

Scott Roy

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

6,138
citations

76196

40
h-index

79541

73
g-index

125
all docs

125
docs citations

125
times ranked

6861
citing authors

#	ARTICLE	IF	CITATIONS
1	Haldane's duel: intragenomic conflict, selfish Y chromosomes and speciation. Trends in Genetics, 2022, 38, 8-11.	2.9	3
2	How did a novel X-linked gene become essential for male determination?. Cell Research, 2022, 32, 7-8.	5.7	1
3	How illuminates why in plant germline methylation. Trends in Plant Science, 2022, , .	4.3	0
4	Distinct Minor Splicing Patterns across Cancers. Genes, 2022, 13, 387.	1.0	3
5	Digest: Study associates squamate rates, traits, and climates. Evolution; International Journal of Organic Evolution, 2022, , .	1.1	0
6	Optimality Versus Opportunity: The Recurrent Evolution of Similar Sex Determination Mechanisms. Journal of Heredity, 2022, 113, 235-237.	1.0	0
7	Gene-rich X chromosomes implicate intragenomic conflict in the evolution of bizarre genetic systems. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	6
8	Noncoding RNA, Intragenomic Conflict, and Rodent SRY Evolution. Trends in Genetics, 2021, 37, 102-104.	2.9	2
9	Analysis of Fungal Genomes Reveals Commonalities of Intron Gain or Loss and Functions in Intron-Poor Species. Molecular Biology and Evolution, 2021, 38, 4166-4186.	3.5	19
10	On the Form and Origins of the Bizarre Sex Chromosomal System of the Mandarin Vole. Journal of Heredity, 2021, 112, 328-334.	1.0	7
11	Mammals with Small Populations Do Not Exhibit Larger Genomes. Molecular Biology and Evolution, 2021, 38, 3737-3741.	3.5	6
12	Inbreeding, male viability, and the remarkable evolutionary stability of the aphid X chromosome. Heredity, 2021, 127, 135-140.	1.2	3
13	Sex chromosome transformation and the origin of a male-specific X chromosome in the creeping vole. Science, 2021, 372, 592-600.	6.0	20
14	CXCR3 Expression and Genome-Wide Δ Splice Site Selection in the TCGA Breast Cancer Cohort. Life, 2021, 11, 746.	1.1	3
15	Expansion and transformation of the minor spliceosomal system in the slime mold Physarum polycephalum. Current Biology, 2021, 31, 3125-3131.e4.	1.8	13
16	ExOrthist: a tool to infer exon orthologies at any evolutionary distance. Genome Biology, 2021, 22, 239.	3.8	11
17	On the utility of oddities: exceptional bee reproduction illuminates fundamental questions of recombination. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211478.	1.2	0
18	Dual Fertilization, Intragenomic Conflict, Genome Downsizing, and Angiosperm Dominance. Trends in Plant Science, 2021, 26, 767-769.	4.3	1

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19	Digest: Three sexes from two loci in one genome: A haploid alga expands the diversity of trioecious species*. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 3002-3003.	1.1	1
20	Coupling of spliceosome complexity to intron diversity. <i>Current Biology</i> , 2021, 31, 4898-4910.e4.	1.8	22
21	CRISPR-Cas Toxin Antitoxin Systems: Selfishness as a Constructive Evolutionary Force. <i>Trends in Microbiology</i> , 2021, 29, 869-870.	3.5	2
22	Costly circRNAs, Effective Population Size, and the Origins of Molecular Complexity. <i>Journal of Molecular Evolution</i> , 2021, 89, 598-600.	0.8	0
23	Sex determination: Ant supergenes link sex ratio to social structure. <i>Current Biology</i> , 2021, 31, R1573-R1575.	1.8	0
24	Comprehensive database and evolutionary dynamics of U12-type introns. <i>Nucleic Acids Research</i> , 2020, 48, 7066-7078.	6.5	35
25	CpG-creating mutations are costly in many human viruses. <i>Evolutionary Ecology</i> , 2020, 34, 339-359.	0.5	14
26	Patterns of conservation of spliceosomal intron structures and spliceosome divergence in representatives of the diplomonad and parabasalid lineages. <i>BMC Evolutionary Biology</i> , 2019, 19, 162.	3.2	17
27	Molecular Evolution: RNA Splicing Machinery Moonlights in Junk Removal. <i>Current Biology</i> , 2019, 29, R920-R922.	1.8	0
28	On the Function of Trans-Splicing: No Evidence for Widespread Proteome Diversification in Trypanosomes. <i>Genome Biology and Evolution</i> , 2019, 11, 3014-3021.	1.1	1
29	Investigating Instructor Talk in Novel Contexts: Widespread Use, Unexpected Categories, and an Emergent Sampling Strategy. <i>CBE Life Sciences Education</i> , 2019, 18, ar47.	1.1	31
30	Collectively Improving Our Teaching: Attempting Biology Department-wide Professional Development in Scientific Teaching. <i>CBE Life Sciences Education</i> , 2018, 17, ar2.	1.1	39
31	Intragenomic Conflict and Immune Tolerance: Do Selfish X-Linked Alleles Drive Skewed X Chromosome Inactivation?. <i>Genome Biology and Evolution</i> , 2018, 10, 857-862.	1.1	3
32	Classroom sound can be used to classify teaching practices in college science courses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3085-3090.	3.3	60
33	The Macronuclear Genome of <i>Stentor coeruleus</i> Reveals Tiny Introns in a Giant Cell. <i>Current Biology</i> , 2017, 27, 569-575.	1.8	105
34	Genomic and Transcriptomic Analysis Reveals Spliced Leader Trans-Splicing in Cryptomonads. <i>Genome Biology and Evolution</i> , 2017, 9, 468-473.	1.1	7
35	Transcriptomic analysis of diplomonad parasites reveals a trans-spliced intron in a helicase gene in <i>Giardia</i> . <i>PeerJ</i> , 2017, 5, e2861.	0.9	7
36	How Common Is Parallel Intron Gain? Rapid Evolution Versus Independent Creation in Recently Created Introns in <i>Daphnia</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 1902-1906.	3.5	13

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37	Is Mutation Random or Targeted?: No Evidence for Hypermutable in Snail Toxin Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2642-2647.	3.5	6
38	Is Genome Complexity a Consequence of Inefficient Selection? Evidence from Intron Creation in Nonrecombining Regions. <i>Molecular Biology and Evolution</i> , 2016, 33, 3088-3094.	3.5	9
39	Mechanism for DNA transposons to generate introns on genomic scales. <i>Nature</i> , 2016, 538, 533-536.	13.7	83
40	HAPCAD: An open-source tool to detect PCR crossovers in next-generation sequencing generated HLA data. <i>Human Immunology</i> , 2016, 77, 257-263.	1.2	4
41	A new model for the origins of allelic dimorphism in <i>Plasmodium falciparum</i> . <i>Parasitology International</i> , 2015, 64, 229-237.	0.6	4
42	Analyses of Alternatively Processed Genes in Ciliates Provide Insights into the Origins of Scrambled Genomes and May Provide a Mechanism for Speciation. <i>MBio</i> , 2015, 6, .	1.8	22
43	The <i>Plasmodium gaboni</i> genome illuminates allelic dimorphism of immunologically important surface antigens in <i>P. falciparum</i> . <i>Infection, Genetics and Evolution</i> , 2015, 36, 441-449.	1.0	7
44	Transcriptome sequencing and analysis of <i>Plasmodium gallinaceum</i> reveals polymorphisms and selection on the apical membrane antigen-1. <i>Malaria Journal</i> , 2014, 13, 382.	0.8	25
45	Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014, 505, 174-179.	13.7	689
46	Origin of Spliceosomal Introns and Alternative Splicing. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016071-a016071.	2.3	112
47	Diversity and Evolution of Spliceosomal Systems. <i>Methods in Molecular Biology</i> , 2014, 1126, 13-33.	0.4	11
48	Ancient cis-regulatory constraints and the evolution of genome architecture. <i>Trends in Genetics</i> , 2013, 29, 521-528.	2.9	30
49	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
50	Evolutionarily conserved A-to-I editing increases protein stability of the alternative splicing factor <i>Nova1</i> . <i>RNA Biology</i> , 2012, 9, 12-21.	1.5	40
51	Widespread Recurrent Evolution of Genomic Features. <i>Genome Biology and Evolution</i> , 2012, 4, 486-500.	1.1	34
52	Numerous Fragmented Spliceosomal Introns, AT-AC Splicing, and an Unusual Dynein Gene Expression Pathway in <i>Giardia lamblia</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 43-49.	3.5	31
53	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	13.7	377
54	Genome Evolution: Where Do New Introns Come From?. <i>Current Biology</i> , 2012, 22, R529-R531.	1.8	13

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55	Extensive conservation of ancient microsynteny across metazoans due to <i>cis</i> -regulatory constraints. <i>Genome Research</i> , 2012, 22, 2356-2367.	2.4	126
56	Contrasting 5' and 3' Evolutionary Histories and Frequent Evolutionary Convergence in Meis/hth Gene Structures. <i>Genome Biology and Evolution</i> , 2011, 3, 551-564.	1.1	16
57	Stepwise assembly of the <i>Nova</i> -regulated alternative splicing network in the vertebrate brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5319-5324.	3.3	38
58	Molecular Characterization of Myostatin Gene from Zhikong scallop <i>Chlamys farreri</i> (Jones et al). <i>Journal of Molecular Evolution</i> , 2010, 70, 622-629.	0.2	29
59	Compensatory Mutations Restore Fitness during the Evolution of Dihydrofolate Reductase. <i>Molecular Biology and Evolution</i> , 2010, 27, 2682-2690.	3.5	93
60	Internal and External Paralogy in the Evolution of Tropomyosin Genes in Metazoans. <i>Molecular Biology and Evolution</i> , 2010, 27, 1504-1517.	3.5	23
61	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	6.0	251
62	Constrained Intron Structures in a Microsporidian. <i>Molecular Biology and Evolution</i> , 2010, 27, 1979-1982.	3.5	30
63	Phylogenomics: Gene Duplication, Unrecognized Paralogy and Outgroup Choice. <i>PLoS ONE</i> , 2009, 4, e4568.	1.1	12
64	Evolution of Alternative Splicing Regulation: Changes in Predicted Exonic Splicing Regulators Are Not Associated with Changes in Alternative Splicing Levels in Primates. <i>PLoS ONE</i> , 2009, 4, e5800.	1.1	16
65	Complex selection on 5' splice sites in intron-rich organisms. <i>Genome Research</i> , 2009, 19, 2021-2027.	2.4	25
66	Mystery of intron gain: new data and new models. <i>Trends in Genetics</i> , 2009, 25, 67-73.	2.9	64
67	Intronization, de-intronization and intron sliding are rare in <i>Cryptococcus</i> . <i>BMC Evolutionary Biology</i> , 2009, 9, 192.	3.2	22
68	Quantitative regulation of alternative splicing in evolution and development. <i>BioEssays</i> , 2009, 31, 40-50.	1.2	49
69	Sequence diversity and evolutionary dynamics of the dimorphic antigen merozoite surface protein-6 and other <i>Msp</i> genes of <i>Plasmodium falciparum</i> . <i>Gene</i> , 2009, 443, 12-21.	1.0	9
70	Splicing in the eukaryotic ancestor: form, function and dysfunction. <i>Trends in Ecology and Evolution</i> , 2009, 24, 447-455.	4.2	47
71	Probing Evolutionary Repeatability: Neutral and Double Changes and the Predictability of Evolutionary Adaptation. <i>PLoS ONE</i> , 2009, 4, e4500.	1.1	13
72	Rare Genomic Characters Do Not Support Coelomata: RGC_CAMs. <i>Journal of Molecular Evolution</i> , 2008, 66, 308-315.	0.8	30

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73	When good transcripts go bad: artifactual RT-PCR "splicing" and genome analysis. <i>BioEssays</i> , 2008, 30, 601-605.	1.2	64
74	In response to letter from Benoit Chabot. <i>BioEssays</i> , 2008, 30, 1257-1258.	1.2	1
75	The <i>Caenorhabditis</i> globin gene family reveals extensive nematode-specific radiation and diversification. <i>BMC Evolutionary Biology</i> , 2008, 8, 279.	3.2	32
76	Origin of introns by "intronization" of exonic sequences. <i>Trends in Genetics</i> , 2008, 24, 378-381.	2.9	74
77	Patterns of polymorphism in genomic regions flanking three highly polymorphic surface antigens in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2008, 159, 1-6.	0.5	5
78	Intron mis-splicing: no alternative?. <i>Genome Biology</i> , 2008, 9, 208.	13.9	33
79	Spliceosomal introns as tools for genomic and evolutionary analysis. <i>Nucleic Acids Research</i> , 2008, 36, 1703-1712.	6.5	91
80	Origins of Human Malaria: Rare Genomic Changes and Full Mitochondrial Genomes Confirm the Relationship of <i>Plasmodium falciparum</i> to Other Mammalian Parasites but Complicate the Origins of <i>Plasmodium vivax</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1192-1198.	3.5	18
81	Rare Genomic Characters Do Not Support Coelomata: Intron Loss/Gain. <i>Molecular Biology and Evolution</i> , 2008, 25, 620-623.	3.5	40
82	Evolutionary Convergence on Highly-Conserved 3' Intron Structures in Intron-Poor Eukaryotes and Insights into the Ancestral Eukaryotic Genome. <i>PLoS Genetics</i> , 2008, 4, e1000148.	1.5	65
83	Widespread Evolutionary Conservation of Alternatively Spliced Exons in <i>Caenorhabditis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 375-382.	3.5	48
84	Evolutionary Conservation of UTR Intron Boundaries in <i>Cryptococcus</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 1140-1148.	3.5	18
85	On the Incidence of Intron Loss and Gain in Paralogous Gene Families. <i>Molecular Biology and Evolution</i> , 2007, 24, 1579-1581.	3.5	38
86	A Very High Fraction of Unique Intron Positions in the Intron-Rich Diatom <i>Thalassiosira pseudonana</i> Indicates Widespread Intron Gain. <i>Molecular Biology and Evolution</i> , 2007, 24, 1447-1457.	3.5	70
87	Widespread Intron Loss Suggests Retrotransposon Activity in Ancient Apicomplexans. <i>Molecular Biology and Evolution</i> , 2007, 24, 1926-1933.	3.5	33
88	Intron length distributions and gene prediction. <i>Nucleic Acids Research</i> , 2007, 35, 4737-4742.	6.5	45
89	Rare Coding Sequence Changes are Consistent with Ecdysozoa, not Coelomata. <i>Molecular Biology and Evolution</i> , 2007, 24, 1604-1607.	3.5	58
90	Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. <i>Genome Biology</i> , 2007, 8, R223.	13.9	115

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91	Functional and evolutionary analysis of alternatively spliced genes is consistent with an early eukaryotic origin of alternative splicing. <i>BMC Evolutionary Biology</i> , 2007, 7, 188.	3.2	75
92	Coevolution of genomic intron number and splice sites. <i>Trends in Genetics</i> , 2007, 23, 321-325.	2.9	93
93	Very little intron loss/gain in <i>Plasmodium</i> : Intron loss/gain mutation rates and intron number. <i>Genome Research</i> , 2006, 16, 750-756.	2.4	66
94	Smoke Without Fire: Most Reported Cases of Intron Gain in Nematodes Instead Reflect Intron Losses. <i>Molecular Biology and Evolution</i> , 2006, 23, 2259-2262.	3.5	55
95	The evolution of spliceosomal introns: patterns, puzzles and progress. <i>Nature Reviews Genetics</i> , 2006, 7, 211-221.	7.7	544
96	Intron-rich ancestors. <i>Trends in Genetics</i> , 2006, 22, 468-471.	2.9	58
97	Very Little Intron Gain in <i>Entamoeba histolytica</i> Genes Laterally Transferred from Prokaryotes. <i>Molecular Biology and Evolution</i> , 2006, 23, 1824-1827.	3.5	30
98	Large-scale intron conservation and order-of-magnitude variation in intron loss/gain rates in apicomplexan evolution. <i>Genome Research</i> , 2006, 16, 1270-1275.	2.4	43
99	Patterns of Intron Loss and Gain in Plants: Intron Loss-Dominated Evolution and Genome-Wide Comparison of <i>O. sativa</i> and <i>A. thaliana</i> . <i>Molecular Biology and Evolution</i> , 2006, 24, 171-181.	3.5	172
100	Rates of intron loss and gain: Implications for early eukaryotic evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5773-5778.	3.3	193
101	The pattern of intron loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 713-718.	3.3	117
102	Complex early genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1986-1991.	3.3	137
103	Resolution of a deep animal divergence by the pattern of intron conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4403-4408.	3.3	58
104	The origin of recent introns: transposons?. <i>Genome Biology</i> , 2004, 5, 251.	13.9	45
105	Recent Evidence for the Exon Theory of Genes. <i>Genetica</i> , 2003, 118, 251-266.	0.5	41
106	Mystery of Intron Gain. <i>Genome Research</i> , 2003, 13, 2236-2241.	2.4	64
107	Large-scale comparison of intron positions in mammalian genes shows intron loss but no gain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7158-7162.	3.3	193
108	Phylogenetically Older Introns Strongly Correlate With Module Boundaries in Ancient Proteins. <i>Genome Research</i> , 2003, 13, 1155-1157.	2.4	26

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109	Recent evidence for the exon theory of genes. <i>Genetica</i> , 2003, 118, 251-66.	0.5	25
110	Nonlinear partial differential equations and applications: The signal of ancient introns is obscured by intron density and homolog number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15513-15517.	3.3	18
111	Footprints of primordial introns on the eukaryotic genome. <i>Trends in Genetics</i> , 2001, 17, 496-499.	2.9	24
112	Centripetal modules and ancient introns. <i>Gene</i> , 1999, 238, 85-91.	1.0	44
113	The correlation between introns and the three-dimensional structure of proteins. <i>Gene</i> , 1997, 205, 141-144.	1.0	16
114	Expansion and Transformation of the Minor Spliceosomal System in the Slime Mold <i>Physarum polycephalum</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0