

# Laurence D Hurst

## List of Publications by Year in descending order

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167  
papers

15,246  
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28736

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172  
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172  
docs citations

172  
times ranked

20228  
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	Dosage sensitivity and the evolution of gene families in yeast. Nature, 2003, 424, 194-197.	13.7	757
3	Hearing silence: non-neutral evolution at synonymous sites in mammals. Nature Reviews Genetics, 2006, 7, 98-108.	7.7	740
4	The evolutionary dynamics of eukaryotic gene order. Nature Reviews Genetics, 2004, 5, 299-310.	7.7	661
5	Highly Expressed Genes in Yeast Evolve Slowly. Genetics, 2001, 158, 927-931.	1.2	556
6	Clustering of housekeeping genes provides a unified model of gene order in the human genome. Nature Genetics, 2002, 31, 180-183.	9.4	496
7	The Genetic Code Is One in a Million. Journal of Molecular Evolution, 1998, 47, 238-248.	0.8	466
8	Comparisons of dN/dS are time dependent for closely related bacterial genomes. Journal of Theoretical Biology, 2006, 239, 226-235.	0.8	400
9	The evolution of isochores. Nature Reviews Genetics, 2001, 2, 549-555.	7.7	379
10	Primate-specific endogenous retrovirus-driven transcription defines naive-like stem cells. Nature, 2014, 516, 405-409.	13.7	372
11	Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast. Nature, 2004, 429, 661-664.	13.7	324
12	Evidence for selection on synonymous mutations affecting stability of mRNA secondary structure in mammals. Genome Biology, 2005, 6, R75.	13.9	266
13	Evolutionary and Physiological Importance of Hub Proteins. PLoS Computational Biology, 2006, 2, e88.	1.5	251
14	Positively Charged Residues Are the Major Determinants of Ribosomal Velocity. PLoS Biology, 2013, 11, e1001508.	2.6	250
15	The Signature of Selection Mediated by Expression on Human Genes. Genome Research, 2003, 13, 2260-2264.	2.4	227
16	Chance and necessity in the evolution of minimal metabolic networks. Nature, 2006, 440, 667-670.	13.7	219
17	Predicting the virulence of MRSA from its genome sequence. Genome Research, 2014, 24, 839-849.	2.4	210
18	Evidence for Purifying Selection Against Synonymous Mutations in Mammalian Exonic Splicing Enhancers. Molecular Biology and Evolution, 2006, 23, 301-309.	3.5	209

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19	Rate of evolution and gene dispensability. <i>Nature</i> , 2003, 421, 496-497.	13.7	205
20	Stratus Not Altocumulus: A New View of the Yeast Protein Interaction Network. <i>PLoS Biology</i> , 2006, 4, e317.	2.6	205
21	Distinct physiological and behavioural functions for parental alleles of imprinted <i>Grb10</i> . <i>Nature</i> , 2011, 469, 534-538.	13.7	204
22	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
23	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
24	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
25	Parental progeny sequencing indicates higher mutation rates in heterozygotes. <i>Nature</i> , 2015, 523, 463-467.	13.7	157
26	Evidence for co-evolution of gene order and recombination rate. <i>Nature Genetics</i> , 2003, 33, 392-395.	9.4	143
27	Leukocyte Tyrosine Kinase Functions in Pigment Cell Development. <i>PLoS Genetics</i> , 2008, 4, e1000026.	1.5	137
28	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
29	Neighboring Genes Show Correlated Evolution in Gene Expression. <i>Molecular Biology and Evolution</i> , 2015, 32, 1748-1766.	3.5	126
30	Natural selection promotes the conservation of linkage of co-expressed genes. <i>Trends in Genetics</i> , 2002, 18, 604-606.	2.9	122
31	A unification of mosaic structures in the human genome. <i>Human Molecular Genetics</i> , 2003, 12, 2411-2415.	1.4	119
32	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
33	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
34	Metabolic trade-offs and the maintenance of the fittest and the flattest. <i>Nature</i> , 2011, 472, 342-346.	13.7	112
35	How do synonymous mutations affect fitness?. <i>BioEssays</i> , 2007, 29, 515-519.	1.2	107
36	Genetics and the understanding of selection. <i>Nature Reviews Genetics</i> , 2009, 10, 83-93.	7.7	107

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37	Evidence against the selfish operon theory. Trends in Genetics, 2004, 20, 232-234.	2.9	106
38	A Mixture of "Cheats" and "Co-Operators" Can Enable Maximal Group Benefit. PLoS Biology, 2010, 8, e1000486.	2.6	103
39	The proteins of linked genes evolve at similar rates. Nature, 2000, 407, 900-903.	13.7	100
40	Exonic Splicing Regulatory Elements Skew Synonymous Codon Usage near Intron-exon Boundaries in Mammals. Molecular Biology and Evolution, 2007, 24, 1600-1603.	3.5	98
41	Direct and indirect consequences of meiotic recombination: implications for genome evolution. Trends in Genetics, 2012, 28, 101-109.	2.9	97
42	Still Stratus Not Altocumulus: Further Evidence against the Date/Party Hub Distinction. PLoS Biology, 2007, 5, e154.	2.6	94
43	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
44	The architecture of intra-organism mutation rate variation in plants. PLoS Biology, 2019, 17, e3000191.	2.6	89
45	Chromatin remodelling is a major source of coexpression of linked genes in yeast. Trends in Genetics, 2007, 23, 480-484.	2.9	87
46	Maternally-inherited Grb10 reduces placental size and efficiency. Developmental Biology, 2010, 337, 1-8.	0.9	85
47	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.	3.5	83
48	The Impact of the Nucleosome Code on Protein-Coding Sequence Evolution in Yeast. PLoS Genetics, 2008, 4, e1000250.	1.5	80
49	Genomic Analysis of Isolates From the United Kingdom 2012 Pertussis Outbreak Reveals That Vaccine Antigen Genes Are Unusually Fast Evolving. Journal of Infectious Diseases, 2015, 212, 294-301.	1.9	79
50	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. Nucleic Acids Research, 2005, 33, 5533-5543.	6.5	78
51	The evolution, impact and properties of exonic splice enhancers. Genome Biology, 2013, 14, R143.	13.9	77
52	Great majority of recombination events in <i>Arabidopsis</i> are gene conversion events. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20992-20997.	3.3	69
53	Evidence for a Trade-Off between Translational Efficiency and Splicing Regulation in Determining Synonymous Codon Usage in <i>Drosophila melanogaster</i> . Molecular Biology and Evolution, 2007, 24, 2755-2762.	3.5	68
54	Evidence for Strong Mutation Bias toward, and Selection against, U Content in SARS-CoV-2: Implications for Vaccine Design. Molecular Biology and Evolution, 2021, 38, 67-83.	3.5	68

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55	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
56	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
57	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
58	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <i>Genetics</i> , 2017, 206, 363-376.	1.2	65
59	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
60	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
61	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.	6.5	63
62	The form of a tradeâ€™off determines the response to competition. <i>Ecology Letters</i> , 2013, 16, 1267-1276.	3.0	63
63	Pluripotency and the endogenous retrovirus HERVH: Conflict or serendipity?. <i>BioEssays</i> , 2016, 38, 109-117.	1.2	63
64	Codon Usage and Splicing Jointly Influence mRNA Localization. <i>Cell Systems</i> , 2020, 10, 351-362.e8.	2.9	61
65	Vertebrate genome evolution: a slow shuffle or a big bang?. <i>BioEssays</i> , 1999, 21, 697-703.	1.2	60
66	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
67	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
68	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
69	The determinants of gene order conservation in yeasts. <i>Genome Biology</i> , 2007, 8, R233.	13.9	58
70	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
71	Comparative evolutionary analysis of VPS33 homologues: genetic and functional insights. <i>Human Molecular Genetics</i> , 2005, 14, 1261-1270.	1.4	56
72	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

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73	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
74	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
75	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
76	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
77	Understanding the limits to generalizability of experimental evolutionary models. <i>Nature</i> , 2008, 455, 220-223.	13.7	49
78	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
79	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	13.7	47
80	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
81	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
82	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
83	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. <i>Genome Biology</i> , 2018, 19, 94.	3.8	43
84	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
85	Exonic splice regulation imposes strong selection at synonymous sites. <i>Genome Research</i> , 2018, 28, 1442-1454.	2.4	39
86	Birt Hogg—Dub— syndrome—associated FLCN mutations disrupt protein stability. <i>Human Mutation</i> , 2011, 32, 921-929.	1.1	38
87	Faster Evolving Primate Genes Are More Likely to Duplicate. <i>Molecular Biology and Evolution</i> , 2018, 35, 107-118.	3.5	38
88	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
89	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
90	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

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91	Teaching genetics prior to teaching evolution improves evolution understanding but not acceptance. <i>PLoS Biology</i> , 2017, 15, e2002255.	2.6	37
92	Causes and Consequences of Purifying Selection on SARS-CoV-2. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	37
93	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
94	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.	1.5	36
95	Sex and the X. <i>Nature</i> , 2001, 411, 149-150.	13.7	35
96	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
97	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
98	Competition between Transposable Elements and Mutator Genes in Bacteria. <i>Molecular Biology and Evolution</i> , 2012, 29, 3153-3159.	3.5	35
99	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
100	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
101	Exome sequencing identifies frequent mutation of MLL2 in non-“small cell lung carcinoma from Chinese patients. <i>Scientific Reports</i> , 2014, 4, 6036.	1.6	33
102	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
103	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
104	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
105	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
106	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
107	DO WOLBACHIA-ASSOCIATED INCOMPATIBILITIES PROMOTE POLYANDRY?. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 107-122.	1.1	28
108	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

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109	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
110	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
111	Estimating the prevalence of functional exonic splice regulatory information. <i>Human Genetics</i> , 2017, 136, 1059-1078.	1.8	26
112	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
113	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
114	Transcription, mRNA Export, and Immune Evasion Shape the Codon Usage of Viruses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	24
115	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
116	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
117	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
118	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in <i>Ascoidea asiatica</i> . <i>Current Biology</i> , 2018, 28, 2046-2057.e5.	1.8	22
119	Purifying Selection on Exonic Splice Enhancers in Intronless Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1396-1418.	3.5	21
120	Is Multiple Paternity Necessary for the Evolution of Genomic Imprinting?. <i>Genetics</i> , 1999, 153, 509-512.	1.2	21
121	A Quantitative Measure of Error Minimization in the Genetic Code. <i>Journal of Molecular Evolution</i> , 1999, 49, 708-708.	0.8	20
122	Mystery of the mutagenic male. <i>Nature</i> , 2002, 420, 365-366.	13.7	20
123	Monoallelic expression and tissue specificity are associated with high crossover rates. <i>Trends in Genetics</i> , 2009, 25, 519-522.	2.9	20
124	Comparison of <i>Iroquois</i> gene expression in limbs/fins of vertebrate embryos. <i>Journal of Anatomy</i> , 2010, 216, 683-691.	0.9	20
125	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
126	Do Alu repeats drive the evolution of the primate transcriptome?. <i>Genome Biology</i> , 2008, 9, R25.	13.9	19

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127	Conditional expression explains molecular evolution of social genes in a microbe. <i>Nature Communications</i> , 2019, 10, 3284.	5.8	19
128	Nonsense-mediated decay targets have multiple sequence-related features that can inhibit translation. <i>Molecular Systems Biology</i> , 2010, 6, 442.	3.2	18
129	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
130	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
131	Mutation rate analysis via parent-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
132	Identification of a New pebp2±A2 Isoform From Zebrafishrunx2Capable of Inducing Osteocalcin Gene Expression In Vitro. <i>Journal of Bone and Mineral Research</i> , 2005, 20, 1440-1453.	3.1	16
133	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
134	Evolutionary genomics and the reach of selection. <i>Journal of Biology</i> , 2009, 8, 12.	2.7	16
135	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
136	Scientific aptitude better explains poor responses to teaching of evolution than psychological conflicts. <i>Nature Ecology and Evolution</i> , 2018, 2, 388-394.	3.4	15
137	Peromysci, promiscuity and imprinting. <i>Nature Genetics</i> , 1998, 20, 315-316.	9.4	14
138	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
139	A positive becomes a negative. <i>Nature</i> , 2009, 457, 543-544.	13.7	13
140	Selfish genes and meiotic drive. <i>Nature</i> , 1998, 391, 223-223.	13.7	12
141	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
142	It's easier to get along with the quiet neighbours. <i>Molecular Systems Biology</i> , 2017, 13, 943.	3.2	12
143	Refining the Ambush Hypothesis: Evidence That GC- and AT-Rich Bacteria Employ Different Frameshift Defence Strategies. <i>Genome Biology and Evolution</i> , 2018, 10, 1153-1173.	1.1	12
144	Depletion of somatic mutations in splicing-associated sequences in cancer genomes. <i>Genome Biology</i> , 2017, 18, 213.	3.8	11

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145	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
146	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.	1.2	9
147	Accelerated molecular evolution of insect orthologues ofERG28/C14orf1: A link with ecdysteroid metabolism?. Journal of Genetics, 2001, 80, 17-21.	0.4	7
148	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.	3.5	7
149	Evidence in disease and non-disease contexts that nonsense mutations cause altered splicing via motif disruption. Nucleic Acids Research, 2021, 49, 9665-9685.	6.5	7
150	Selfish centromeres and the wastefulness of human reproduction. PLoS Biology, 2022, 20, e3001671.	2.6	7
151	Evolutionary genomics: reading the bands. BioEssays, 2000, 22, 105-107.	1.2	6
152	Open questions: A logic (or lack thereof) of genome organization. BMC Biology, 2013, 11, 58.	1.7	6
153	Evidence for Deep Phylogenetic Conservation of Exonic Splice-Related Constraints: Splice-Related Skews at Exonic Ends in the Brown Alga Ectocarpus Are Common and Resemble Those Seen in Humans. Genome Biology and Evolution, 2013, 5, 1731-1745.	1.1	6
154	Identification of Two Maternal Transmission Ratio Distortion Loci in Pedigrees of the Framingham Heart Study. Scientific Reports, 2013, 3, 2147.	1.6	6
155	Male Mutation Bias Is the Main Force Shaping Chromosomal Substitution Rates in Monotreme Mammals. Genome Biology and Evolution, 2017, 9, 2198-2210.	1.1	6
156	Dissecting dispensability. Nature Genetics, 2005, 37, 214-215.	9.4	5
157	Intronic AT Skew is a Defendable Proxy for Germline Transcription but does not Predict Crossing-Over or Protein Evolution Rates in Drosophila melanogaster. Journal of Molecular Evolution, 2010, 71, 415-426.	0.8	5
158	Late Replicating Domains Are Highly Recombining in Females but Have Low Male Recombination Rates: Implications for Isochore Evolution. PLoS ONE, 2011, 6, e24480.	1.1	5
159	Mitotic gene conversion can be as important as meiotic conversion in driving genetic variability in plants and other species without early germline segregation. PLoS Biology, 2021, 19, e3001164.	2.6	5
160	Does negative auto-regulation increase gene duplicability?. BMC Evolutionary Biology, 2009, 9, 193.	3.2	4
161	Effective Population Size Predicts Local Rates but Not Local Mitigation of Read-through Errors. Molecular Biology and Evolution, 2021, 38, 244-262.	3.5	4
162	Evidence from Drosophila Supports Higher Duplicability of Faster Evolving Genes. Genome Biology and Evolution, 2022, 14, .	1.1	4

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163	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
164	OUP accepted manuscript. <i>Molecular Biology and Evolution</i> , 2021, , .	3.5	2
165	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
166	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
167	Transgene-design: a web application for the design of mammalian transgenes. <i>Bioinformatics</i> , 2022, 38, 2626-2627.	1.8	1