

List of Publications by Year in descending order

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238
papers

20,929
citations

13827

67
h-index

12558

132
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249
all docs

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docs citations

249
times ranked

21179
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence from <i>Drosophila</i> Supports Higher Duplicability of Faster Evolving Genes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	4
2	In rice splice variants that restore the reading frame after frameshifting indel introduction are common, often induced by the indels and sometimes lead to organism-level rescue. <i>PLoS Genetics</i> , 2022, 18, e1010071.	1.5	2
3	Transgene-design: a web application for the design of mammalian transgenes. <i>Bioinformatics</i> , 2022, 38, 2626-2627.	1.8	1
4	Selfish centromeres and the wastefulness of human reproduction. <i>PLoS Biology</i> , 2022, 20, e3001671.	2.6	7
5	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
6	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
7	Effective Population Size Predicts Local Rates but Not Local Mitigation of Read-through Errors. <i>Molecular Biology and Evolution</i> , 2021, 38, 244-262.	3.5	4
8	Mitotic gene conversion can be as important as meiotic conversion in driving genetic variability in plants and other species without early germline segregation. <i>PLoS Biology</i> , 2021, 19, e3001164.	2.6	5
9	Inferring Adaptive Codon Preference to Understand Sources of Selection Shaping Codon Usage Bias. <i>Molecular Biology and Evolution</i> , 2021, 38, 3247-3266.	3.5	14
10	Transcription, mRNA Export, and Immune Evasion Shape the Codon Usage of Viruses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	24
11	Causes and Consequences of Purifying Selection on SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	37
12	Evidence in disease and non-disease contexts that nonsense mutations cause altered splicing via motif disruption. <i>Nucleic Acids Research</i> , 2021, 49, 9665-9685.	6.5	7
13	OUP accepted manuscript. <i>Molecular Biology and Evolution</i> , 2021, , .	3.5	2
14	A Depletion of Stop Codons in lincRNA is Owing to Transfer of Selective Constraint from Coding Sequences. <i>Molecular Biology and Evolution</i> , 2020, 37, 1148-1164.	3.5	1
15	Codon Usage and Splicing Jointly Influence mRNA Localization. <i>Cell Systems</i> , 2020, 10, 351-362.e8.	2.9	61
16	A RCT for assessment of active human-centred learning finds teacher-centric non-human teaching of evolution optimal. <i>Npj Science of Learning</i> , 2020, 5, 19.	1.5	3
17	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
18	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

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19	Evidence for the Success of a Quantitative Assessment Instrument for Teaching Evolution in Primary Schools in England. , 2019, , 21-40.		2
20	Conditional expression explains molecular evolution of social genes in a microbe. Nature Communications, 2019, 10, 3284.	5.8	19
21	A century of bias in genetics and evolution. Heredity, 2019, 123, 33-43.	1.2	11
22	The architecture of intra-organism mutation rate variation in plants. PLoS Biology, 2019, 17, e3000191.	2.6	89
23	In eubacteria, unlike eukaryotes, there is no evidence for selection favouring fail-safe 3â€™™ additional stop codons. PLoS Genetics, 2019, 15, e1008386.	1.5	11
24	Refining the Ambush Hypothesis: Evidence That GC- and AT-Rich Bacteria Employ Different Frameshift Defence Strategies. Genome Biology and Evolution, 2018, 10, 1153-1173.	1.1	12
25	Scientific aptitude better explains poor responses to teaching of evolution than psychological conflicts. Nature Ecology and Evolution, 2018, 2, 388-394.	3.4	15
26	Tetrad analysis in plants and fungi finds large differences in gene conversion rates but no GC bias. Nature Ecology and Evolution, 2018, 2, 164-173.	3.4	65
27	Exonic splice regulation imposes strong selection at synonymous sites. Genome Research, 2018, 28, 1442-1454.	2.4	39
28	Faster Evolving Primate Genes Are More Likely to Duplicate. Molecular Biology and Evolution, 2018, 35, 107-118.	3.5	38
29	Identifying a large number of high-yield genes in rice by pedigree analysis, whole-genome sequencing, and CRISPR-Cas9 gene knockout. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7559-E7567.	3.3	50
30	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. Genome Biology, 2018, 19, 94.	3.8	43
31	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. Genetics, 2017, 206, 363-376.	1.2	65
32	Engineering of PEDF-Expressing Primary Pigment Epithelial Cells by the SB Transposon System Delivered by pFAR4 Plasmids. Molecular Therapy - Nucleic Acids, 2017, 6, 302-314.	2.3	24
33	<scp>SDHA</scp> related tumorigenesis: a new case series and literature review for variant interpretation and pathogenicity. Molecular Genetics & Genomic Medicine, 2017, 5, 237-250.	0.6	46
34	Direct Determination of the Mutation Rate in the Bumblebee Reveals Evidence for Weak Recombination-Associated Mutation and an Approximate Rate Constancy in Insects. Molecular Biology and Evolution, 2017, 34, 119-130.	3.5	93
35	It's easier to getÂ along with the quiet neighbours. Molecular Systems Biology, 2017, 13, 943.	3.2	12
36	How to tame an endogenous retrovirus: HERVH and the evolution of human pluripotency. Current Opinion in Virology, 2017, 25, 49-58.	2.6	35

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37	Estimating the prevalence of functional exonic splice regulatory information. <i>Human Genetics</i> , 2017, 136, 1059-1078.	1.8	26
38	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
39	Depletion of somatic mutations in splicing-associated sequences in cancer genomes. <i>Genome Biology</i> , 2017, 18, 213.	3.8	11
40	Male Mutation Bias Is the Main Force Shaping Chromosomal Substitution Rates in Monotreme Mammals. <i>Genome Biology and Evolution</i> , 2017, 9, 2198-2210.	1.1	6
41	Adenine Enrichment at the Fourth CDS Residue in Bacterial Genes Is Consistent with Error Proofing for +1 Frameshifts. <i>Molecular Biology and Evolution</i> , 2017, 34, 3064-3080.	3.5	7
42	Teaching genetics prior to teaching evolution improves evolution understanding but not acceptance. <i>PLoS Biology</i> , 2017, 15, e2002255.	2.6	37
43	Pluripotency and the endogenous retrovirus HERVH: Conflict or serendipity?. <i>BioEssays</i> , 2016, 38, 109-117.	1.2	63
44	Open questions in the study of de novo genes: what, how and why. <i>Nature Reviews Genetics</i> , 2016, 17, 567-578.	7.7	179
45	Mutation rate analysis via parentâ€“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
46	Mutation rate analysis via parentâ€“progeny sequencing of the perennial peach. II. No evidence for recombination-associated mutation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161785.	1.2	17
47	Purifying Selection on Exonic Splice Enhancers in Intronless Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1396-1418.	3.5	21
48	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
49	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
50	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
51	Parentâ€“progeny sequencing indicates higher mutation rates in heterozygotes. <i>Nature</i> , 2015, 523, 463-467.	13.7	157
52	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
53	Neighboring Genes Show Correlated Evolution in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1748-1766.	3.5	126
54	Why Selection Might Be Stronger When Populations Are Small: Intron Size and Density Predict within and between-Species Usage of Exonic Splice Associated <i>cis</i> -Motifs. <i>Molecular Biology and Evolution</i> , 2015, 32, 1847-1861.	3.5	28

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55	A simple metric of promoter architecture robustly predicts expression breadth of human genes suggesting that most transcription factors are positive regulators. <i>Genome Biology</i> , 2014, 15, 413.	3.8	20
56	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
57	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
58	Environmentally responsive genome-wide accumulation of de novo <i>Arabidopsis thaliana</i> mutations and epimutations. <i>Genome Research</i> , 2014, 24, 1821-1829.	2.4	194
59	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. <i>Nature</i> , 2014, 516, 405-409.	13.7	372
60	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	2.4	210
61	The form of a trade-off determines the response to competition. <i>Ecology Letters</i> , 2013, 16, 1267-1276.	3.0	63
62	Open questions: A logic (or lack thereof) of genome organization. <i>BMC Biology</i> , 2013, 11, 58.	1.7	6
63	The evolution, impact and properties of exonic splice enhancers. <i>Genome Biology</i> , 2013, 14, R143.	13.9	77
64	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
65	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
66	Positively Charged Residues Are the Major Determinants of Ribosomal Velocity. <i>PLoS Biology</i> , 2013, 11, e1001508.	2.6	250
67	Evidence for Deep Phylogenetic Conservation of Exonic Splice-Related Constraints: Splice-Related Skews at Exonic Ends in the Brown Alga <i>Ectocarpus</i> Are Common and Resemble Those Seen in Humans. <i>Genome Biology and Evolution</i> , 2013, 5, 1731-1745.	1.1	6
68	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
69	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
70	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
71	Direct and indirect consequences of meiotic recombination: implications for genome evolution. <i>Trends in Genetics</i> , 2012, 28, 101-109.	2.9	97
72	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

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73	Metabolic trade-offs and the maintenance of the fittest and the flattest. <i>Nature</i> , 2011, 472, 342-346.	13.7	112
74	Late Replicating Domains Are Highly Recombining in Females but Have Low Male Recombination Rates: Implications for Isochore Evolution. <i>PLoS ONE</i> , 2011, 6, e24480.	1.1	5
75	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
76	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
77	Distinct physiological and behavioural functions for parental alleles of imprinted <i>Grb10</i> . <i>Nature</i> , 2011, 469, 534-538.	13.7	204
78	The sound of silence. <i>Nature</i> , 2011, 471, 582-583.	13.7	35
79	Birt Hoggâ€“DubÃ© syndromeâ€“associated <i>FLCN</i> mutations disrupt protein stability. <i>Human Mutation</i> , 2011, 32, 921-929.	1.1	38
80	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.	1.5	36
81	Unique Cost Dynamics Elucidate the Role of Frameshifting Errors in Promoting Translational Robustness. <i>Genome Biology and Evolution</i> , 2010, 2, 636-645.	1.1	9
82	Intronic AT Skew is a Defendable Proxy for Germline Transcription but does not Predict Crossing-Over or Protein Evolution Rates in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2010, 71, 415-426.	0.8	5
83	Transcriptional coupling of neighbouring genes and gene expression noise: evidence that gene orientation and non-coding transcripts are modulators of noise. <i>Nature Precedings</i> , 2010, , .	0.1	0
84	GroEL dependency affects codon usageâ€“support for a critical role of misfolding in gene evolution. <i>Molecular Systems Biology</i> , 2010, 6, 340.	3.2	53
85	Nonsenseâ€“mediated decay targets have multiple sequenceâ€“related features that can inhibit translation. <i>Molecular Systems Biology</i> , 2010, 6, 442.	3.2	18
86	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
87	A Mixture of â€“Cheatsâ€“and â€“Co-Operatorsâ€“Can Enable Maximal Group Benefit. <i>PLoS Biology</i> , 2010, 8, e1000486.	2.6	103
88	Maternally-inherited <i>Grb10</i> reduces placental size and efficiency. <i>Developmental Biology</i> , 2010, 337, 1-8.	0.9	85
89	Protein Rates of Evolution Are Predicted by Double-Strand Break Events, Independent of Crossing-over Rates. <i>Genome Biology and Evolution</i> , 2009, 1, 340-349.	1.1	17
90	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

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91	Evidence That Replication-Associated Mutation Alone Does Not Explain Between-Chromosome Differences In Substitution Rates. <i>Genome Biology and Evolution</i> , 2009, 1, 13-22.	1.1	16
92	Monoallelic expression and tissue specificity are associated with high crossover rates. <i>Trends in Genetics</i> , 2009, 25, 519-522.	2.9	20
93	Does negative auto-regulation increase gene duplicability?. <i>BMC Evolutionary Biology</i> , 2009, 9, 193.	3.2	4
94	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
95	Evolutionary genomics and the reach of selection. <i>Journal of Biology</i> , 2009, 8, 12.	2.7	16
96	A positive becomes a negative. <i>Nature</i> , 2009, 457, 543-544.	13.7	13
97	Genetics and the understanding of selection. <i>Nature Reviews Genetics</i> , 2009, 10, 83-93.	7.7	107
98	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
99	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
100	DO WOLBACHIA-ASSOCIATED INCOMPATIBILITIES PROMOTE POLYANDRY?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 107-122.	1.1	28
101	Understanding the limits to generalizability of experimental evolutionary models. <i>Nature</i> , 2008, 455, 220-223.	13.7	49
102	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
103	Do Alu repeats drive the evolution of the primate transcriptome?. <i>Genome Biology</i> , 2008, 9, R25.	13.9	19
104	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
105	The Impact of the Nucleosome Code on Protein-Coding Sequence Evolution in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000250.	1.5	80
106	A Test of the Null Model for 5' UTR Evolution Based on GC Content. <i>Molecular Biology and Evolution</i> , 2008, 25, 801-804.	3.5	15
107	Splicing and the Evolution of Proteins in Mammals. <i>PLoS Biology</i> , 2007, 5, e14.	2.6	94
108	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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109	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
110	The determinants of gene order conservation in yeasts. <i>Genome Biology</i> , 2007, 8, R233.	13.9	58
111	Still Stratus Not Altocumulus: Further Evidence against the Date/Party Hub Distinction. <i>PLoS Biology</i> , 2007, 5, e154.	2.6	94
112	How do synonymous mutations affect fitness?. <i>BioEssays</i> , 2007, 29, 515-519.	1.2	107
113	Evolution of chromosome organization driven by selection for reduced gene expression noise. <i>Nature Genetics</i> , 2007, 39, 945-949.	9.4	202
114	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
115	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
116	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
117	Hearing silence: non-neutral evolution at synonymous sites in mammals. <i>Nature Reviews Genetics</i> , 2006, 7, 98-108.	7.7	740
118	Chance and necessity in the evolution of minimal metabolic networks. <i>Nature</i> , 2006, 440, 667-670.	13.7	219
119	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	13.7	47
120	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
121	Comparisons of dN/dS are time dependent for closely related bacterial genomes. <i>Journal of Theoretical Biology</i> , 2006, 239, 226-235.	0.8	400
122	Is optimal gene order impossible?. <i>Trends in Genetics</i> , 2006, 22, 420-423.	2.9	29
123	Evolutionary and Physiological Importance of Hub Proteins. <i>PLoS Computational Biology</i> , 2006, 2, e88.	1.5	251
124	Evidence for Purifying Selection Against Synonymous Mutations in Mammalian Exonic Splicing Enhancers. <i>Molecular Biology and Evolution</i> , 2006, 23, 301-309.	3.5	209
125	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
126	Stratus Not Altocumulus: A New View of the Yeast Protein Interaction Network. <i>PLoS Biology</i> , 2006, 4, e317.	2.6	205

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127	Dissecting dispensability. <i>Nature Genetics</i> , 2005, 37, 214-215.	9.4	5
128	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
129	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
130	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
131	Unusual linkage patterns of ligands and their cognate receptors indicate a novel reason for non-random gene order in the human genome. <i>BMC Evolutionary Biology</i> , 2005, 5, 62.	3.2	12
132	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
133	Comparative evolutionary analysis of VPS33 homologues: genetic and functional insights. <i>Human Molecular Genetics</i> , 2005, 14, 1261-1270.	1.4	56
134	The Small Introns of Antisense Genes Are Better Explained by Selection for Rapid Transcription Than by "Genomic Design". <i>Genetics</i> , 2005, 171, 2151-2155.	1.2	17
135	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
136	Evidence for selection on synonymous mutations affecting stability of mRNA secondary structure in mammals. <i>Genome Biology</i> , 2005, 6, R75.	13.9	266
137	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	3.3	830
138	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
139	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
140	The evolutionary dynamics of eukaryotic gene order. <i>Nature Reviews Genetics</i> , 2004, 5, 299-310.	7.7	661
141	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. <i>Nature</i> , 2004, 429, 661-664.	13.7	324
142	Evidence against the selfish operon theory. <i>Trends in Genetics</i> , 2004, 20, 232-234.	2.9	106
143	How biologically relevant are interaction-based modules in protein networks?. <i>Genome Biology</i> , 2004, 5, R93.	13.9	47
144	Evolution of cis-regulatory elements in duplicated genes of yeast. <i>Trends in Genetics</i> , 2003, 19, 417-422.	2.9	127

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145	Rate of evolution and gene dispensability. <i>Nature</i> , 2003, 421, 496-497.	13.7	205
146	Evidence for co-evolution of gene order and recombination rate. <i>Nature Genetics</i> , 2003, 33, 392-395.	9.4	143
147	Dosage sensitivity and the evolution of gene families in yeast. <i>Nature</i> , 2003, 424, 194-197.	13.7	757
148	A unification of mosaic structures in the human genome. <i>Human Molecular Genetics</i> , 2003, 12, 2411-2415.	1.4	119
149	Coexpression of Neighboring Genes in <i>Caenorhabditis Elegans</i> Is Mostly Due to Operons and Duplicate Genes. <i>Genome Research</i> , 2003, 13, 238-243.	2.4	194
150	The Signature of Selection Mediated by Expression on Human Genes. <i>Genome Research</i> , 2003, 13, 2260-2264.	2.4	227
151	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
152	Imprinted Chromosomal Regions of the Human Genome Have Unusually High Recombination Rates. <i>Genetics</i> , 2003, 165, 1629-1632.	1.2	39
153	Is the Synonymous Substitution Rate in Mammals Gene-Specific?. <i>Molecular Biology and Evolution</i> , 2002, 19, 1395-1398.	3.5	23
154	Survival and anisogamy. <i>Trends in Ecology and Evolution</i> , 2002, 17, 358.	4.2	9
155	Can mutation or fixation biases explain the allele frequency distribution of human single nucleotide polymorphisms (SNPs)?. <i>Gene</i> , 2002, 300, 53-58.	1.0	14
156	Human SNP variability and mutation rate are higher in regions of high recombination. <i>Trends in Genetics</i> , 2002, 18, 337-340.	2.9	326
157	The Ka/Ks ratio: diagnosing the form of sequence evolution. <i>Trends in Genetics</i> , 2002, 18, 486-487.	2.9	939
158	Natural selection promotes the conservation of linkage of co-expressed genes. <i>Trends in Genetics</i> , 2002, 18, 604-606.	2.9	122
159	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
160	Mystery of the mutagenic male. <i>Nature</i> , 2002, 420, 365-366.	13.7	20
161	Clustering of housekeeping genes provides a unified model of gene order in the human genome. <i>Nature Genetics</i> , 2002, 31, 180-183.	9.4	496
162	The Evolution of Isochores: Evidence From SNP Frequency Distributions. <i>Genetics</i> , 2002, 162, 1805-1810.	1.2	56

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163	Understanding the Distribution and Effects of Wolbachia. <i>Selection</i> , 2002, 2, 237-248.	0.8	1
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