

Laurence D Hurst

List of Publications by Year in descending order

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Version: 2024-02-01

167
papers

15,246
citations

25034

57
h-index

20961

115
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172
all docs

172
docs citations

172
times ranked

17939
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, .	2.5	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.	3.5	2
3	Transgene-design: a web application for the design of mammalian transgenes. <i>Bioinformatics</i> , 2022, 38, 2626-2627.	4.1	1
4	Selfish centromeres and the wastefulness of human reproduction. <i>PLoS Biology</i> , 2022, 20, e3001671.	5.6	7
5	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.	8.9	68
6	Effective Population Size Predicts Local Rates but Not Local Mitigation of Read-through Errors. <i>Molecular Biology and Evolution</i> , 2021, 38, 244-262.	8.9	4
7	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.	5.6	5
8	Inferring Adaptive Codon Preference to Understand Sources of Selection Shaping Codon Usage Bias. <i>Molecular Biology and Evolution</i> , 2021, 38, 3247-3266.	8.9	14
9	Transcription, mRNA Export, and Immune Evasion Shape the Codon Usage of Viruses. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	24
10	Causes and Consequences of Purifying Selection on SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	37
11	Evidence in disease and non-disease contexts that nonsense mutations cause altered splicing via a motif disruption. <i>Nucleic Acids Research</i> , 2021, 49, 9665-9685.	14.5	7
12	OUP accepted manuscript. <i>Molecular Biology and Evolution</i> , 2021, , .	8.9	2
13	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.	8.9	1
14	Codon Usage and Splicing Jointly Influence mRNA Localization. <i>Cell Systems</i> , 2020, 10, 351-362.e8.	6.2	61
15	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.	2.8	3
16	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.	8.8	24
17	Conditional expression explains molecular evolution of social genes in a microbe. <i>Nature Communications</i> , 2019, 10, 3284.	12.8	19
18	The architecture of intra-organism mutation rate variation in plants. <i>PLoS Biology</i> , 2019, 17, e3000191.	5.6	89

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19	In eubacteria, unlike eukaryotes, there is no evidence for selection favouring fail-safe 3â€™™ additional stop codons. PLoS Genetics, 2019, 15, e1008386.	3.5	11
20	Refining the Ambush Hypothesis: Evidence That GC- and AT-Rich Bacteria Employ Different Frameshift Defence Strategies. Genome Biology and Evolution, 2018, 10, 1153-1173.	2.5	12
21	Scientific aptitude better explains poor responses to teaching of evolution than psychological conflicts. Nature Ecology and Evolution, 2018, 2, 388-394.	7.8	15
22	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.	7.8	65
23	Exonic splice regulation imposes strong selection at synonymous sites. Genome Research, 2018, 28, 1442-1454.	5.5	39
24	Faster Evolving Primate Genes Are More Likely to Duplicate. Molecular Biology and Evolution, 2018, 35, 107-118.	8.9	38
25	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. Genome Biology, 2018, 19, 94.	8.8	43
26	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in Ascoidea asiatica. Current Biology, 2018, 28, 2046-2057.e5.	3.9	22
27	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. Genetics, 2017, 206, 363-376.	2.9	65
28	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.	5.1	24
29	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.	8.9	93
30	It's easier to getÂalong with the quiet neighbours. Molecular Systems Biology, 2017, 13, 943.	7.2	12
31	Estimating the prevalence of functional exonic splice regulatory information. Human Genetics, 2017, 136, 1059-1078.	3.8	26
32	Both maintenance and avoidance of RNA-binding protein interactions constrain coding sequence evolution. Molecular Biology and Evolution, 2017, 34, msx061.	8.9	22
33	Depletion of somatic mutations in splicing-associated sequences in cancer genomes. Genome Biology, 2017, 18, 213.	8.8	11
34	Male Mutation Bias Is the Main Force Shaping Chromosomal Substitution Rates in Monotreme Mammals. Genome Biology and Evolution, 2017, 9, 2198-2210.	2.5	6
35	Adenine Enrichment at the Fourth CDS Residue in Bacterial Genes Is Consistent with Error Proofing for +1 Frameshifts. Molecular Biology and Evolution, 2017, 34, 3064-3080.	8.9	7
36	Teaching genetics prior to teaching evolution improves evolution understanding but not acceptance. PLoS Biology, 2017, 15, e2002255.	5.6	37

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37	Pluripotency and the endogenous retrovirus HERVH: Conflict or serendipity?. <i>BioEssays</i> , 2016, 38, 109-117.	2.5	63
38	Open questions in the study of de novo genes: what, how and why. <i>Nature Reviews Genetics</i> , 2016, 17, 567-578.	16.3	179
39	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.	2.6	64
40	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.	2.6	17
41	Purifying Selection on Exonic Splice Enhancers in Intronless Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1396-1418.	8.9	21
42	Isolation and cultivation of naive-like human pluripotent stem cells based on HERVH expression. <i>Nature Protocols</i> , 2016, 11, 327-346.	12.0	32
43	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.	8.9	43
44	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315.	5.6	32
45	Parentâ€“progeny sequencing indicates higher mutation rates in heterozygotes. <i>Nature</i> , 2015, 523, 463-467.	27.8	157
46	Causes and consequences of crossing-over evidenced via a high-resolution recombinational landscape of the honey bee. <i>Genome Biology</i> , 2015, 16, 15.	8.8	67
47	Neighboring Genes Show Correlated Evolution in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1748-1766.	8.9	126
48	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.	8.9	28
49	Genomic Analysis of Isolates From the United Kingdom 2012 Pertussis Outbreak Reveals That Vaccine Antigen Genes Are Unusually Fast Evolving. <i>Journal of Infectious Diseases</i> , 2015, 212, 294-301.	4.0	79
50	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.	8.8	20
51	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.	8.9	58
52	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.	8.9	26
53	Environmentally responsive genome-wide accumulation of de novo <i>Arabidopsis thaliana</i> mutations and epimutations. <i>Genome Research</i> , 2014, 24, 1821-1829.	5.5	194
54	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. <i>Nature</i> , 2014, 516, 405-409.	27.8	372

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55	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	5.5	210
56	Exome sequencing identifies frequent mutation of MLL2 in nonâ€‘small cell lung carcinoma from Chinese patients. <i>Scientific Reports</i> , 2014, 4, 6036.	3.3	33
57	The form of a tradeâ€‘off determines the response to competition. <i>Ecology Letters</i> , 2013, 16, 1267-1276.	6.4	63
58	Open questions: A logic (or lack thereof) of genome organization. <i>BMC Biology</i> , 2013, 11, 58.	3.8	6
59	The evolution, impact and properties of exonic splice enhancers. <i>Genome Biology</i> , 2013, 14, R143.	9.6	77
60	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.	8.9	113
61	Duplication and Retention Biases of Essential and Non-Essential Genes Revealed by Systematic Knockdown Analyses. <i>PLoS Genetics</i> , 2013, 9, e1003330.	3.5	48
62	Positively Charged Residues Are the Major Determinants of Ribosomal Velocity. <i>PLoS Biology</i> , 2013, 11, e1001508.	5.6	250
63	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.	2.5	6
64	Identification of Two Maternal Transmission Ratio Distortion Loci in Pedigrees of the Framingham Heart Study. <i>Scientific Reports</i> , 2013, 3, 2147.	3.3	6
65	Young intragenic miRNAs are less coexpressed with host genes than old ones: implications of miRNAâ€‘host gene coevolution. <i>Nucleic Acids Research</i> , 2012, 40, 4002-4012.	14.5	63
66	Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159.	8.9	35
67	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.	7.1	69
68	Late-Replicating Domains Have Higher Divergence and Diversity in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 873-882.	8.9	30
69	Direct and indirect consequences of meiotic recombination: implications for genome evolution. <i>Trends in Genetics</i> , 2012, 28, 101-109.	6.7	97
70	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.	9.6	51
71	Metabolic trade-offs and the maintenance of the fittest and the flattest. <i>Nature</i> , 2011, 472, 342-346.	27.8	112
72	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.	2.5	5

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73	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.	2.5	52
74	Error prevention and mitigation as forces in the evolution of genes and genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 875-881.	16.3	37
75	Distinct physiological and behavioural functions for parental alleles of imprinted Grb10. <i>Nature</i> , 2011, 469, 534-538.	27.8	204
76	Birt Hoggâ€DubÃ© syndromeâ€associated FLCN mutations disrupt protein stability. <i>Human Mutation</i> , 2011, 32, 921-929.	2.5	38
77	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.	3.5	36
78	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.	1.8	5
79	Comparison of <i>Iroquois</i> gene expression in limbs/fins of vertebrate embryos. <i>Journal of Anatomy</i> , 2010, 216, 683-691.	1.5	20
80	GroEL dependency affects codon usageâ€support for a critical role of misfolding in gene evolution. <i>Molecular Systems Biology</i> , 2010, 6, 340.	7.2	53
81	Nonsenseâ€mediated decay targets have multiple sequenceâ€related features that can inhibit translation. <i>Molecular Systems Biology</i> , 2010, 6, 442.	7.2	18
82	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.	8.9	26
83	A Mixture of â€Cheatsâ€and â€Co-Operatorsâ€Can Enable Maximal Group Benefit. <i>PLoS Biology</i> , 2010, 8, e1000486.	5.6	103
84	Maternally-inherited Grb10 reduces placental size and efficiency. <i>Developmental Biology</i> , 2010, 337, 1-8.	2.0	85
85	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.	2.5	17
86	Stochasticity in Protein Levels Drives Colinearity of Gene Order in Metabolic Operons of <i>Escherichia coli</i> . <i>PLoS Biology</i> , 2009, 7, e1000115.	5.6	35
87	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.	2.5	16
88	Monoallelic expression and tissue specificity are associated with high crossover rates. <i>Trends in Genetics</i> , 2009, 25, 519-522.	6.7	20
89	Does negative auto-regulation increase gene duplicability?. <i>BMC Evolutionary Biology</i> , 2009, 9, 193.	3.2	4
90	Noisy splicing, more than expression regulation, explains why some exons are subject to nonsense-mediated mRNA decay. <i>BMC Biology</i> , 2009, 7, 23.	3.8	67

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91	Evolutionary genomics and the reach of selection. <i>Journal of Biology</i> , 2009, 8, 12.	2.7	16
92	A positive becomes a negative. <i>Nature</i> , 2009, 457, 543-544.	27.8	13
93	Genetics and the understanding of selection. <i>Nature Reviews Genetics</i> , 2009, 10, 83-93.	16.3	107
94	Dosage compensation on the active X chromosome minimizes transcriptional noise of X-linked genes in mammals. <i>Genome Biology</i> , 2009, 10, R74.	9.6	35
95	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.	3.4	33
96	DO WOLBACHIA-ASSOCIATED INCOMPATIBILITIES PROMOTE POLYANDRY?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 107-122.	2.3	28
97	Understanding the limits to generalizability of experimental evolutionary models. <i>Nature</i> , 2008, 455, 220-223.	27.8	49
98	Leukocyte Tyrosine Kinase Functions in Pigment Cell Development. <i>PLoS Genetics</i> , 2008, 4, e1000026.	3.5	137
99	Evidence for common short natural trans sense-antisense pairing between transcripts from protein coding genes. <i>Genome Biology</i> , 2008, 9, R169.	9.6	22
100	Do Alu repeats drive the evolution of the primate transcriptome?. <i>Genome Biology</i> , 2008, 9, R25.	9.6	19
101	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.	9.6	37
102	The Impact of the Nucleosome Code on Protein-Coding Sequence Evolution in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000250.	3.5	80
103	A Test of the Null Model for 5' UTR Evolution Based on GC Content. <i>Molecular Biology and Evolution</i> , 2008, 25, 801-804.	8.9	15
104	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.	8.9	68
105	Exonic Splicing Regulatory Elements Skew Synonymous Codon Usage near Intron-exon Boundaries in Mammals. <i>Molecular Biology and Evolution</i> , 2007, 24, 1600-1603.	8.9	98
106	The determinants of gene order conservation in yeasts. <i>Genome Biology</i> , 2007, 8, R233.	9.6	58
107	Still Stratus Not Altocumulus: Further Evidence against the Date/Party Hub Distinction. <i>PLoS Biology</i> , 2007, 5, e154.	5.6	94
108	How do synonymous mutations affect fitness?. <i>BioEssays</i> , 2007, 29, 515-519.	2.5	107

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109	Chromatin remodelling is a major source of coexpression of linked genes in yeast. Trends in Genetics, 2007, 23, 480-484.	6.7	87
110	How Common Are Intragenic Windows with $K_A > K_S$ Owing to Purifying Selection on Synonymous Mutations?. Journal of Molecular Evolution, 2007, 64, 646-655.	1.8	33
111	Co-expressed Yeast Genes Cluster Over a Long Range but are not Regularly Spaced. Journal of Molecular Biology, 2006, 359, 825-831.	4.2	36
112	Hearing silence: non-neutral evolution at synonymous sites in mammals. Nature Reviews Genetics, 2006, 7, 98-108.	16.3	740
113	Chance and necessity in the evolution of minimal metabolic networks. Nature, 2006, 440, 667-670.	27.8	219
114	Causes of trends in amino-acid gain and loss. Nature, 2006, 442, E11-E12.	27.8	47
115	Preliminary Assessment of the Impact of MicroRNA-Mediated Regulation on Coding Sequence Evolution in Mammals. Journal of Molecular Evolution, 2006, 63, 174-182.	1.8	37
116	Comparisons of dN/dS are time dependent for closely related bacterial genomes. Journal of Theoretical Biology, 2006, 239, 226-235.	1.7	400
117	Evolutionary and Physiological Importance of Hub Proteins. PLoS Computational Biology, 2006, 2, e88.	3.2	251
118	Evidence for Purifying Selection Against Synonymous Mutations in Mammalian Exonic Splicing Enhancers. Molecular Biology and Evolution, 2006, 23, 301-309.	8.9	209
119	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity. Genome Research, 2006, 16, 922-933.	5.5	40
120	Stratus Not Altocumulus: A New View of the Yeast Protein Interaction Network. PLoS Biology, 2006, 4, e317.	5.6	205
121	Identification of a New pebp2 \pm A2 Isoform From Zebrafishrunx2Capable of Inducing Osteocalcin Gene Expression In Vitro. Journal of Bone and Mineral Research, 2005, 20, 1440-1453.	2.8	16
122	Dissecting dispensability. Nature Genetics, 2005, 37, 214-215.	21.4	5
123	Human antisense genes have unusually short introns: evidence for selection for rapid transcription. Trends in Genetics, 2005, 21, 203-207.	6.7	60
124	Biased codon usage near intron-exon junctions: selection on splicing enhancers, splice-site recognition or something else?. Trends in Genetics, 2005, 21, 256-259.	6.7	65
125	Unusual linkage patterns of ligands and their cognate receptors indicate a novel reason for non-random gene order in the human genome. BMC Evolutionary Biology, 2005, 5, 62.	3.2	12
126	Gametophytic Selection in Arabidopsis thaliana Supports the Selective Model of Intron Length Reduction. PLoS Genetics, 2005, 1, e13.	3.5	60

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127	Comparative evolutionary analysis of VPS33 homologues: genetic and functional insights. Human Molecular Genetics, 2005, 14, 1261-1270.	2.9	56
128	The Small Introns of Antisense Genes Are Better Explained by Selection for Rapid Transcription Than by "Genomic Design" Genetics, 2005, 171, 2151-2155.	2.9	17
129	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. Nucleic Acids Research, 2005, 33, 5533-5543.	14.5	78
130	Evidence for selection on synonymous mutations affecting stability of mRNA secondary structure in mammals. Genome Biology, 2005, 6, R75.	9.6	266
131	Genomic Regionality in Rates of Evolution Is Not Explained by Clustering of Genes of Comparable Expression Profile. Genome Research, 2004, 14, 1002-1013.	5.5	43
132	Similar Rates but Different Modes of Sequence Evolution in Introns and at Exonic Silent Sites in Rodents: Evidence for Selectively Driven Codon Usage. Molecular Biology and Evolution, 2004, 21, 1014-1023.	8.9	83
133	The evolutionary dynamics of eukaryotic gene order. Nature Reviews Genetics, 2004, 5, 299-310.	16.3	661
134	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. Nature, 2004, 429, 661-664.	27.8	324
135	Evidence against the selfish operon theory. Trends in Genetics, 2004, 20, 232-234.	6.7	106
136	Rate of evolution and gene dispensability. Nature, 2003, 421, 496-497.	27.8	205
137	Evidence for co-evolution of gene order and recombination rate. Nature Genetics, 2003, 33, 392-395.	21.4	143
138	Dosage sensitivity and the evolution of gene families in yeast. Nature, 2003, 424, 194-197.	27.8	757
139	Evidence for a priming effect on maternal resource allocation: implications for interbrood competition. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, S100-3.	2.6	9
140	A unification of mosaic structures in the human genome. Human Molecular Genetics, 2003, 12, 2411-2415.	2.9	119
141	Coexpression of Neighboring Genes in Caenorhabditis Elegans Is Mostly Due to Operons and Duplicate Genes. Genome Research, 2003, 13, 238-243.	5.5	194
142	The Signature of Selection Mediated by Expression on Human Genes. Genome Research, 2003, 13, 2260-2264.	5.5	227
143	Evidence That the Human X Chromosome Is Enriched for Male-Specific but not Female-Specific Genes. Molecular Biology and Evolution, 2003, 20, 1113-1116.	8.9	112
144	The Ka/Ks ratio: diagnosing the form of sequence evolution. Trends in Genetics, 2002, 18, 486-487.	6.7	939

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145	Natural selection promotes the conservation of linkage of co-expressed genes. Trends in Genetics, 2002, 18, 604-606.	6.7	122
146	Clustering of Tissue-Specific Genes Underlies Much of the Similarity in Rates of Protein Evolution of Linked Genes. Journal of Molecular Evolution, 2002, 54, 511-518.	1.8	28
147	Mystery of the mutagenic male. Nature, 2002, 420, 365-366.	27.8	20
148	Clustering of housekeeping genes provides a unified model of gene order in the human genome. Nature Genetics, 2002, 31, 180-183.	21.4	496
149	Accelerated molecular evolution of insect orthologues ofERG28/C14orf1: A link with ecdysteroid metabolism?. Journal of Genetics, 2001, 80, 17-21.	0.7	7
150	Sex and the X. Nature, 2001, 411, 149-150.	27.8	35
151	The evolution of isochores. Nature Reviews Genetics, 2001, 2, 549-555.	16.3	379
152	Highly Expressed Genes in Yeast Evolve Slowly. Genetics, 2001, 158, 927-931.	2.9	556
153	Codon Usage Bias Covaries With Expression Breadth and the Rate of Synonymous Evolution in Humans, but This Is Not Evidence for Selection. Genetics, 2001, 159, 1191-1199.	2.9	135
154	Evolutionary genomics: reading the bands. BioEssays, 2000, 22, 105-107.	2.5	6
155	The proteins of linked genes evolve at similar rates. Nature, 2000, 407, 900-903.	27.8	100
156	Male killing can select for male mate choice: a novel solution to the paradox of the lek. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 867-874.	2.6	59
157	A Quantitative Measure of Error Minimization in the Genetic Code. Journal of Molecular Evolution, 1999, 49, 708-708.	1.8	20
158	Vertebrate genome evolution: a slow shuffle or a big bang?. BioEssays, 1999, 21, 697-703.	2.5	60
159	The Causes of Synonymous Rate Variation in the Rodent Genome: Can Substitution Rates Be Used to Estimate the Sex Bias in Mutation Rate?. Genetics, 1999, 152, 661-673.	2.9	54
160	Is Multiple Paternity Necessary for the Evolution of Genomic Imprinting?. Genetics, 1999, 153, 509-512.	2.9	21
161	The Effect of Tandem Substitutions on the Correlation Between Synonymous and Nonsynonymous Rates in Rodents. Genetics, 1999, 153, 1395-1402.	2.9	50
162	The Genetic Code Is One in a Million. Journal of Molecular Evolution, 1998, 47, 238-248.	1.8	466

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163	Selfish genes and meiotic drive. <i>Nature</i> , 1998, 391, 223-223.	27.8	12
164	Peromysci, promiscuity and imprinting. <i>Nature Genetics</i> , 1998, 20, 315-316.	21.4	14
165	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.	1.8	23
166	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.	2.9	30
167	Molecular evolution of imprinted genes: no evidence for antagonistic coevolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1997, 264, 739-746.	2.6	44