

List of Publications by Year in descending order

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238
papers

20,929
citations

13827

67
h-index

12558

132
g-index

249
all docs

249
docs citations

249
times ranked

21179
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ka/Ks ratio: diagnosing the form of sequence evolution. Trends in Genetics, 2002, 18, 486-487.	2.9	939
2	Complete genomes of two clinical Staphylococcus aureus strains: Evidence for the rapid evolution of virulence and drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9786-9791.	3.3	830
3	Dosage sensitivity and the evolution of gene families in yeast. Nature, 2003, 424, 194-197.	13.7	757
4	Hearing silence: non-neutral evolution at synonymous sites in mammals. Nature Reviews Genetics, 2006, 7, 98-108.	7.7	740
5	The evolutionary dynamics of eukaryotic gene order. Nature Reviews Genetics, 2004, 5, 299-310.	7.7	661
6	Highly Expressed Genes in Yeast Evolve Slowly. Genetics, 2001, 158, 927-931.	1.2	556
7	Clustering of housekeeping genes provides a unified model of gene order in the human genome. Nature Genetics, 2002, 31, 180-183.	9.4	496
8	The Genetic Code Is One in a Million. Journal of Molecular Evolution, 1998, 47, 238-248.	0.8	466
9	Comparisons of dN/dS are time dependent for closely related bacterial genomes. Journal of Theoretical Biology, 2006, 239, 226-235.	0.8	400
10	The evolution of isochores. Nature Reviews Genetics, 2001, 2, 549-555.	7.7	379
11	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. Nature, 2014, 516, 405-409.	13.7	372
12	Recent advances in understanding of the evolution and maintenance of sex. Trends in Ecology and Evolution, 1996, 11, 46-52.	4.2	341
13	Human SNP variability and mutation rate are higher in regions of high recombination. Trends in Genetics, 2002, 18, 337-340.	2.9	326
14	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. Nature, 2004, 429, 661-664.	13.7	324
15	A quantitative measure of error minimization in the genetic code. Journal of Molecular Evolution, 1991, 33, 412-417.	0.8	296
16	Do essential genes evolve slowly?. Current Biology, 1999, 9, 747-750.	1.8	287
17	Genetic Conflicts. Quarterly Review of Biology, 1996, 71, 317-364.	0.0	286
18	Evidence for selection on synonymous mutations affecting stability of mRNA secondary structure in mammals. Genome Biology, 2005, 6, R75.	13.9	266

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19	Evolutionary and Physiological Importance of Hub Proteins. PLoS Computational Biology, 2006, 2, e88.	1.5	251
20	Positively Charged Residues Are the Major Determinants of Ribosomal Velocity. PLoS Biology, 2013, 11, e1001508.	2.6	250
21	The Signature of Selection Mediated by Expression on Human Genes. Genome Research, 2003, 13, 2260-2264.	2.4	227
22	Early Fixation of an Optimal Genetic Code. Molecular Biology and Evolution, 2000, 17, 511-518.	3.5	226
23	Chance and necessity in the evolution of minimal metabolic networks. Nature, 2006, 440, 667-670.	13.7	219
24	Predicting the virulence of MRSA from its genome sequence. Genome Research, 2014, 24, 839-849.	2.4	210
25	Evidence for Purifying Selection Against Synonymous Mutations in Mammalian Exonic Splicing Enhancers. Molecular Biology and Evolution, 2006, 23, 301-309.	3.5	209
26	Rate of evolution and gene dispensability. Nature, 2003, 421, 496-497.	13.7	205
27	Stratus Not Altocumulus: A New View of the Yeast Protein Interaction Network. PLoS Biology, 2006, 4, e317.	2.6	205
28	Distinct physiological and behavioural functions for parental alleles of imprinted Grb10. Nature, 2011, 469, 534-538.	13.7	204
29	Evolution of chromosome organization driven by selection for reduced gene expression noise. Nature Genetics, 2007, 39, 945-949.	9.4	202
30	Coexpression of Neighboring Genes in Caenorhabditis Elegans Is Mostly Due to Operons and Duplicate Genes. Genome Research, 2003, 13, 238-243.	2.4	194
31	Environmentally responsive genome-wide accumulation of de novo <i>Arabidopsis thaliana</i> mutations and epimutations. Genome Research, 2014, 24, 1821-1829.	2.4	194
32	Sex and Conflict. , 1998, 281, 2003-2008.		189
33	Open questions in the study of de novo genes: what, how and why. Nature Reviews Genetics, 2016, 17, 567-578.	7.7	179
34	High guanine-cytosine content is not an adaptation to high temperature: a comparative analysis amongst prokaryotes. Proceedings of the Royal Society B: Biological Sciences, 2001, 268, 493-497.	1.2	171
35	THE INCIDENCES. MECHANISMS AND EVOLUTION OF CYTOPLASMIC SEX RATIO DISTORTERS IN ANIMALS. Biological Reviews, 1993, 68, 121-194.	4.7	164
36	Sex biases in the mutation rate. Trends in Genetics, 1998, 14, 446-452.	2.9	160

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37	Parentâ€™ progeny sequencing indicates higher mutation rates in heterozygotes. <i>Nature</i> , 2015, 523, 463-467.	13.7	157
38	Evidence for a selectively favourable reduction in the mutation rate of the X chromosome. <i>Nature</i> , 1997, 386, 388-392.	13.7	144
39	Evidence for co-evolution of gene order and recombination rate. <i>Nature Genetics</i> , 2003, 33, 392-395.	9.4	143
40	Codon Usage Bias Covaries With Expression Breadth and the Rate of Synonymous Evolution in Humans, but This Is Not Evidence for Selection. <i>Genetics</i> , 2001, 159, 1191-1199.	1.2	135
41	Genome-wide analysis of coordinate expression and evolution of human encoded sense-antisense transcripts. <i>Trends in Genetics</i> , 2005, 21, 326-329.	2.9	133
42	Evolution of cis-regulatory elements in duplicated genes of yeast. <i>Trends in Genetics</i> , 2003, 19, 417-422.	2.9	127
43	Neighboring Genes Show Correlated Evolution in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1748-1766.	3.5	126
44	The evolution of cytoplasmic incompatibility or when spite can be successful. <i>Journal of Theoretical Biology</i> , 1991, 148, 269-277.	0.8	122
45	Natural selection promotes the conservation of linkage of co-expressed genes. <i>Trends in Genetics</i> , 2002, 18, 604-606.	2.9	122
46	A unification of mosaic structures in the human genome. <i>Human Molecular Genetics</i> , 2003, 12, 2411-2415.	1.4	119
47	Genes That Escape X-Inactivation in Humans Have High Intraspecific Variability in Expression, Are Associated with Mental Impairment but Are Not Slow Evolving. <i>Molecular Biology and Evolution</i> , 2013, 30, 2588-2601.	3.5	113
48	Evidence That the Human X Chromosome Is Enriched for Male-Specific but not Female-Specific Genes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1113-1116.	3.5	112
49	Metabolic trade-offs and the maintenance of the fittest and the flattest. <i>Nature</i> , 2011, 472, 342-346.	13.7	112
50	How do synonymous mutations affect fitness?. <i>BioEssays</i> , 2007, 29, 515-519.	1.2	107
51	Genetics and the understanding of selection. <i>Nature Reviews Genetics</i> , 2009, 10, 83-93.	7.7	107
52	Evidence against the selfish operon theory. <i>Trends in Genetics</i> , 2004, 20, 232-234.	2.9	106
53	A Mixture of â€™Cheatsâ€™ and â€™Co-Operatorsâ€™ Can Enable Maximal Group Benefit. <i>PLoS Biology</i> , 2010, 8, e1000486.	2.6	103
54	The proteins of linked genes evolve at similar rates. <i>Nature</i> , 2000, 407, 900-903.	13.7	100

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55	Exonic Splicing Regulatory Elements Skew Synonymous Codon Usage near Intron-exon Boundaries in Mammals. <i>Molecular Biology and Evolution</i> , 2007, 24, 1600-1603.	3.5	98
56	Direct and indirect consequences of meiotic recombination: implications for genome evolution. <i>Trends in Genetics</i> , 2012, 28, 101-109.	2.9	97
57	Splicing and the Evolution of Proteins in Mammals. <i>PLoS Biology</i> , 2007, 5, e14.	2.6	94
58	Still Stratus Not Altocumulus: Further Evidence against the Date/Party Hub Distinction. <i>PLoS Biology</i> , 2007, 5, e154.	2.6	94
59	Local Similarity in Evolutionary Rates Extends over Whole Chromosomes in Human-Rodent and Mouse-Rat Comparisons: Implications for Understanding the Mechanistic Basis of the Male Mutation Bias. <i>Molecular Biology and Evolution</i> , 2001, 18, 2032-2039.	3.5	93
60	Direct Determination of the Mutation Rate in the Bumblebee Reveals Evidence for Weak Recombination-Associated Mutation and an Approximate Rate Constancy in Insects. <i>Molecular Biology and Evolution</i> , 2017, 34, 119-130.	3.5	93
61	Growth effects of uniparental disomies and the conflict theory of genomic imprinting. <i>Trends in Genetics</i> , 1997, 13, 436-443.	2.9	92
62	The architecture of intra-organism mutation rate variation in plants. <i>PLoS Biology</i> , 2019, 17, e3000191.	2.6	89
63	Chromatin remodelling is a major source of coexpression of linked genes in yeast. <i>Trends in Genetics</i> , 2007, 23, 480-484.	2.9	87
64	Evidence for purifying selection acting on silent sites in BRCA1. <i>Trends in Genetics</i> , 2001, 17, 62-65.	2.9	85
65	Maternally-inherited Grb10 reduces placental size and efficiency. <i>Developmental Biology</i> , 2010, 337, 1-8.	0.9	85
66	Do we understand the evolution of genomic imprinting?. <i>Current Opinion in Genetics and Development</i> , 1998, 8, 701-708.	1.5	84
67	Similar Rates but Different Modes of Sequence Evolution in Introns and at Exonic Silent Sites in Rodents: Evidence for Selectively Driven Codon Usage. <i>Molecular Biology and Evolution</i> , 2004, 21, 1014-1023.	3.5	83
68	The Impact of the Nucleosome Code on Protein-Coding Sequence Evolution in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000250.	1.5	80
69	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. <i>Nucleic Acids Research</i> , 2005, 33, 5533-5543.	6.5	78
70	The evolution, impact and properties of exonic splice enhancers. <i>Genome Biology</i> , 2013, 14, R143.	13.9	77
71	Great majority of recombination events in <i>Arabidopsis</i> are gene conversion events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20992-20997.	3.3	69
72	Evidence for a Trade-Off between Translational Efficiency and Splicing Regulation in Determining Synonymous Codon Usage in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2755-2762.	3.5	68

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73	Evidence for Strong Mutation Bias toward, and Selection against, U Content in SARS-CoV-2: Implications for Vaccine Design. <i>Molecular Biology and Evolution</i> , 2021, 38, 67-83.	3.5	68
74	Noisy splicing, more than expression regulation, explains why some exons are subject to nonsense-mediated mRNA decay. <i>BMC Biology</i> , 2009, 7, 23.	1.7	67
75	Causes and consequences of crossing-over evidenced via a high-resolution recombinational landscape of the honey bee. <i>Genome Biology</i> , 2015, 16, 15.	3.8	67
76	Active and repressed biosynthetic gene clusters have spatially distinct chromosome states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13800-13809.	3.3	66
77	Biased codon usage near intron-exon junctions: selection on splicing enhancers, splice-site recognition or something else?. <i>Trends in Genetics</i> , 2005, 21, 256-259.	2.9	65
78	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <i>Genetics</i> , 2017, 206, 363-376.	1.2	65
79	Tetrad analysis in plants and fungi finds large differences in gene conversion rates but no GC bias. <i>Nature Ecology and Evolution</i> , 2018, 2, 164-173.	3.4	65
80	The uncertain evolution of the sexes. <i>Trends in Ecology and Evolution</i> , 2001, 16, 571-579.	4.2	64
81	Mutation rate analysis via parent-progeny sequencing of the perennial peach. I. A low rate in woody perennials and a higher mutagenicity in hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161016.	1.2	64
82	Covert sex. <i>Trends in Ecology and Evolution</i> , 1992, 7, 144-145.	4.2	63
83	Young intragenic miRNAs are less coexpressed with host genes than old ones: implications of miRNA-host gene coevolution. <i>Nucleic Acids Research</i> , 2012, 40, 4002-4012.	6.5	63
84	The form of a trade-off determines the response to competition. <i>Ecology Letters</i> , 2013, 16, 1267-1276.	3.0	63
85	Pluripotency and the endogenous retrovirus HERVH: Conflict or serendipity?. <i>BioEssays</i> , 2016, 38, 109-117.	1.2	63
86	Codon Usage and Splicing Jointly Influence mRNA Localization. <i>Cell Systems</i> , 2020, 10, 351-362.e8.	2.9	61
87	Human antisense genes have unusually short introns: evidence for selection for rapid transcription. <i>Trends in Genetics</i> , 2005, 21, 203-207.	2.9	60
88	Gametophytic Selection in <i>Arabidopsis thaliana</i> Supports the Selective Model of Intron Length Reduction. <i>PLoS Genetics</i> , 2005, 1, e13.	1.5	60
89	Male killing can select for male mate choice: a novel solution to the paradox of the lek. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 867-874.	1.2	59
90	Further Evidence Consistent With <i>Stellate's</i> Involvement in Meiotic Drive. <i>Genetics</i> , 1996, 142, 641-643.	1.2	59

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91	Parasite diversity and the evolution of diploidy, multicellularity and anisogamy. <i>Journal of Theoretical Biology</i> , 1990, 144, 429-443.	0.8	58
92	The evolutionary dynamics of male-killers and their hosts. <i>Heredity</i> , 2000, 84, 152-160.	1.2	58
93	The molecular evolution of signal peptides. <i>Gene</i> , 2000, 253, 313-322.	1.0	58
94	The determinants of gene order conservation in yeasts. <i>Genome Biology</i> , 2007, 8, R233.	13.9	58
95	Purifying Selection on Splice-Related Motifs, Not Expression Level nor RNA Folding, Explains Nearly All Constraint on Human lincRNAs. <i>Molecular Biology and Evolution</i> , 2014, 31, 3164-3183.	3.5	58
96	Comparative evolutionary analysis of VPS33 homologues: genetic and functional insights. <i>Human Molecular Genetics</i> , 2005, 14, 1261-1270.	1.4	56
97	The Evolution of Isochores: Evidence From SNP Frequency Distributions. <i>Genetics</i> , 2002, 162, 1805-1810.	1.2	56
98	Molecular evolutionary evidence that H19 mRNA is functional. <i>Trends in Genetics</i> , 1999, 15, 134-135.	2.9	54
99	The Causes of Synonymous Rate Variation in the Rodent Genome: Can Substitution Rates Be Used to Estimate the Sex Bias in Mutation Rate?. <i>Genetics</i> , 1999, 152, 661-673.	1.2	54
100	Embryonic growth and the evolution of the mammalian Y chromosome. I. The Y as an attractor for selfish growth factors. <i>Heredity</i> , 1994, 73, 223-232.	1.2	53
101	GroEL dependency affects codon usage—support for a critical role of misfolding in gene evolution. <i>Molecular Systems Biology</i> , 2010, 6, 340.	3.2	53
102	Does the Recombination Rate Affect the Efficiency of Purifying Selection? The Yeast Genome Provides a Partial Answer. <i>Molecular Biology and Evolution</i> , 2001, 18, 2323-2326.	3.5	52
103	Transcriptional Coupling of Neighboring Genes and Gene Expression Noise: Evidence that Gene Orientation and Noncoding Transcripts Are Modulators of Noise. <i>Genome Biology and Evolution</i> , 2011, 3, 320-331.	1.1	52
104	Support for multiple classes of local expression clusters in <i>Drosophila melanogaster</i> , but no evidence for gene order conservation. <i>Genome Biology</i> , 2011, 12, R23.	13.9	51
105	Identifying a large number of high-yield genes in rice by pedigree analysis, whole-genome sequencing, and CRISPR-Cas9 gene knockout. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7559-E7567.	3.3	50
106	The Effect of Tandem Substitutions on the Correlation Between Synonymous and Nonsynonymous Rates in Rodents. <i>Genetics</i> , 1999, 153, 1395-1402.	1.2	50
107	Understanding the limits to generalizability of experimental evolutionary models. <i>Nature</i> , 2008, 455, 220-223.	13.7	49
108	Duplication and Retention Biases of Essential and Non-Essential Genes Revealed by Systematic Knockdown Analyses. <i>PLoS Genetics</i> , 2013, 9, e1003330.	1.5	48

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109	Shellfish genes kept in line. <i>Nature</i> , 1994, 368, 811-812.	13.7	47
110	Covariation of GC content and the silent site substitution rate in rodents: implications for methodology and for the evolution of isochores. <i>Gene</i> , 2000, 261, 107-114.	1.0	47
111	How biologically relevant are interaction-based modules in protein networks?. <i>Genome Biology</i> , 2004, 5, R93.	13.9	47
112	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	13.7	47
113	<scp>SDHA</scp> related tumorigenesis: a new case series and literature review for variant interpretation and pathogenicity. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 237-250.	0.6	46
114	An eXceptional chromosome. <i>Trends in Genetics</i> , 1999, 15, 383-385.	2.9	45
115	The Elevated GC Content at Exonic Third Sites Is Not Evidence Against Neutralist Models of Isochore Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 757-762.	3.5	45
116	Molecular evolution of imprinted genes: no evidence for antagonistic coevolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997, 264, 739-746.	1.2	44
117	Genomic Regionality in Rates of Evolution Is Not Explained by Clustering of Genes of Comparable Expression Profile. <i>Genome Research</i> , 2004, 14, 1002-1013.	2.4	43
118	Determinants of the Usage of Splice-Associated <i>cis</i> -Motifs Predict the Distribution of Human Pathogenic SNPs. <i>Molecular Biology and Evolution</i> , 2016, 33, 518-529.	3.5	43
119	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. <i>Genome Biology</i> , 2018, 19, 94.	3.8	43
120	Selfish genes move sideways. <i>Nature</i> , 1992, 356, 659-660.	13.7	41
121	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity. <i>Genome Research</i> , 2006, 16, 922-933.	2.4	40
122	Exonic splice regulation imposes strong selection at synonymous sites. <i>Genome Research</i> , 2018, 28, 1442-1454.	2.4	39
123	Imprinted Chromosomal Regions of the Human Genome Have Unusually High Recombination Rates. <i>Genetics</i> , 2003, 165, 1629-1632.	1.2	39
124	Birt Hoggâ€DubÃ© syndromeâ€ associated FLCN mutations disrupt protein stability. <i>Human Mutation</i> , 2011, 32, 921-929.	1.1	38
125	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	3.5	38
126	scat+ is a selfish gene analogous to Medea of <i>tribolium castaneum</i> . <i>Cell</i> , 1993, 75, 407-408.	13.5	37

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127	Preliminary Assessment of the Impact of MicroRNA-Mediated Regulation on Coding Sequence Evolution in Mammals. <i>Journal of Molecular Evolution</i> , 2006, 63, 174-182.	0.8	37
128	Finding exonic islands in a sea of non-coding sequence: splicing related constraints on protein composition and evolution are common in intron-rich genomes. <i>Genome Biology</i> , 2008, 9, R29.	13.9	37
129	Error prevention and mitigation as forces in the evolution of genes and genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 875-881.	7.7	37
130	Teaching genetics prior to teaching evolution improves evolution understanding but not acceptance. <i>PLoS Biology</i> , 2017, 15, e2002255.	2.6	37
131	Causes and Consequences of Purifying Selection on SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	37
132	Co-expressed Yeast Genes Cluster Over a Long Range but are not Regularly Spaced. <i>Journal of Molecular Biology</i> , 2006, 359, 825-831.	2.0	36
133	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.	1.5	36
134	Embryonic growth and the evolution of the mammalian Y chromosome. II. Suppression of selfish Y-linked growth factors may explain escape from X-inactivation and rapid evolution of Sry. <i>Heredity</i> , 1994, 73, 233-243.	1.2	35
135	Sex and the X. <i>Nature</i> , 2001, 411, 149-150.	13.7	35
136	Stochasticity in Protein Levels Drives Colinearity of Gene Order in Metabolic Operons of <i>Escherichia coli</i> . <i>PLoS Biology</i> , 2009, 7, e1000115.	2.6	35
137	Dosage compensation on the active X chromosome minimizes transcriptional noise of X-linked genes in mammals. <i>Genome Biology</i> , 2009, 10, R74.	13.9	35
138	The sound of silence. <i>Nature</i> , 2011, 471, 582-583.	13.7	35
139	How to tame an endogenous retrovirus: HERVH and the evolution of human pluripotency. <i>Current Opinion in Virology</i> , 2017, 25, 49-58.	2.6	35
140	Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. <i>Cell Stem Cell</i> , 2022, 29, 1031-1050.e12.	5.2	34
141	How Common Are Intragenic Windows with $K_A > K_S$ Owing to Purifying Selection on Synonymous Mutations?. <i>Journal of Molecular Evolution</i> , 2007, 64, 646-655.	0.8	33
142	Why there is more to protein evolution than protein function: splicing, nucleosomes and dual-coding sequence. <i>Biochemical Society Transactions</i> , 2009, 37, 756-761.	1.6	33
143	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315.	2.6	32
144	Isolation and cultivation of naive-like human pluripotent stem cells based on HERVH expression. <i>Nature Protocols</i> , 2016, 11, 327-346.	5.5	32

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145	Late-Replicating Domains Have Higher Divergence and Diversity in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 873-882.	3.5	30
146	Molecular Evolution of an Imprinted Gene: Repeatability of Patterns of Evolution Within the Mammalian Insulin-Like Growth Factor Type II Receptor. <i>Genetics</i> , 1998, 150, 823-833.	1.2	30
147	Is optimal gene order impossible?. <i>Trends in Genetics</i> , 2006, 22, 420-423.	2.9	29
148	Clustering of Tissue-Specific Genes Underlies Much of the Similarity in Rates of Protein Evolution of Linked Genes. <i>Journal of Molecular Evolution</i> , 2002, 54, 511-518.	0.8	28
149	DO WOLBACHIA-ASSOCIATED INCOMPATIBILITIES PROMOTE POLYANDRY?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 107-122.	1.1	28
150	Why Selection Might Be Stronger When Populations Are Small: Intron Size and Density Predict within and between-Species Usage of Exonic Splice Associated cis-Motifs. <i>Molecular Biology and Evolution</i> , 2015, 32, 1847-1861.	3.5	28
151	Genetic Conflicts and the Paradox of Sex Determination: Three Paths to the Evolution of Female Intersexuality in a Mammal. <i>Journal of Theoretical Biology</i> , 1996, 179, 199-211.	0.8	26
152	Timing of Replication Is a Determinant of Neutral Substitution Rates but Does Not Explain Slow Y Chromosome Evolution in Rodents. <i>Molecular Biology and Evolution</i> , 2010, 27, 1077-1086.	3.5	26
153	Positive Charge Loading at Protein Termini Is Due to Membrane Protein Topology, Not a Translational Ramp. <i>Molecular Biology and Evolution</i> , 2014, 31, 70-84.	3.5	26
154	Estimating the prevalence of functional exonic splice regulatory information. <i>Human Genetics</i> , 2017, 136, 1059-1078.	1.8	26
155	Maintaining mendelism: Might prevention be better than cure?. <i>BioEssays</i> , 1991, 13, 489-490.	1.2	25
156	Intranuclear conflict and its role in evolution. <i>Trends in Ecology and Evolution</i> , 1992, 7, 373-378.	4.2	25
157	The uncertain origin of introns. <i>Nature</i> , 1994, 371, 381-382.	13.7	25
158	Genetic conflict and evolution of mammalian X-chromosome inactivation. <i>Genesis</i> , 1995, 17, 206-211.	3.1	24
159	Engineering of PEDF-Expressing Primary Pigment Epithelial Cells by the SB Transposon System Delivered by pFAR4 Plasmids. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 6, 302-314.	2.3	24
160	Repeat-induced point mutation in <i>Neurospora crassa</i> causes the highest known mutation rate and mutational burden of any cellular life. <i>Genome Biology</i> , 2020, 21, 142.	3.8	24
161	Transcription, mRNA Export, and Immune Evasion Shape the Codon Usage of Viruses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	24
162	Sensitivity of Patterns of Molecular Evolution to Alterations in Methodology: A Critique of Hughes and Yeager. <i>Journal of Molecular Evolution</i> , 1998, 47, 493-500.	0.8	23

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163	Is the Synonymous Substitution Rate in Mammals Gene-Specific?. <i>Molecular Biology and Evolution</i> , 2002, 19, 1395-1398.	3.5	23
164	Evidence for common short natural trans sense-antisense pairing between transcripts from protein coding genes. <i>Genome Biology</i> , 2008, 9, R169.	13.9	22
165	Both maintenance and avoidance of RNA-binding protein interactions constrain coding sequence evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, msx061.	3.5	22
166	Sex, slime and selfish genes. <i>Nature</i> , 1991, 354, 23-24.	13.7	21
167	Riding the evolutionary streetcar: where population genetics and game theory meet. <i>Trends in Ecology and Evolution</i> , 1996, 11, 445-446.	4.2	21
168	Purifying Selection on Exonic Splice Enhancers in Intronless Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1396-1418.	3.5	21
169	Is Multiple Paternity Necessary for the Evolution of Genomic Imprinting?. <i>Genetics</i> , 1999, 153, 509-512.	1.2	21
170	Driving sexual preference. <i>Trends in Ecology and Evolution</i> , 1999, 14, 425-426.	4.2	20
171	Mystery of the mutagenic male. <i>Nature</i> , 2002, 420, 365-366.	13.7	20
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