List of Publications by Year in descending order

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ΙΙΛΝΖΗΙ ΖΗΛΝΟ

#	Article	IF	CITATIONS
1	Evaluation of an Improved Branch-Site Likelihood Method for Detecting Positive Selection at the Molecular Level. Molecular Biology and Evolution, 2005, 22, 2472-2479.	8.9	1,650
2	Why Do Hubs Tend to Be Essential in Protein Networks?. PLoS Genetics, 2006, 2, e88.	3.5	634
3	The pleiotropic structure of the genotype–phenotype map: the evolvability of complex organisms. Nature Reviews Genetics, 2011, 12, 204-213.	16.3	577
4	Determinants of the rate of protein sequence evolution. Nature Reviews Genetics, 2015, 16, 409-420.	16.3	294
5	Rates of Conservative and Radical Nonsynonymous Nucleotide Substitutions in Mammalian Nuclear Genes. Journal of Molecular Evolution, 2000, 50, 56-68.	1.8	274
6	Balanced Codon Usage Optimizes Eukaryotic Translational Efficiency. PLoS Genetics, 2012, 8, e1002603.	3.5	263
7	Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. Journal of Molecular Evolution, 1997, 44, S139-S146.	1.8	256
8	Evolutionary deterioration of the vomeronasal pheromone transduction pathway in catarrhine primates. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8337-8341.	7.1	240
9	Genomic patterns of pleiotropy and the evolution of complexity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18034-18039.	7.1	218
10	Null mutations in human and mouse orthologs frequently result in different phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6987-6992.	7.1	217
11	Accelerated Protein Evolution and Origins of Human-Specific Features: FOXP2 as an Example. Genetics, 2002, 162, 1825-1835.	2.9	217
12	Parallel adaptive origins of digestive RNases in Asian and African leaf monkeys. Nature Genetics, 2006, 38, 819-823.	21.4	189
13	Evolution of the Human <i>ASPM</i> Gene, a Major Determinant of Brain Size. Genetics, 2003, 165, 2063-2070.	2.9	184
14	Toward a Molecular Understanding of Pleiotropy. Genetics, 2006, 173, 1885-1891.	2.9	182
15	The hearing gene Prestin unites echolocating bats and whales. Current Biology, 2010, 20, R55-R56.	3.9	178
16	Impact of gene expression noise on organismal fitness and the efficacy of natural selection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E67-76.	7.1	177
17	The Genomic Landscape and Evolutionary Resolution of Antagonistic Pleiotropy in Yeast. Cell Reports, 2012, 2, 1399-1410.	6.4	177
18	Rapid evolution of primate antiviral enzyme APOBEC3G. Human Molecular Genetics, 2004, 13, 1785-1791.	2.9	170

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19	The fitness landscape of a tRNA gene. Science, 2016, 352, 837-840.	12.6	168
20	Protein misinteraction avoidance causes highly expressed proteins to evolve slowly. Proceedings of the United States of America, 2012, 109, E831-40.	7.1	160
21	Synonymous mutations in representative yeast genes are mostly strongly non-neutral. Nature, 2022, 606, 725-731.	27.8	157
22	Frequent False Detection of Positive Selection by the Likelihood Method with Branch-Site Models. Molecular Biology and Evolution, 2004, 21, 1332-1339.	8.9	155
23	Prevalent positive epistasis in Escherichia coli and Saccharomyces cerevisiae metabolic networks. Nature Genetics, 2010, 42, 272-276.	21.4	134
24	Human coding RNA editing is generally nonadaptive. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3769-3774.	7.1	128
25	Are Convergent and Parallel Amino Acid Substitutions in Protein Evolution More Prevalent Than Neutral Expectations?. Molecular Biology and Evolution, 2015, 32, 2085-2096.	8.9	124
26	Significant Impact of Protein Dispensability on the Instantaneous Rate of Protein Evolution. Molecular Biology and Evolution, 2005, 22, 1147-1155.	8.9	114
27	Positive selection for elevated gene expression noise in yeast. Molecular Systems Biology, 2009, 5, 299.	7.2	112
28	Genomic evidence for adaptation by gene duplication. Genome Research, 2014, 24, 1356-1362.	5.5	107
29	Phylostratigraphic Bias Creates Spurious Patterns of Genome Evolution. Molecular Biology and Evolution, 2015, 32, 258-267.	8.9	107
30	Codon-by-Codon Modulation of Translational Speed and Accuracy Via mRNA Folding. PLoS Biology, 2014, 12, e1001910.	5.6	101
31	Evolutionary adaptations to new environments generally reverse plastic phenotypic changes. Nature Communications, 2018, 9, 350.	12.8	96
32	No Genome-Wide Protein Sequence Convergence for Echolocation. Molecular Biology and Evolution, 2015, 32, 1237-1241.	8.9	94
33	Human RNase 7: a new cationic ribonuclease of the RNase A superfamily. Nucleic Acids Research, 2003, 31, 602-607.	14.5	83
34	Evaluating Phylostratigraphic Evidence for Widespread De Novo Gene Birth in Genome Evolution. Molecular Biology and Evolution, 2016, 33, 1245-1256.	8.9	83
35	Yeast Spontaneous Mutation Rate and Spectrum Vary with Environment. Current Biology, 2019, 29, 1584-1591.e3.	3.9	82
36	Dissimilation of synonymous codon usage bias in virus–host coevolution due to translational selection. Nature Ecology and Evolution, 2020, 4, 589-600.	7.8	79

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37	The Genomic Landscape of Position Effects on Protein Expression Level and Noise in Yeast. Cell Systems, 2016, 2, 347-354.	6.2	78
38	Abundant Indispensable Redundancies in Cellular Metabolic Networks. Genome Biology and Evolution, 2009, 1, 23-33.	2.5	72
39	Why Is the Correlation between Gene Importance and Gene Evolutionary Rate So Weak?. PLoS Genetics, 2009, 5, e1000329.	3.5	64
40	Multi-environment fitness landscapes of a tRNA gene. Nature Ecology and Evolution, 2018, 2, 1025-1032.	7.8	62
41	Stop-codon read-through arises largely from molecular errors and is generally nonadaptive. PLoS Genetics, 2019, 15, e1008141.	3.5	59
42	Human C-to-U Coding RNA Editing Is Largely Nonadaptive. Molecular Biology and Evolution, 2018, 35, 963-969.	8.9	56
43	Morphological and molecular convergences in mammalian phylogenetics. Nature Communications, 2016, 7, 12758.	12.8	55
44	Testing the Chromosomal Speciation Hypothesis for Humans and Chimpanzees. Genome Research, 2004, 14, 845-851.	5.5	52
45	Is Phylotranscriptomics as Reliable as Phylogenomics?. Molecular Biology and Evolution, 2020, 37, 3672-3683.	8.9	52
46	Genetic Redundancies and Their Evolutionary Maintenance. Advances in Experimental Medicine and Biology, 2012, 751, 279-300.	1.6	51
47	Molecular evidence for the loss of three basic tastes in penguins. Current Biology, 2015, 25, R141-R142.	3.9	51
48	Measuring the evolutionary rate of protein–protein interaction. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8725-8730.	7.1	50
49	Are Human Translated Pseudogenes Functional?. Molecular Biology and Evolution, 2016, 33, 755-760.	8.9	48
50	Idiosyncratic epistasis creates universals in mutational effects and evolutionary trajectories. Nature Ecology and Evolution, 2020, 4, 1685-1693.	7.8	48
51	Mammalian circular RNAs result largely from splicing errors. Cell Reports, 2021, 36, 109439.	6.4	48
52	Parallel Functional Changes in the Digestive RNases of Ruminants and Colobines by Divergent Amino Acid Substitutions. Molecular Biology and Evolution, 2003, 20, 1310-1317.	8.9	47
53	Further Simulations and Analyses Demonstrate Open Problems of Phylostratigraphy. Genome Biology and Evolution, 2017, 9, 1519-1527.	2.5	47
54	No X-Chromosome Dosage Compensation in Human Proteomes. Molecular Biology and Evolution, 2015, 32, 1456-1460.	8.9	46

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55	Evidence that alternative transcriptional initiation is largely nonadaptive. PLoS Biology, 2019, 17, e3000197.	5.6	46
56	Antagonistic pleiotropy conceals molecular adaptations in changing environments. Nature Ecology and Evolution, 2020, 4, 461-469.	7.8	46
57	He et al. reply. Nature Genetics, 2011, 43, 1171-1172.	21.4	45
58	Correlation Between the Substitution Rate and Rate Variation Among Sites in Protein Evolution. Genetics, 1998, 149, 1615-1625.	2.9	44
59	Most m6A RNA Modifications in Protein-Coding Regions Are Evolutionarily Unconserved and Likely Nonfunctional. Molecular Biology and Evolution, 2018, 35, 666-675.	8.9	43
60	Deciphering the Genic Basis of Yeast Fitness Variation by Simultaneous Forward and Reverse Genetics. Molecular Biology and Evolution, 2017, 34, 2486-2502.	8.9	42
61	Evolution of DMY, a Newly Emergent Male Sex-Determination Gene of Medaka Fish. Genetics, 2004, 166, 1887-1895.	2.9	41
62	Coexpression of Linked Genes in Mammalian Genomes Is Generally Disadvantageous. Molecular Biology and Evolution, 2008, 25, 1555-1565.	8.9	40
63	Testing the neutral hypothesis of phenotypic evolution. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12219-12224.	7.1	38
64	Neutral Theory and Phenotypic Evolution. Molecular Biology and Evolution, 2018, 35, 1327-1331.	8.9	38
65	Alternative Polyadenylation of Mammalian Transcripts Is Generally Deleterious, Not Adaptive. Cell Systems, 2018, 6, 734-742.e4.	6.2	38
66	The preponderance of nonsynonymous A-to-I RNA editing in coleoids is nonadaptive. Nature Communications, 2019, 10, 5411.	12.8	38
67	The Genotype–Phenotype Map of Yeast Complex Traits: Basic Parameters and the Role of Natural Selection. Molecular Biology and Evolution, 2014, 31, 1568-1580.	8.9	36
68	Patterns and Mechanisms of Diminishing Returns from Beneficial Mutations. Molecular Biology and Evolution, 2019, 36, 1008-1021.	8.9	36
69	Disulfide-Bond Reshuffling in the Evolution of an Ape Placental Ribonuclease. Molecular Biology and Evolution, 2007, 24, 505-512.	8.9	33
70	Human Long Noncoding RNAs Are Substantially Less Folded than Messenger RNAs. Molecular Biology and Evolution, 2015, 32, 970-977.	8.9	32
71	Adaptive Genetic Robustness of <i>Escherichia coli</i> Metabolic Fluxes. Molecular Biology and Evolution, 2016, 33, 1164-1176.	8.9	32
72	Genetic Gene Expression Changes during Environmental Adaptations Tend to Reverse Plastic Changes Even after the Correction for Statistical Nonindependence. Molecular Biology and Evolution, 2019, 36, 604-612.	8.9	32

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73	Deep Residual Neural Networks Resolve Quartet Molecular Phylogenies. Molecular Biology and Evolution, 2020, 37, 1495-1507.	8.9	32
74	The optimal mating distance resulting from heterosis and genetic incompatibility. Science Advances, 2018, 4, eaau5518.	10.3	30
75	Intra and Interspecific Variations of Gene Expression Levels in Yeast Are Largely Neutral: (Nei Lecture,) Tj ETQq1 1	0,784314 8.9	1 rgBT /Overl
76	Genome-Wide Evolutionary Conservation of N-Glycosylation Sites. Molecular Biology and Evolution, 2011, 28, 2351-2357.	8.9	27
77	In Search of Beneficial Coding RNA Editing. Molecular Biology and Evolution, 2015, 32, 536-541.	8.9	26
78	EVOLUTION:Molecular Origin of Species. , 1998, 282, 1428-1429.		25
79	Why Are Genes Encoded on the Lagging Strand of the Bacterial Genome?. Genome Biology and Evolution, 2013, 5, 2436-2439.	2.5	25
80	Evolution of the Yeast Recombination Landscape. Molecular Biology and Evolution, 2019, 36, 412-422.	8.9	24
81	Phenotypic plasticity as a long-term memory easing readaptations to ancestral environments. Science Advances, 2020, 6, eaba3388.	10.3	24
82	On the Evolution of Codon Volatility. Genetics, 2005, 169, 495-501.	2.9	23
83	Yeast mutation accumulation experiment supports elevated mutation rates at highly transcribed sites. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4062.	7.1	23
84	Why Human Disease-Associated Residues Appear as the Wild-Type in Other Species: Genome-Scale Structural Evidence for the Compensation Hypothesis. Molecular Biology and Evolution, 2014, 31, 1787-1792.	8.9	23
85	A Simple Method for Estimating the Strength of Natural Selection on Overlapping Genes. Genome Biology and Evolution, 2015, 7, 381-390.	2.5	23
86	Allele-specific single-cell RNA sequencing reveals different architectures of intrinsic and extrinsic gene expression noises. Nucleic Acids Research, 2020, 48, 533-547.	14.5	23
87	Population Genomic Analysis Reveals Contrasting Demographic Changes of Two Closely Related Dolphin Species in the Last Glacial. Molecular Biology and Evolution, 2018, 35, 2026-2033.	8.9	22
88	Nascent RNA folding mitigates transcription-associated mutagenesis. Genome Research, 2016, 26, 50-59.	5.5	21
89	Toward Reducing Phylostratigraphic Errors and Biases. Genome Biology and Evolution, 2018, 10, 2037-2048.	2.5	20
90	Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. PLoS Genetics, 2019, 15, e1008389.	3.5	20

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91	Environment-dependent pleiotropic effects of mutations on the maximum growth rate r and carrying capacity K of population growth. PLoS Biology, 2019, 17, e3000121.	5.6	20
92	Universal pleiotropy is not a valid null hypothesis: reply to Hill and Zhang. Nature Reviews Genetics, 2012, 13, 296-296.	16.3	19
93	The Genomic Architecture of Interactions Between Natural Genetic Polymorphisms and Environments in Yeast Growth. Genetics, 2017, 205, 925-937.	2.9	19
94	Synchronization of stochastic expressions drives the clustering of functionally related genes. Science Advances, 2019, 5, eaax6525.	10.3	18
95	The rate and molecular spectrum of mutation are selectively maintained in yeast. Nature Communications, 2021, 12, 4044.	12.8	18
96	Why Phenotype Robustness Promotes Phenotype Evolvability. Genome Biology and Evolution, 2017, 9, 3509-3515.	2.5	15
97	The X to Autosome Expression Ratio in Haploid and Diploid Human Embryonic Stem Cells. Molecular Biology and Evolution, 2016, 33, 3104-3107.	8.9	14
98	A different perspective on alternative cleavage and polyadenylation. Nature Reviews Genetics, 2020, 21, 63-63.	16.3	14
99	Pseudogenization of the tumor-growth promoter angiogenin in a leaf-eating monkey. Gene, 2003, 308, 95-101.	2.2	13
100	Amino acid exchangeabilities vary across the tree of life. Science Advances, 2019, 5, eaax3124.	10.3	13
101	Mammalian Alternative Translation Initiation Is Mostly Nonadaptive. Molecular Biology and Evolution, 2020, 37, 2015-2028.	8.9	13
102	Fly wing evolution explained by a neutral model with mutational pleiotropy. Evolution; International Journal of Organic Evolution, 2020, 74, 2158-2167.	2.3	12
103	Are Nonsynonymous Transversions Generally More Deleterious than Nonsynonymous Transitions?. Molecular Biology and Evolution, 2021, 38, 181-191.	8.9	12
104	Evolution of DMY, a Newly Emergent Male Sex-Determination Gene of Medaka Fish. Genetics, 2004, 166, 1887-1895.	2.9	11
105	Gene Tree Discordance Does Not Explain Away the Temporal Decline of Convergence in Mammalian Protein Sequence Evolution. Molecular Biology and Evolution, 2017, 34, 1682-1688.	8.9	10
106	Retesting the influences of mutation accumulation and antagonistic pleiotropy on human senescence and disease. Nature Ecology and Evolution, 2019, 3, 992-993.	7.8	10
107	Higher Germline Mutagenesis of Genes with Stronger Testis Expressions Refutes the Transcriptional Scanning Hypothesis. Molecular Biology and Evolution, 2020, 37, 3225-3231.	8.9	10
108	Determinative Developmental Cell Lineages Are Robust to Cell Deaths. PLoS Genetics, 2014, 10, e1004501.	3.5	9

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109	Gene product diversity: adaptive or not?. Trends in Genetics, 2022, 38, 1112-1122.	6.7	9
110	Rampant False Detection of Adaptive Phenotypic Optimization by ParTI-Based Pareto Front Inference. Molecular Biology and Evolution, 2021, 38, 1653-1664.	8.9	8
111	Paleomolecular biology unravels the evolutionary mystery of vertebrate UV vision: Fig. 1 Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8045-8047.	7.1	7
112	Epistasis Analysis Goes Genome-Wide. PLoS Genetics, 2017, 13, e1006558.	3.5	7
113	Asexual Experimental Evolution of Yeast Does Not Curtail Transposable Elements. Molecular Biology and Evolution, 2021, 38, 2831-2842.	8.9	7
114	On the Origin of Frameshift-Robustness of the Standard Genetic Code. Molecular Biology and Evolution, 2021, 38, 4301-4309.	8.9	7
115	The drifting human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20147-20148.	7.1	7
116	The Coupon Collection Behavior in Human Reproduction. Current Biology, 2020, 30, 3856-3861.e1.	3.9	6
117	Natural selection contributes to the myopia epidemic. National Science Review, 2021, 8, .	9.5	6
118	Impact of structure space continuity on protein fold classification. Scientific Reports, 2016, 6, 23263.	3.3	5
119	Unbiased inference of the fitness landscape ruggedness from imprecise fitness estimates. Evolution; International Journal of Organic Evolution, 2021, 75, 2658-2671.	2.3	5
120	Transposon insertional mutagenesis of diverse yeast strains suggests coordinated gene essentiality polymorphisms. Nature Communications, 2022, 13, 1490.	12.8	5
121	Is the Genetic Code Optimized for Resource Conservation?. Molecular Biology and Evolution, 2021, 38, 5122-5126.	8.9	4
122	Testing the adaptive hypothesis of lagging-strand encoding in bacterial genomes. Nature Communications, 2022, 13, 2628.	12.8	4
123	Codon usage bias and nuclear mRNA concentration: Correlation vs. causation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	3
124	Parallel transcriptomic changes in the origins of divergent monogamous vertebrates?. Proceedings of the United States of America, 2019, 116, 17627-17628.	7.1	2
125	On the Origin of Compositional Features of Ribosomes. Genome Biology and Evolution, 2018, 10, 2010-2016.	2.5	1
126	Caution in testing phenotypic selection. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2022180118.	7.1	1

JIANZHI ZHANG

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127	Toward understanding the evolutionary histories and mechanisms of mangroves. National Science Review, 2017, 4, 737-737.	9.5	0
128	Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389.		0
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130	Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389.		0
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