PLoS Genetics, 2008, 4, e11.	1.5	53

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163	Human DNA Sequence Variation in a 6.6-kb Region Containing the Melanocortin 1 Receptor Promoter. Genetics, 2001, 158, 1253-1268.	1.2	52
164	Molecular cloning and expression of partial cDNAs and deduced amino acid sequence of a carboxyl-terminal fragment of human apolipoprotein B-100.. Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 7265-7269.	3.3	51
165	Expression Divergence of Chemosensory Genes betweenDrosophila sechelliaand Its Sibling Species and Its Implications for Host Shift. Genome Biology and Evolution, 2015, 7, 2843-2858.	1.1	51
166	Integrating an algal Î²-carotene hydroxylase gene into a designed carotenoid-biosynthesis pathway increases carotenoid production in yeast. Bioresource Technology, 2015, 184, 2-8.	4.8	50
167	Large numbers of vertebrates began rapid population decline in the late 19th century. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14079-14084.	3.3	50
168	Gene number expansion and contraction in vertebrate genomes with respect to invertebrate genomes. Genome Research, 2008, 18, 221-232.	2.4	49
169	Evolutionary Conservation of Histone Modifications in Mammals. Molecular Biology and Evolution, 2012, 29, 1757-1767.	3.5	49
170	The prognostic significance of RUNX2 and miR-10a/10b and their inter-relationship in breast cancer. Journal of Translational Medicine, 2014, 12, 257.	1.8	49
171	Evolution of 5' Untranslated Region Length and Gene Expression Reprogramming in Yeasts. Molecular Biology and Evolution, 2012, 29, 81-89.	3.5	48
172	Probability of identical monomorphism in related species. Genetical Research, 1975, 26, 31-43.	0.3	47
173	Allelic Variation in the Squirrel Monkey X-Linked Color Vision Gene: Biogeographical and Behavioral Correlates. Journal of Molecular Evolution, 2002, 54, 734-745.	0.8	47
174	PERSISTENCE OF COMMON ALLELES IN TWO RELATED POPULATIONS OR SPECIES. Genetics, 1977, 86, 901-914.	1.2	47
175	Features and Trend of Loss of Promoter-Associated CpG Islands in the Human and Mouse Genomes. Molecular Biology and Evolution, 2007, 24, 1991-2000.	3.5	46
176	Metabolite Profiles for Antrodia cinnamomea Fruiting Bodies Harvested at Different Culture Ages and from Different Wood Substrates. Journal of Agricultural and Food Chemistry, 2011, 59, 7626-7635.	2.4	46
177	Multiple Regulatory Modules Are Required for Scale-to-Feather Conversion. Molecular Biology and Evolution, 2018, 35, 417-430.	3.5	46
178	Expression evolution in yeast genes of single-input modules is mainly due to changes in trans-acting factors. Genome Research, 2007, 17, 1161-1169.	2.4	45
179	A model for the correlation of mutation rate with GC content and the origin of GC-rich isochores. Journal of Molecular Evolution, 1994, 38, 468-475.	0.8	44
180	Effects of GC Content and Mutational Pressure on the Lengths of Exons and Coding Sequences. Journal of Molecular Evolution, 2003, 56, 362-370.	0.8	44

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181	Comment on "Chromosomal Speciation and Molecular Divergence-Accelerated Evolution in Rearranged Chromosomes". Science, 2003, 302, 988b-988.	6.0	44
182	Constructing a yeast to express the largest cellulosome complex on the cell surface. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2385-2394.	3.3	44
183	Estimating the intensity of male-driven evolution in rodents by using X-linked and Y-linked Ube 1 genes and pseudogenes. Journal of Molecular Evolution, 1995, 40, 70-77.	0.8	43
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