Scott Roy

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1127173/publications.pdf

Version: 2024-02-01

114 papers	6,138 citations	76326 40 h-index	79698 73 g-index
125 all docs	125 docs citations	125 times ranked	6861 citing authors

#	ARTICLE	IF	CITATIONS
1	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	27.8	689
2	The evolution of spliceosomal introns: patterns, puzzles and progress. Nature Reviews Genetics, 2006, 7, 211-221.	16.3	544
3	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	27.8	377
4	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	9.6	296
5	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. Science, 2010, 330, 1381-1385.	12.6	251
6	Large-scale comparison of intron positions in mammalian genes shows intron loss but no gain. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7158-7162.	7.1	193
7	Rates of intron loss and gain: Implications for early eukaryotic evolution. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5773-5778.	7.1	193
8	Patterns of Intron Loss and Gain in Plants: Intron Loss-Dominated Evolution and Genome-Wide Comparison of O. sativa and A. thaliana. Molecular Biology and Evolution, 2006, 24, 171-181.	8.9	172
9	Complex early genes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1986-1991.	7.1	137
10	Extensive conservation of ancient microsynteny across metazoans due to <i>cis</i>-regulatory constraints. Genome Research, 2012, 22, 2356-2367.	5.5	126
11	The pattern of intron loss. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 713-718.	7.1	117
12	Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. Genome Biology, 2007, 8, R223.	9.6	115
13	Origin of Spliceosomal Introns and Alternative Splicing. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016071-a016071.	5.5	112
14	The Macronuclear Genome of Stentor coeruleus Reveals Tiny Introns in a Giant Cell. Current Biology, 2017, 27, 569-575.	3.9	105
15	Coevolution of genomic intron number and splice sites. Trends in Genetics, 2007, 23, 321-325.	6.7	93
16	Compensatory Mutations Restore Fitness during the Evolution of Dihydrofolate Reductase. Molecular Biology and Evolution, 2010, 27, 2682-2690.	8.9	93
17	Spliceosomal introns as tools for genomic and evolutionary analysis. Nucleic Acids Research, 2008, 36, 1703-1712.	14.5	91
18	Mechanism for DNA transposons to generate introns on genomic scales. Nature, 2016, 538, 533-536.	27.8	83

#	ARTICLE	IF	CITATIONS
19	Functional and evolutionary analysis of alternatively spliced genes is consistent with an early eukaryotic origin of alternative splicing. BMC Evolutionary Biology, 2007, 7, 188.	3.2	75
20	Origin of introns by â€˜intronizationâ€™ of exonic sequences. Trends in Genetics, 2008, 24, 378-381.	6.7	74
21	A Very High Fraction of Unique Intron Positions in the Intron-Rich Diatom Thalassiosira pseudonana Indicates Widespread Intron Gain. Molecular Biology and Evolution, 2007, 24, 1447-1457.	8.9	70
22	Very little intron loss/gain in Plasmodium: Intron loss/gain mutation rates and intron number. Genome Research, 2006, 16, 750-756.	5.5	66
23	Evolutionary Convergence on Highly-Conserved 3â€² Intron Structures in Intron-Poor Eukaryotes and Insights into the Ancestral Eukaryotic Genome. PLoS Genetics, 2008, 4, e1000148.	3.5	65
24	Mystery of Intron Gain. Genome Research, 2003, 13, 2236-2241.	5.5	64
25	When good transcripts go bad: artifactual RTâ€PCR â€˜splicingâ€™ and genome analysis. BioEssays, 2008, 30, 601-605.	2.5	64
26	Mystery of intron gain: new data and new models. Trends in Genetics, 2009, 25, 67-73.	6.7	64
27	Classroom sound can be used to classify teaching practices in college science courses. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3085-3090.	7.1	60
28	Resolution of a deep animal divergence by the pattern of intron conservation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4403-4408.	7.1	58
29	Intron-rich ancestors. Trends in Genetics, 2006, 22, 468-471.	6.7	58
30	Rare Coding Sequence Changes are Consistent with Ecdysozoa, not Coelomata. Molecular Biology and Evolution, 2007, 24, 1604-1607.	8.9	58
31	Smoke Without Fire: Most Reported Cases of Intron Gain in Nematodes Instead Reflect Intron Losses. Molecular Biology and Evolution, 2006, 23, 2259-2262.	8.9	55
32	Quantitative regulation of alternative splicing in evolution and development. BioEssays, 2009, 31, 40-50.	2.5	49
33	Widespread Evolutionary Conservation of Alternatively Spliced Exons in Caenorhabditis. Molecular Biology and Evolution, 2008, 25, 375-382.	8.9	48
34	Splicing in the eukaryotic ancestor: form, function and dysfunction. Trends in Ecology and Evolution, 2009, 24, 447-455.	8.7	47
35	The origin of recent introns: transposons?. Genome Biology, 2004, 5, 251.	9.6	45
36	Intron length distributions and gene prediction. Nucleic Acids Research, 2007, 35, 4737-4742.	14.5	45

#	ARTICLE	IF	CITATIONS
37	Centripetal modules and ancient introns. Gene, 1999, 238, 85-91.	2.2	44
38	Large-scale intron conservation and order-of-magnitude variation in intron loss/gain rates in apicomplexan evolution. Genome Research, 2006, 16, 1270-1275.	5.5	43
39	Recent Evidence for the Exon Theory of Genes. Genetica, 2003, 118, 251-266.	1.1	41
40	Rare Genomic Characters Do Not Support Coelomata: Intron Loss/Gain. Molecular Biology and Evolution, 2008, 25, 620-623.	8.9	40
41	Evolutionarily conserved A-to-I editing increases protein stability of the alternative splicing factor<i>Nova1</i>. RNA Biology, 2012, 9, 12-21.	3.1	40
42	Collectively Improving Our Teaching: Attempting Biology Departmentâ€“wide Professional Development in Scientific Teaching. CBE Life Sciences Education, 2018, 17, ar2.	2.3	39
43	On the Incidence of Intron Loss and Gain in Paralogous Gene Families. Molecular Biology and Evolution, 2007, 24, 1579-1581.	8.9	38
44	Stepwise assembly of the <i>Nova</i> -regulated alternative splicing network in the vertebrate brain. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5319-5324.	7.1	38
45	Comprehensive database and evolutionary dynamics of U12-type introns. Nucleic Acids Research, 2020, 48, 7066-7078.	14.5	35
46	Widespread Recurrent Evolution of Genomic Features. Genome Biology and Evolution, 2012, 4, 486-500.	2.5	34
47	Widespread Intron Loss Suggests Retrotransposon Activity in Ancient Apicomplexans. Molecular Biology and Evolution, 2007, 24, 1926-1933.	8.9	33
48	Intron mis-splicing: no alternative?. Genome Biology, 2008, 9, 208.	9.6	33
49	The Caenorhabditis globin gene family reveals extensive nematode-specific radiation and diversification. BMC Evolutionary Biology, 2008, 8, 279.	3.2	32
50	Numerous Fragmented Spliceosomal Introns, AT-AC Splicing, and an Unusual Dynein Gene Expression Pathway in Giardia lamblia. Molecular Biology and Evolution, 2012, 29, 43-49.	8.9	31
51	Investigating Instructor Talk in Novel Contexts: Widespread Use, Unexpected Categories, and an Emergent Sampling Strategy. CBE Life Sciences Education, 2019, 18, ar47.	2.3	31
52	Very Little Intron Gain in Entamoeba histolytica Genes Laterally Transferred from Prokaryotes. Molecular Biology and Evolution, 2006, 23, 1824-1827.	8.9	30
53	Rare Genomic Characters Do Not Support Coelomata: RGC_CAMs. Journal of Molecular Evolution, 2008, 66, 308-315.	1.8	30
54	Constrained Intron Structures in a Microsporidian. Molecular Biology and Evolution, 2010, 27, 1979-1982.	8.9	30

#	ARTICLE	IF	CITATIONS
55	Ancient cis-regulatory constraints and the evolution of genome architecture. Trends in Genetics, 2013, 29, 521-528.	6.7	30
56	Molecular Characterization of Myostatin Gene from Zhikong scallop Chlamys farreri (Jones et) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	0.7	29
57	Phylogenetically Older Introns Strongly Correlate With Module Boundaries in Ancient Proteins. Genome Research, 2003, 13, 1155-1157.	5.5	26
58	Complex selection on 5â€² splice sites in intron-rich organisms. Genome Research, 2009, 19, 2021-2027.	5.5	25
59	Transcriptome sequencing and analysis of Plasmodium gallinaceum reveals polymorphisms and selection on the apical membrane antigen-1. Malaria Journal, 2014, 13, 382.	2.3	25
60	Recent evidence for the exon theory of genes. Genetica, 2003, 118, 251-66.	1.1	25
61	Footprints of primordial introns on the eukaryotic genome. Trends in Genetics, 2001, 17, 496-499.	6.7	24
62	Internal and External Paralogy in the Evolution of Tropomyosin Genes in Metazoans. Molecular Biology and Evolution, 2010, 27, 1504-1517.	8.9	23
63	Intronization, de-intronization and intron sliding are rare in Cryptococcus. BMC Evolutionary Biology, 2009, 9, 192.	3.2	22
64	Analyses of Alternatively Processed Genes in Ciliates Provide Insights into the Origins of Scrambled Genomes and May Provide a Mechanism for Speciation. MBio, 2015, 6, .	4.1	22
65	Coupling of spliceosome complexity to intron diversity. Current Biology, 2021, 31, 4898-4910.e4.	3.9	22
66	Sex chromosome transformation and the origin of a male-specific X chromosome in the creeping vole. Science, 2021, 372, 592-600.	12.6	20
67	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.	8.9	19
68	Nonlinear partial differential equations and applications: The signal of ancient introns is obscured by intron density and homolog number. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15513-15517.	7.1	18
69	Evolutionary Conservation of UTR Intron Boundaries in Cryptococcus. Molecular Biology and Evolution, 2007, 24, 1140-1148.	8.9	18
70	Origins of Human Malaria: Rare Genomic Changes and Full Mitochondrial Genomes Confirm the Relationship of Plasmodium falciparum to Other Mammalian Parasites but Complicate the Origins of Plasmodium vivax. Molecular Biology and Evolution, 2008, 25, 1192-1198.	8.9	18
71	Patterns of conservation of spliceosomal intron structures and spliceosome divergence in representatives of the diplomonad and parabasalid lineages. BMC Evolutionary Biology, 2019, 19, 162.	3.2	17
72	The correlation between introns and the three-dimensional structure of proteins. Gene, 1997, 205, 141-144.	2.2	16

#	ARTICLE	IF	CITATIONS
73	Evolution of Alternative Splicing Regulation: Changes in Predicted Exonic Splicing Regulators Are Not Associated with Changes in Alternative Splicing Levels in Primates. PLoS ONE, 2009, 4, e5800.	2.5	16
74	Contrasting 5' and 3' Evolutionary Histories and Frequent Evolutionary Convergence in Meis/hth Gene Structures. Genome Biology and Evolution, 2011, 3, 551-564.	2.5	16
75	CpG-creating mutations are costly in many human viruses. Evolutionary Ecology, 2020, 34, 339-359.	1.2	14
76	Genome Evolution: Where Do New Introns Come From?. Current Biology, 2012, 22, R529-R531.	3.9	13
77	How Common Is Parallel Intron Gain? Rapid Evolution Versus Independent Creation in Recently Created Introns in<i>Daphnia</i>. Molecular Biology and Evolution, 2016, 33, 1902-1906.	8.9	13
78	Expansion and transformation of the minor spliceosomal system in the slime mold Physarum polycephalum. Current Biology, 2021, 31, 3125-3131.e4.	3.9	13
79	Probing Evolutionary Repeatability: Neutral and Double Changes and the Predictability of Evolutionary Adaptation. PLoS ONE, 2009, 4, e4500.	2.5	13
80	Phylogenomics: Gene Duplication, Unrecognized Paralogy and Outgroup Choice. PLoS ONE, 2009, 4, e4568.	2.5	12
81	ExOrthist: a tool to infer exon orthologies at any evolutionary distance. Genome Biology, 2021, 22, 239.	8.8	11
82	Diversity and Evolution of Spliceosomal Systems. Methods in Molecular Biology, 2014, 1126, 13-33.	0.9	11
83	Sequence diversity and evolutionary dynamics of the dimorphic antigen merozoite surface protein-6 and other Msp genes of Plasmodium falciparum. Gene, 2009, 443, 12-21.	2.2	9
84	Is Genome Complexity a Consequence of Inefficient Selection? Evidence from Intron Creation in Nonrecombining Regions. Molecular Biology and Evolution, 2016, 33, 3088-3094.	8.9	9
85	The Plasmodium gaboni genome illuminates allelic dimorphism of immunologically important surface antigens in P. falciparum. Infection, Genetics and Evolution, 2015, 36, 441-449.	2.3	7
86	Genomic and Transcriptomic Analysis Reveals Spliced Leader Trans-Splicing in Cryptomonads. Genome Biology and Evolution, 2017, 9, 468-473.	2.5	7
87	On the Form and Origins of the Bizarre Sex Chromosomal System of the Mandarin Vole. Journal of Heredity, 2021, 112, 328-334.	2.4	7
88	Transcriptomic analysis of diplomonad parasites reveals a trans-spliced intron in a helicase gene in <i>Giardia</i>. PeerJ, 2017, 5, e2861.	2.0	7
89	Is Mutation Random or Targeted?: No Evidence for Hypermutability in Snail Toxin Genes. Molecular Biology and Evolution, 2016, 33, 2642-2647.	8.9	6
90	Mammals with Small Populations Do Not Exhibit Larger Genomes. Molecular Biology and Evolution, 2021, 38, 3737-3741.	8.9	6

#	ARTICLE	IF	CITATIONS
91	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, .	7.1	6
92	Patterns of polymorphism in genomic regions flanking three highly polymorphic surface antigens in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2008, 159, 1-6.	1.1	5
93	A new model for the origins of allelic dimorphism in Plasmodium falciparum. Parasitology International, 2015, 64, 229-237.	1.3	4
94	HAPCAD: An open-source tool to detect PCR crossovers in next-generation sequencing generated HLA data. Human Immunology, 2016, 77, 257-263.	2.4	4
95	Intragenomic Conflict and Immune Tolerance: Do Selfish X-Linked Alleles Drive Skewed X Chromosome Inactivation?. Genome Biology and Evolution, 2018, 10, 857-862.	2.5	3
96	Inbreeding, male viability, and the remarkable evolutionary stability of the aphid X chromosome. Heredity, 2021, 127, 135-140.	2.6	3
97	Haldaneâ€™s duel: intragenomic conflict, selfish Y chromosomes and speciation. Trends in Genetics, 2022, 38, 8-11.	6.7	3
98	CXCR3 Expression and Genome-Wide 3â€² Splice Site Selection in the TCGA Breast Cancer Cohort. Life, 2021, 11, 746.	2.4	3
99	Distinct Minor Splicing Patterns across Cancers. Genes, 2022, 13, 387.	2.4	3
100	Noncoding RNA, Intragenomic Conflict, and Rodent SRY Evolution. Trends in Genetics, 2021, 37, 102-104.	6.7	2
101	CRISPR-Cas Toxinâ€“Antitoxin Systems: Selfishness as a Constructive Evolutionary Force. Trends in Microbiology, 2021, 29, 869-870.	7.7	2
102	In response to letter from Benoit Chabot. BioEssays, 2008, 30, 1257-1258.	2.5	1
103	On the Function of Trans-Splicing: No Evidence for Widespread Proteome Diversification in Trypanosomes. Genome Biology and Evolution, 2019, 11, 3014-3021.	2.5	1
104	Dual Fertilization, Intragenomic Conflict, Genome Downsizing, and Angiosperm Dominance. Trends in Plant Science, 2021, 26, 767-769.	8.8	1
105	Digest: Three sexes from two loci in one genome: A haploid alga expands the diversity of trioecious species*. Evolution; International Journal of Organic Evolution, 2021, 75, 3002-3003.	2.3	1
106	How did a novel X-linked gene become essential for male determination?. Cell Research, 2022, 32, 7-8.	12.0	1
107	Molecular Evolution: RNA Splicing Machinery Moonlights in Junk Removal. Current Biology, 2019, 29, R920-R922.	3.9	0
108	On the utility of oddities: exceptional bee reproduction illuminates fundamental questions of recombination. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20211478.	2.6	0

#	ARTICLE	IF	CITATIONS
109	Costly circRNAs, Effective Population Size, and the Origins of Molecular Complexity. Journal of Molecular Evolution, 2021, 89, 598-600.	1.8	0
110	Expansion and Transformation of the Minor Spliceosomal System in the Slime Mold <i>Physarum polycephalum</i>. SSRN Electronic Journal, 0, , .	0.4	0
111	How illuminates why in plant germline methylation. Trends in Plant Science, 2022, , .	8.8	0
112	Digest: Study associates squamate rates, traits, and climates. Evolution; International Journal of Organic Evolution, 2022, , .	2.3	0
113	Optimality Versus Opportunity: The Recurrent Evolution of Similar Sex Determination Mechanisms. Journal of Heredity, 2022, 113, 235-237.	2.4	0
114	Sex determination: Ant supergenes link sex ratio toÂsocial structure. Current Biology, 2021, 31, R1573-R1575.	3.9	0