

Wen-Hsiung Li

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

353
papers

28,786
citations

82
h-index

159
g-index

364
ext. papers

32,379
ext. citations

8.9
avg, IF

7.13
L-index

#	Paper	IF	Citations
353	Identifying mutations in sd1, Pi54 and Pi-ta, and positively selected genes of TN1, the first semidwarf rice in Green Revolution.. <i>Botanical Studies</i> , 2022 , 63, 9	2.3	
352	Maize Golden2-like transcription factors boost rice chloroplast development, photosynthesis and grain yield. <i>Plant Physiology</i> , 2021 ,	6.6	4
351	Identifying Primate ACE2 Variants That Confer Resistance to SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2715-2731	8.3	7
350	Rice transcription factor GAMYB modulates bHLH142 and is homeostatically regulated by TDR during anther tapetal and pollen development. <i>Journal of Experimental Botany</i> , 2021 , 72, 4888-4903	7	4
349	Chromosomal-level genome assembly of the semi-dwarf rice Taichung Native 1, an initiator of Green Revolution. <i>Genomics</i> , 2021 , 113, 2656-2674	4.3	4
348	Constructing a human complex type N-linked glycosylation pathway in <i>Kluyveromyces marxianus</i> . <i>PLoS ONE</i> , 2020 , 15, e0233492	3.7	0
347	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	6	8
346	Constructing a yeast to express the largest cellulosome complex on the cell surface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 2385-2394	11.5	25
345	Maize ANT1 modulates vascular development, chloroplast development, photosynthesis, and plant growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21747-21755	11.5	21755
344	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
343	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
342	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
341	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
340	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
339	Behavioral and brain- transcriptomic synchronization between the two opponents of a fighting pair of the fish <i>Betta splendens</i> 2020 , 16, e1008831		
338	Many human RNA viruses show extraordinarily stringent selective constraints on protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 19009-19018	11.5	13
337	Comparative transcriptomics method to infer gene coexpression networks and its applications to maize and rice leaf transcriptomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3091-3099	11.5	22

336	Characterizing an engineered carotenoid-producing yeast as an anti-stress chassis for building cell factories. <i>Microbial Cell Factories</i> , 2019 , 18, 155	6.4	3
335	Feather Evolution from Precocial to Altricial Birds. <i>Zoological Studies</i> , 2019 , 58, e24	0.6	3
334	Experimental Evolution of Yeast for High-Temperature Tolerance. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1823-1839	8.3	29
333	Multiple Regulatory Modules Are Required for Scale-to-Feather Conversion. <i>Molecular Biology and Evolution</i> , 2018 , 35, 417-430	8.3	26
332	Engineering the oleaginous red yeast <i>Rhodotorula glutinis</i> for simultaneous β -carotene and cellulase production. <i>Scientific Reports</i> , 2018 , 8, 10850	4.9	23
331	Genome-wide prediction of CRISPR/Cas9 targets in <i>Kluyveromyces marxianus</i> and its application to obtain a stable haploid strain. <i>Scientific Reports</i> , 2018 , 8, 7305	4.9	14
330	Constructing a cellulosic yeast host with an efficient cellulase cocktail. <i>Biotechnology and Bioengineering</i> , 2018 , 115, 751-761	4.9	9
329	Genetic and Molecular Basis of Feather Diversity in Birds. <i>Genome Biology and Evolution</i> , 2018 , 10, 2572-2586	3.9	17
328	Identification and evolutionary analysis of long non-coding RNAs in zebra finch. <i>BMC Genomics</i> , 2017 , 18, 117	4.5	10
327	Predicting Transcription Factor Binding Sites and Their Cognate Transcription Factors Using Gene Expression Data. <i>Methods in Molecular Biology</i> , 2017 , 1629, 271-282	1.4	3
326	Metabolic engineering a yeast to produce astaxanthin. <i>Bioresource Technology</i> , 2017 , 245, 899-905	11	36
325	Elevated auxin biosynthesis and transport underlie high vein density in <i>C</i> leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6884-E6891	11.5	18
324	The rises and falls of opsin genes in 59 ray-finned fish genomes and their implications for environmental adaptation. <i>Scientific Reports</i> , 2017 , 7, 15568	4.9	42
323	Genomic signatures for the origin, adaptation and diversification of mangroves. <i>National Science Review</i> , 2017 , 4, 735-736	10.8	
322	Regulatory Divergence among Beta-Keratin Genes during Bird Evolution. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2769-2780	8.3	8
321	Large numbers of vertebrates began rapid population decline in the late 19th century. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 14079-14084	11.5	33
320	Positional distribution of transcription factor binding sites in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2016 , 6, 25164	4.9	56
319	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016 , 6, 35076	4.9	6

318	Insights into the regulation of C4 leaf development from comparative transcriptomic analysis. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 1-10	9.9	8
317	Integrating RNA-seq and ChIP-seq data to characterize long non-coding RNAs in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2016 , 17, 220	4.5	14
316	Regulatory Differences in Natal Down Development between Altricial Zebra Finch and Precocial Chicken. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2030-43	8.3	10
315	Transcriptome dynamics of developing maize leaves and genomewide prediction of cis elements and their cognate transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2477-86	11.5	53
314	Gains and Losses of Transcription Factor Binding Sites in <i>Saccharomyces cerevisiae</i> and <i>Saccharomyces paradoxus</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 2245-57	3.9	2
313	Topographical mapping of β and β keratins on developing chicken skin integuments: Functional interaction and evolutionary perspectives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6770-9	11.5	53
312	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6496-505	11.5	236
311	Integrating an algal β carotene hydroxylase gene into a designed carotenoid-biosynthesis pathway increases carotenoid production in yeast. <i>Bioresource Technology</i> , 2015 , 184, 2-8	11	44
310	Uncovering MicroRNA Regulatory Hubs that Modulate Plasma Cell Differentiation. <i>Scientific Reports</i> , 2015 , 5, 17957	4.9	13
309	Transcriptomic analyses of regenerating adult feathers in chicken. <i>BMC Genomics</i> , 2015 , 16, 756	4.5	24
308	Dynamic association rules for gene expression data analysis. <i>BMC Genomics</i> , 2015 , 16, 786	4.5	13
307	Expression Divergence of Chemosensory Genes between <i>Drosophila sechellia</i> and Its Sibling Species and Its Implications for Host Shift. <i>Genome Biology and Evolution</i> , 2015 , 7, 2843-58	3.9	34
306	Down-Regulation of Cytokinin Oxidase 2 Expression Increases Tiller Number and Improves Rice Yield. <i>Rice</i> , 2015 , 8, 36	5.8	77
305	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. <i>PLoS Computational Biology</i> , 2015 , 11, e1004497	5	57
304	MicroRNA-like small RNAs prediction in the development of <i>Antrodia cinnamomea</i> . <i>PLoS ONE</i> , 2015 , 10, e0123245	3.7	21
303	Genomic and transcriptomic analyses of the medicinal fungus <i>Antrodia cinnamomea</i> for its metabolite biosynthesis and sexual development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4743-52	11.5	55
302	Studying tumorigenesis through network evolution and somatic mutational perturbations in the cancer interactome. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2156-69	8.3	68
301	Functional evolution of cardiac microRNAs in heart development and functions. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2722-34	8.3	17

300	A thermo- and toxin-tolerant kefir yeast for biorefinery and biofuel production. <i>Applied Energy</i> , 2014 , 132, 465-474	10.7	14
299	The genome and occlusion bodies of marine <i>Penaeus monodon</i> nudivirus (PmNV, also known as MBV and PemoNPV) suggest that it should be assigned to a new nudivirus genus that is distinct from the terrestrial nudiviruses. <i>BMC Genomics</i> , 2014 , 15, 628	4.5	32
298	Genomic organization, transcriptomic analysis, and functional characterization of avian β and β keratins in diverse feather forms. <i>Genome Biology and Evolution</i> , 2014 , 6, 2258-73	3.9	44
297	Maize and millet transcription factors annotated using comparative genomic and transcriptomic data. <i>BMC Genomics</i> , 2014 , 15, 818	4.5	16
296	The prognostic significance of RUNX2 and miR-10a/10b and their inter-relationship in breast cancer. <i>Journal of Translational Medicine</i> , 2014 , 12, 257	8.5	37
295	Comparative Genomics and Evolutionary Genetics of Yeast Carbon Metabolism 2014 , 97-120		
294	Assembling a cellulase cocktail and a cellodextrin transporter into a yeast host for CBP ethanol production. <i>Biotechnology for Biofuels</i> , 2013 , 6, 19	7.8	62
293	Anatomical and transcriptional dynamics of maize embryonic leaves during seed germination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 3979-84	11.5	59
292	Assembler for de novo assembly of large genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E3417-24	11.5	24
291	Systematic screening of glycosylation- and trafficking-associated gene knockouts in <i>Saccharomyces cerevisiae</i> identifies mutants with improved heterologous exocellulase activity and host secretion. <i>BMC Biotechnology</i> , 2013 , 13, 71	3.5	25
290	Transcriptional profiling of adult <i>Drosophila</i> antennae by high-throughput sequencing. <i>Zoological Studies</i> , 2013 , 52, 42	0.6	19
289	Historical profiling of maize duplicate genes sheds light on the evolution of C4 photosynthesis in grasses. <i>Molecular Phylogenetics and Evolution</i> , 2013 , 66, 453-62	4.1	2
288	Establishment of the metabolite profile for an <i>Antrodia cinnamomea</i> health food product and investigation of its chemoprevention activity. <i>Journal of Agricultural and Food Chemistry</i> , 2013 , 61, 8556-64	5.7	23
287	Predicting the probability of H3K4me3 occupation at a base pair from the genome sequence context. <i>Bioinformatics</i> , 2013 , 29, 1199-205	7.2	5
286	Identifying cis-regulatory changes involved in the evolution of aerobic fermentation in yeasts. <i>Genome Biology and Evolution</i> , 2013 , 5, 1065-78	3.9	11
285	Inheritance of gene expression level and selective constraints on trans- and cis-regulatory changes in yeast. <i>Molecular Biology and Evolution</i> , 2013 , 30, 2121-33	8.3	51
284	Genome-wide patterns of genetic variation in two domestic chickens. <i>Genome Biology and Evolution</i> , 2013 , 5, 1376-92	3.9	49
283	A highly efficient β glucosidase from the buffalo rumen fungus <i>Neocallimastix patriciarum</i> W5. <i>Biotechnology for Biofuels</i> , 2012 , 5, 24	7.8	51

282	PGASO: A synthetic biology tool for engineering a cellulolytic yeast. <i>Biotechnology for Biofuels</i> , 2012 , 5, 53	7.8	35
281	Development of cellulosic ethanol production process via co-culturing of artificial cellulosomal Bacillus and kefir yeast. <i>Applied Energy</i> , 2012 , 100, 27-32	10.7	19
280	DNA replication timing and selection shape the landscape of nucleotide variation in cancer genomes. <i>Nature Communications</i> , 2012 , 3, 1004	17.4	91
279	MicroRNA 3' end nucleotide modification patterns and arm selection preference in liver tissues. <i>BMC Systems Biology</i> , 2012 , 6 Suppl 2, S14	3.5	29
278	The chicken frizzle feather is due to an Ekeratin (KRT75) mutation that causes a defective rachis. <i>PLoS Genetics</i> , 2012 , 8, e1002748	6	70
277	Revealing the anti-tumor effect of artificial miRNA p-27-5p on human breast carcinoma cell line T-47D. <i>International Journal of Molecular Sciences</i> , 2012 , 13, 6352-69	6.3	4
276	Transcriptomes of mouse olfactory epithelium reveal sexual differences in odorant detection. <i>Genome Biology and Evolution</i> , 2012 , 4, 703-12	3.9	34
275	Evolution of 5' untranslated region length and gene expression reprogramming in yeasts. <i>Molecular Biology and Evolution</i> , 2012 , 29, 81-9	8.3	40
274	PSC: protein surface classification. <i>Nucleic Acids Research</i> , 2012 , 40, W435-9	20.1	4
273	Evolutionary conservation of histone modifications in mammals. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1757-67	8.3	37
272	Classification of protein functional surfaces using structural characteristics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1170-5	11.5	21
271	Characterizing regulatory and functional differentiation between maize mesophyll and bundle sheath cells by transcriptomic analysis. <i>Plant Physiology</i> , 2012 , 160, 165-77	6.6	111
270	Contribution of transcription factor binding site motif variants to condition-specific gene expression patterns in budding yeast. <i>PLoS ONE</i> , 2012 , 7, e32274	3.7	
269	Antroquinonol from ethanolic extract of mycelium of <i>Antrodia cinnamomea</i> protects hepatic cells from ethanol-induced oxidative stress through Nrf-2 activation. <i>Journal of Ethnopharmacology</i> , 2011 , 136, 168-77	5	77
268	Gene clustering pattern, promoter architecture, and gene expression stability in eukaryotic genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3306-11	11.5	29
267	Functional characterization of cellulases identified from the cow rumen fungus <i>Neocallimastix patriciarum</i> W5 by transcriptomic and secretomic analyses. <i>Biotechnology for Biofuels</i> , 2011 , 4, 24	7.8	51
266	Metabolite profiles for <i>Antrodia cinnamomea</i> fruiting bodies harvested at different culture ages and from different wood substrates. <i>Journal of Agricultural and Food Chemistry</i> , 2011 , 59, 7626-35	5.7	31
265	Mixed culture fermentation from lignocellulosic materials using thermophilic lignocellulose-degrading anaerobes. <i>Process Biochemistry</i> , 2011 , 46, 489-493	4.8	48

264	Expansion of hexose transporter genes was associated with the evolution of aerobic fermentation in yeasts. <i>Molecular Biology and Evolution</i> , 2011 , 28, 131-42	8.3	60
263	Coordinated histone modifications are associated with gene expression variation within and between species. <i>Genome Research</i> , 2011 , 21, 590-8	9.7	126
262	The relationships among microRNA regulation, intrinsically disordered regions, and other indicators of protein evolutionary rate. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2513-20	8.3	25
261	A simple method using Pyrosequencing™ to identify de novo SNPs in pooled DNA samples. <i>Nucleic Acids Research</i> , 2011 , 39, e28	20.1	6
260	Functional compensation of primary and secondary metabolites by duplicate genes in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2011 , 28, 377-82	8.3	51
259	Genetically distinct coelacanth population off the northern Tanzanian coast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 18009-13	11.5	15
258	Evolutionary approach to predicting the binding site residues of a protein from its primary sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5313-8	11.5	9
257	Signalling pathway for RKIP and Let-7 regulates and predicts metastatic breast cancer. <i>EMBO Journal</i> , 2011 , 30, 4500-14	13	143
256	The evolution of aerobic fermentation in <i>Schizosaccharomyces pombe</i> was associated with regulatory reprogramming but not nucleosome reorganization. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1407-13	8.3	9
255	The genetic basis of evolutionary change in gene expression levels. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 2581-90	5.8	47
254	Adverse interactions between micro-RNAs and target genes from different species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 12935-40	11.5	29
253	Phosphorylated and nonphosphorylated serine and threonine residues evolve at different rates in mammals. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2548-54	8.3	29
252	fPOP: footprinting functional pockets of proteins by comparative spatial patterns. <i>Nucleic Acids Research</i> , 2010 , 38, D288-95	20.1	20
251	Gene family size conservation is a good indicator of evolutionary rates. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1750-8	8.3	23
250	Natural selection on cis and trans regulation in yeasts. <i>Genome Research</i> , 2010 , 20, 826-36	9.7	114
249	Omics Applications to Biofuel Research 2010 , 265-276		6
248	The spatial distribution of cis regulatory elements in yeast promoters and its implications for transcriptional regulation. <i>BMC Genomics</i> , 2010 , 11, 581	4.5	36
247	A novel puf-A gene predicted from evolutionary analysis is involved in the development of eyes and primordial germ-cells. <i>PLoS ONE</i> , 2009 , 4, e4980	3.7	28

246	SplitPocket: identification of protein functional surfaces and characterization of their spatial patterns. <i>Nucleic Acids Research</i> , 2009 , 37, W384-9	20.1	29
245	Uncovering small RNA-mediated responses to phosphate deficiency in Arabidopsis by deep sequencing. <i>Plant Physiology</i> , 2009 , 151, 2120-32	6.6	520
244	Parallel Evolution between Aromatase and Androgen Receptor in the Animal Kingdom. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1191-1191	8.3	78
243	Evolutionary persistence of functional compensation by duplicate genes in Arabidopsis. <i>Genome Biology and Evolution</i> , 2009 , 1, 409-14	3.9	56
242	Roles of trans and cis variation in yeast intraspecies evolution of gene expression. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2533-8	8.3	30
241	Parallel evolution between aromatase and androgen receptor in the animal kingdom. <i>Molecular Biology and Evolution</i> , 2009 , 26, 123-9	8.3	13
240	Lowly expressed human microRNA genes evolve rapidly. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1195-8	8.3	79
239	Functional compensation by duplicated genes in mouse. <i>Trends in Genetics</i> , 2009 , 25, 441-2	8.5	19
238	Sulfate activation enzymes: phylogeny and association with pyrophosphatase. <i>Journal of Molecular Evolution</i> , 2009 , 68, 1-13	3.1	21
237	Identification of protein functional surfaces by the concept of a split pocket. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 959-76	4.2	20
236	Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009 , 22, 2430-7	4.7	17
235	Increasing MicroRNA target prediction confidence by the relative R(2) method. <i>Journal of Theoretical Biology</i> , 2009 , 259, 793-8	2.3	21
234	Multidimensional scaling for large genomic data sets. <i>BMC Bioinformatics</i> , 2008 , 9, 179	3.6	69
233	Systematic identification of yeast cell cycle transcription factors using multiple data sources. <i>BMC Bioinformatics</i> , 2008 , 9, 522	3.6	36
232	Overlapping genes in the human and mouse genomes. <i>BMC Genomics</i> , 2008 , 9, 169	4.5	45
231	Identifying gene regulatory modules of heat shock response in yeast. <i>BMC Genomics</i> , 2008 , 9, 439	4.5	39
230	Whole genome transcriptome polymorphisms in Arabidopsis thaliana. <i>Genome Biology</i> , 2008 , 9, R165	18.3	26
229	CpG island density and its correlations with genomic features in mammalian genomes. <i>Genome Biology</i> , 2008 , 9, R79	18.3	91

228	Roles of cis- and trans-changes in the regulatory evolution of genes in the gluconeogenic pathway in yeast. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1863-75	8.3	12
227	Discovering gapped binding sites of yeast transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 2527-32	11.5	19
226	Prediction of human miRNAs using tissue-selective motifs in 3QTRs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17061-6	11.5	12
225	Gene number expansion and contraction in vertebrate genomes with respect to invertebrate genomes. <i>Genome Research</i> , 2008 , 18, 221-32	9.7	29
224	RNA landscape of evolution for optimal exon and intron discrimination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 5797-802	11.5	86
223	Fast evolution of core promoters in primate genomes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1239-44	8.3	13
222	Protein under-wrapping causes dosage sensitivity and decreases gene duplicability. <i>PLoS Genetics</i> , 2008 , 4, e11	6	45
221	Reconstructing a network of stress-response regulators via dynamic system modeling of gene regulation. <i>Gene Regulation and Systems Biology</i> , 2008 , 2, 53-62	2	2
220	Improved variance estimators for one- and two-parameter models of nucleotide substitution. <i>Journal of Theoretical Biology</i> , 2008 , 254, 164-7	2.3	5
219	On the robust circuit design schemes of biochemical networks: steady-state approach. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2007 , 1, 91-104	5.1	29
218	Identifying regulatory targets of cell cycle transcription factors using gene expression and CHIP-chip data. <i>BMC Bioinformatics</i> , 2007 , 8, 188	3.6	29
217	A systematic approach to detecting transcription factors in response to environmental stresses. <i>BMC Bioinformatics</i> , 2007 , 8, 473	3.6	12
216	External factors accelerate expression divergence between duplicate genes. <i>Trends in Genetics</i> , 2007 , 23, 162-6	8.5	52
215	Gene essentiality, gene duplicability and protein connectivity in human and mouse. <i>Trends in Genetics</i> , 2007 , 23, 375-8	8.5	95
214	Mathematical properties of some measures of evolutionary distance. <i>Journal of Theoretical Biology</i> , 2007 , 245, 790-2	2.3	
213	Human-specific insertions and deletions inferred from mammalian genome sequences. <i>Genome Research</i> , 2007 , 17, 16-22	9.7	51
212	Expression evolution in yeast genes of single-input modules is mainly due to changes in trans-acting factors. <i>Genome Research</i> , 2007 , 17, 1161-9	9.7	39
211	Simultaneous amino acid substitutions at antigenic sites drive influenza A hemagglutinin evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 6283-8	11.5	170

210	Human polymorphism at microRNAs and microRNA target sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3300-5	11.5	562
209	Features and trend of loss of promoter-associated CpG islands in the human and mouse genomes. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1991-2000	8.3	40
208	The nonsynonymous/synonymous substitution rate ratio versus the radical/conservative replacement rate ratio in the evolution of mammalian genes. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2235-41	8.3	58
207	Proportion of solvent-exposed amino acids in a protein and rate of protein evolution. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1005-11	8.3	73
206	MicroRNA regulation of human protein protein interaction network. <i>Rna</i> , 2007 , 13, 1402-8	5.8	134
205	MYBS: a comprehensive web server for mining transcription factor binding sites in yeast. <i>Nucleic Acids Research</i> , 2007 , 35, W221-6	20.1	26
204	A large number of novel coding small open reading frames in the intergenic regions of the <i>Arabidopsis thaliana</i> genome are transcribed and/or under purifying selection. <i>Genome Research</i> , 2007 , 17, 632-40	9.7	120
203	Human TRIM71 and its nematode homologue are targets of let-7 microRNA and its zebrafish orthologue is essential for development. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2525-34	8.3	66
202	On the Adaptive Design Rules of Biochemical Networks in Evolution. <i>Evolutionary Bioinformatics</i> , 2007 , 3, 117693430700300	1.9	11
201	Protein complexity, gene duplicability and gene dispensability in the yeast genome. <i>Gene</i> , 2007 , 387, 109-17	3.8	12
200	Patterns of internal gene duplication in the course of metazoan evolution. <i>Gene</i> , 2007 , 396, 59-65	3.8	7
199	On the adaptive design rules of biochemical networks in evolution. <i>Evolutionary Bioinformatics</i> , 2007 , 3, 27-39	1.9	5
198	Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. <i>BMC Bioinformatics</i> , 2006 , 7, 421	3.6	47
197	Reorganization of adjacent gene relationships in yeast genomes by whole-genome duplication and gene deletion. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1136-43	8.3	31
196	Alternatively and constitutively spliced exons are subject to different evolutionary forces. <i>Molecular Biology and Evolution</i> , 2006 , 23, 675-82	8.3	50
195	Protein function, connectivity, and duplicability in yeast. <i>Molecular Biology and Evolution</i> , 2006 , 23, 30-9	8.3	69
194	Role of positive selection in the retention of duplicate genes in mammalian genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 2232-6	11.5	70
193	Method for identifying transcription factor binding sites in yeast. <i>Bioinformatics</i> , 2006 , 22, 1675-81	7.2	21

192	Codon-usage bias versus gene conversion in the evolution of yeast duplicate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14412-6	11.5	29
191	Nucleotide variation and haplotype diversity in a 10-kb noncoding region in three continental human populations. <i>Genetics</i> , 2006 , 174, 399-409	4	23
190	Patterns of expansion and expression divergence in the plant polygalacturonase gene family. <i>Genome Biology</i> , 2006 , 7, R87	18.3	102
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6	Probability of identical monomorphism in related species. <i>Genetical Research</i> , 1975 , 26, 31-43	1.1	35
5	Drift variances of heterozygosity and genetic distance in transient states. <i>Genetical Research</i> , 1975 , 25, 229-48	1.1	76
4	Total number of individuals affected by deleterious mutant genes in a finite population. <i>Annals of Human Genetics</i> , 1975 , 38, 333-40	2.2	4
3	Stable linkage disequilibrium without epistasis in subdivided populations. <i>Theoretical Population Biology</i> , 1974 , 6, 173-83	1.2	92
2	Linkage disequilibrium in subdivided populations. <i>Genetics</i> , 1973 , 75, 213-9	4	213
1	Computational Reconstruction of Transcriptional Regulatory Modules of the Yeast Cell Cycle331-354		0