

Laurent Duret

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

13,669
citations

20817

60
h-index

24258

110
g-index

126
all docs

126
docs citations

126
times ranked

14158
citing authors

#	ARTICLE	IF	CITATIONS
1	DILS: Demographic inferences with linked selection by using ABC. <i>Molecular Ecology Resources</i> , 2021, 21, 2629-2644.	4.8	32
2	Massive colonization of protein-coding exons by selfish genetic elements in <i>Paramecium</i> germline genomes. <i>PLoS Biology</i> , 2021, 19, e3001309.	5.6	30
3	Evolutionary Plasticity of Mating-Type Determination Mechanisms in <i>Paramecium aurelia</i> Sibling Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	13
4	Population genomics supports clonal reproduction and multiple independent gains and losses of parasitic abilities in the most devastating nematode pest. <i>Evolutionary Applications</i> , 2020, 13, 442-457.	3.1	23
5	How consistent is RAD-seq divergence with DNA barcode based clustering in insects?. <i>Molecular Ecology Resources</i> , 2020, 20, 1294-1298.	4.8	4
6	Bedrock radioactivity influences the rate and spectrum of mutation. <i>ELife</i> , 2020, 9, .	6.0	8
7	Global survey of mobile DNA horizontal transfer in arthropods reveals Lepidoptera as a prime hotspot. <i>PLoS Genetics</i> , 2019, 15, e1007965.	3.5	41
8	Evolution of replication origins in vertebrate genomes: rapid turnover despite selective constraints. <i>Nucleic Acids Research</i> , 2019, 47, 5114-5125.	14.5	10
9	GC-biased gene conversion conceals the prediction of the nearly neutral theory in avian genomes. <i>Genome Biology</i> , 2019, 20, 5.	8.8	37
10	PRDM9 Methyltransferase Activity Is Essential for Meiotic DNA Double-Strand Break Formation at Its Binding Sites. <i>Molecular Cell</i> , 2018, 69, 853-865.e6.	9.7	110
11	Codon Usage Bias in Animals: Disentangling the Effects of Natural Selection, Effective Population Size, and GC-Biased Gene Conversion. <i>Molecular Biology and Evolution</i> , 2018, 35, 1092-1103.	8.9	111
12	Unbiased Estimate of Synonymous and Nonsynonymous Substitution Rates with Nonstationary Base Composition. <i>Molecular Biology and Evolution</i> , 2018, 35, 734-742.	8.9	43
13	Life History Traits Impact the Nuclear Rate of Substitution but Not the Mitochondrial Rate in Isopods. <i>Molecular Biology and Evolution</i> , 2018, 35, 2900-2912.	8.9	28
14	Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017, 27, 1016-1028.	5.5	75
15	In vivo binding of PRDM9 reveals interactions with noncanonical genomic sites. <i>Genome Research</i> , 2017, 27, 580-590.	5.5	67
16	The Red Queen model of recombination hot-spot evolution: a theoretical investigation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160463.	4.0	32
17	The fitness cost of mis-splicing is the main determinant of alternative splicing patterns. <i>Genome Biology</i> , 2017, 18, 208.	8.8	76
18	Recombination, meiotic expression and human codon usage. <i>ELife</i> , 2017, 6, .	6.0	59

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19	No Evidence That Nitrogen Limitation Influences the Elemental Composition of Isopod Transcriptomes and Proteomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2605-2620.	8.9	9
20	Occurrence of a non deleterious gene conversion event in the <i>BRCA1</i> gene. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 646-652.	2.8	3
21	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228.	5.5	127
22	Optimization of multiplexed RADseq libraries using low-cost adaptors. <i>Genetica</i> , 2015, 143, 139-143.	1.1	4
23	GC-Content Evolution in Bacterial Genomes: The Biased Gene Conversion Hypothesis Expands. <i>PLoS Genetics</i> , 2015, 11, e1004941.	3.5	200
24	The Spatiotemporal Program of DNA Replication Is Associated with Specific Combinations of Chromatin Marks in Human Cells. <i>PLoS Genetics</i> , 2014, 10, e1004282.	3.5	123
25	The Red Queen Model of Recombination Hotspots Evolution in the Light of Archaic and Modern Human Genomes. <i>PLoS Genetics</i> , 2014, 10, e1004790.	3.5	62
26	Strong Heterogeneity in Mutation Rate Causes Misleading Hallmarks of Natural Selection on Indel Mutations in the Human Genome. <i>Molecular Biology and Evolution</i> , 2014, 31, 23-36.	8.9	16
27	Estimation of the RNU2 macrosatellite mutation rate by BRCA1 mutation tracing. <i>Nucleic Acids Research</i> , 2014, 42, 9121-9130.	14.5	4
28	XACT, a long noncoding transcript coating the active X chromosome in human pluripotent cells. <i>Nature Genetics</i> , 2013, 45, 239-241.	21.4	125
29	The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. <i>Genome Research</i> , 2013, 23, 749-761.	5.5	206
30	GC-Biased Gene Conversion in Yeast Is Specifically Associated with Crossovers: Molecular Mechanisms and Evolutionary Significance. <i>Molecular Biology and Evolution</i> , 2013, 30, 1409-1419.	8.9	87
31	Genome-scale coestimation of species and gene trees. <i>Genome Research</i> , 2013, 23, 323-330.	5.5	223
32	Is RADseq suitable for phylogenetic inference? An in silico assessment and optimization. <i>Ecology and Evolution</i> , 2013, 3, 846-852.	1.9	162
33	The Paramecium Germline Genome Provides a Niche for Intragenic Parasitic DNA: Evolutionary Dynamics of Internal Eliminated Sequences. <i>PLoS Genetics</i> , 2012, 8, e1002984.	3.5	154
34	Evidence for Widespread GC-biased Gene Conversion in Eukaryotes. <i>Genome Biology and Evolution</i> , 2012, 4, 675-682.	2.5	154
35	Ultra-fast sequence clustering from similarity networks with SiLiX. <i>BMC Bioinformatics</i> , 2011, 12, 116.	2.6	271
36	Meiotic recombination favors the spreading of deleterious mutations in human populations. <i>Human Mutation</i> , 2011, 32, 198-206.	2.5	37

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37	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	12.8	481
38	Ftx is a non-coding RNA which affects Xist expression and chromatin structure within the X-inactivation center region. <i>Human Molecular Genetics</i> , 2011, 20, 705-718.	2.9	222
39	Preventing Dangerous Nonsense: Selection for Robustness to Transcriptional Error in Human Genes. <i>PLoS Genetics</i> , 2011, 7, e1002276.	3.5	39
40	Gene expression in a paleopolyploid: a transcriptome resource for the ciliate <i>Paramecium tetraurelia</i> . <i>BMC Genomics</i> , 2010, 11, 547.	2.8	64
41	Detecting positive selection within genomes: the problem of biased gene conversion. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 2571-2580.	4.0	130
42	The Relationship among Gene Expression, the Evolution of Gene Dosage, and the Rate of Protein Evolution. <i>PLoS Genetics</i> , 2010, 6, e1000944.	3.5	189
43	<i>Paramecium tetraurelia</i> : The Renaissance of an Early Unicellular Model. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.emo140.	0.3	43
44	Silencing Specific <i>Paramecium tetraurelia</i> Genes by Feeding Double-Stranded RNA. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5363.	0.3	27
45	Mutation Patterns in the Human Genome: More Variable Than Expected. <i>PLoS Biology</i> , 2009, 7, e1000028.	5.6	42
46	The Relationship between DNA Replication and Human Genome Organization. <i>Molecular Biology and Evolution</i> , 2009, 26, 729-741.	8.9	43
47	Comment on "Human-Specific Gain of Function in a Developmental Enhancer". <i>Science</i> , 2009, 323, 714-714.	12.6	30
48	GC-biased gene conversion promotes the fixation of deleterious amino acid changes in primates. <i>Trends in Genetics</i> , 2009, 25, 1-5.	6.7	167
49	Monoallelic expression and tissue specificity are associated with high crossover rates. <i>Trends in Genetics</i> , 2009, 25, 519-522.	6.7	20
50	Databases of homologous gene families for comparative genomics. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	118
51	Biased Gene Conversion and the Evolution of Mammalian Genomic Landscapes. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 285-311.	6.2	607
52	Differential Retention of Metabolic Genes Following Whole-Genome Duplication. <i>Molecular Biology and Evolution</i> , 2009, 26, 1067-1072.	8.9	38
53	Translational control of intron splicing in eukaryotes. <i>Nature</i> , 2008, 451, 359-362.	27.8	200
54	Genome-wide studies highlight indirect links between human replication origins and gene regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15837-15842.	7.1	267

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55	Analysis of sequence variability in the macronuclear DNA of <i>Paramecium tetraurelia</i> : A somatic view of the germline. <i>Genome Research</i> , 2008, 18, 585-596.	5.5	82
56	The Impact of Recombination on Nucleotide Substitutions in the Human Genome. <i>PLoS Genetics</i> , 2008, 4, e1000071.	3.5	303
57	ISG20L2, a Novel Vertebrate Nucleolar Exoribonuclease Involved in Ribosome Biogenesis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 546-559.	3.8	38
58	Pervasive positive selection on duplicated and nonduplicated vertebrate protein coding genes. <i>Genome Research</i> , 2008, 18, 1393-1402.	5.5	73
59	Identification and characterization of human Mex-3 proteins, a novel family of evolutionarily conserved RNA-binding proteins differentially localized to processing bodies. <i>Nucleic Acids Research</i> , 2007, 35, 1289-1300.	14.5	127
60	Unexpected observations after mapping LongSAGE tags to the human genome. <i>BMC Bioinformatics</i> , 2007, 8, 154.	2.6	14
61	Adaptation or biased gene conversion? Extending the null hypothesis of molecular evolution. <i>Trends in Genetics</i> , 2007, 23, 273-277.	6.7	214
62	A new perspective on isochore evolution. <i>Gene</i> , 2006, 385, 71-74.	2.2	88
63	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	27.8	744
64	The Xist RNA Gene Evolved in Eutherians by Pseudogenization of a Protein-Coding Gene. <i>Science</i> , 2006, 312, 1653-1655.	12.6	371
65	GC Content Evolution of the Human and Mouse Genomes: Insights from the Study of Processed Pseudogenes in Regions of Different Recombination Rates. <i>Journal of Molecular Evolution</i> , 2006, 62, 745-752.	1.8	23
66	The GC Content of Primates and Rodents Genomes Is Not at Equilibrium: A Reply to Antezana. <i>Journal of Molecular Evolution</i> , 2006, 62, 803-806.	1.8	18
67	No Evidence for Tissue-Specific Adaptation of Synonymous Codon Usage in Humans. <i>Molecular Biology and Evolution</i> , 2006, 23, 523-529.	8.9	73
68	Evolutionary Origin and Maintenance of Coexpressed Gene Clusters in Mammals. <i>Molecular Biology and Evolution</i> , 2006, 23, 1715-1723.	8.9	123
69	Relationship between gene expression and GC-content in mammals: statistical significance and biological relevance. <i>Human Molecular Genetics</i> , 2005, 14, 421-427.	2.9	85
70	Homology-dependent methylation in primate repetitive DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5471-5476.	7.1	50
71	Tree pattern matching in phylogenetic trees: automatic search for orthologs or paralogs in homologous gene sequence databases. <i>Bioinformatics</i> , 2005, 21, 2596-2603.	4.1	161
72	Natural history of the ERVWE1 endogenous retroviral locus. <i>Retrovirology</i> , 2005, 2, 57.	2.0	19

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73	Evidence of Selection on the Domesticated ERVWE1 env Retroviral Element Involved in Placentation. <i>Molecular Biology and Evolution</i> , 2004, 21, 1895-1901.	8.9	53
74	Polymorphix: a sequence polymorphism database. <i>Nucleic Acids Research</i> , 2004, 33, D481-D484.	14.5	17
75	The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1731-1736.	7.1	192
76	Recombination Drives the Evolution of GC-Content in the Human Genome. <i>Molecular Biology and Evolution</i> , 2004, 21, 984-990.	8.9	302
77	Physical and transcript map of the autosomal dominant colobomatous microphthalmia locus on chromosome 15q12-q15 and refinement to a 4.4%Mb region. <i>European Journal of Human Genetics</i> , 2004, 12, 574-578.	2.8	10
78	Evidence that functional transcription units cover at least half of the human genome. <i>Trends in Genetics</i> , 2004, 20, 229-232.	6.7	35
79	The Decline of Isochores in Mammals: An Assessment of the GC Content Variation Along the Mammalian Phylogeny. <i>Journal of Molecular Evolution</i> , 2004, 58, 653-660.	1.8	63
80	HOPPSIGEN: a database of human and mouse processed pseudogenes. <i>Nucleic Acids Research</i> , 2004, 33, D59-D66.	14.5	44
81	Subcellular localization of 14-3-3 proteins in <i>Toxoplasma gondii</i> tachyzoites and evidence for a lipid raft-associated form. <i>FEMS Microbiology Letters</i> , 2003, 224, 161-168.	1.8	35
82	Placenta-Specific INSL4 Expression Is Mediated by a Human Endogenous Retrovirus Element 1. <i>Biology of Reproduction</i> , 2003, 68, 1422-1429.	2.7	86
83	Integrated databanks access and sequence/structure analysis services at the PBIL. <i>Nucleic Acids Research</i> , 2003, 31, 3393-3399.	14.5	28
84	Neutral effect of recombination on base composition in <i>Drosophila</i> . <i>Genetical Research</i> , 2003, 81, 79-87.	0.9	69
85	Patterns of Selection Against Transposons Inferred From the Distribution of Tc1, Tc3 and Tc5 Insertions in the <i>mut-7</i> Line of the Nematode <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2003, 165, 1127-1135.	2.9	31
86	Hovergen: Comparative Analysis of Homologous Vertebrate Genes. , 2002, , 21-35.		0
87	Evolution of synonymous codon usage in metazoans. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 640-649.	3.3	460
88	Expected Relationship Between the Silent Substitution Rate and the GC Content: Implications for the Evolution of Isochores. <i>Journal of Molecular Evolution</i> , 2002, 54, 129-133.	1.8	41
89	Vanishing GC-Rich Isochores in Mammalian Genomes. <i>Genetics</i> , 2002, 162, 1837-1847.	2.9	157
90	Comparative Sequence Analysis of the X-Inactivation Center Region in Mouse, Human, and Bovine. <i>Genome Research</i> , 2002, 12, 894-908.	5.5	212

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91	A <i>Medicago truncatula</i> Homogluthathione Synthetase Is Derived from Glutathione Synthetase by Gene Duplication. <i>Plant Physiology</i> , 2001, 126, 1706-1715.	4.8	62
92	Determinants of CpG Islands: Expression in Early Embryo and Isochore Structure. <i>Genome Research</i> , 2001, 11, 1854-1860.	5.5	105
93	Synonymous Codon Usage, Accuracy of Translation, and Gene Length in <i>Caenorhabditis elegans</i> . <i>Journal of Molecular Evolution</i> , 2001, 52, 275-280.	1.8	121
94	The Elevated GC Content at Exonic Third Sites Is Not Evidence Against Neutralist Models of Isochore Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 757-762.	8.9	45
95	Determinants of Substitution Rates in Mammalian Genes: Expression Pattern Affects Selection Intensity but Not Mutation Rate. <i>Molecular Biology and Evolution</i> , 2000, 17, 68-070.	8.9	475
96	The Covariation Between TpA Deficiency, CpG Deficiency, and G+C Content of Human Isochores Is Due to a Mathematical Artifact. <i>Molecular Biology and Evolution</i> , 2000, 17, 1620-1625.	8.9	77
97	tRNA gene number and codon usage in the <i>C. elegans</i> genome are co-adapted for optimal translation of highly expressed genes. <i>Trends in Genetics</i> , 2000, 16, 287-289.	6.7	375
98	Chromosomal Distribution and Coding Capacity of the Human Endogenous Retrovirus HERV-W Family. <i>AIDS Research and Human Retroviruses</i> , 2000, 16, 731-740.	1.1	90
99	Nature and Structure of Human Genes that Generate Retropseudogenes. <i>Genome Research</i> , 2000, 10, 672-678.	5.5	167
100	HOBACGEN: Database System for Comparative Genomics in Bacteria. <i>Genome Research</i> , 2000, 10, 379-385.	5.5	69
101	Identification and molecular analysis of BANP. <i>Gene</i> , 2000, 253, 189-196.	2.2	21
102	Transposons but Not Retrotransposons Are Located Preferentially in Regions of High Recombination Rate in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2000, 156, 1661-1669.	2.9	124
103	Use of a TT virus ORF1 recombinant protein to detect anti-TT virus antibodies in human sera. <i>Journal of General Virology</i> , 2000, 81, 2949-2958.	2.9	56
104	Molecular Characterization and Placental Expression of HERV-W, a New Human Endogenous Retrovirus Family. <i>Journal of Virology</i> , 1999, 73, 1175-1185.	3.4	333
105	Regulation of dauer larva development in <i>Caenorhabditis elegans</i> by daf-18, a homologue of the tumour suppressor PTEN. <i>Current Biology</i> , 1999, 9, 329-334.	3.9	202
106	Human and nematode orthologs " lessons from the analysis of 1800 human genes and the proteome of <i>Caenorhabditis elegans</i> . <i>Gene</i> , 1999, 238, 163-170.	2.2	51
107	New Insulin-Like Proteins with Atypical Disulfide Bond Pattern Characterized in <i>Caenorhabditis elegans</i> by Comparative Sequence Analysis and Homology Modeling. <i>Genome Research</i> , 1998, 8, 348-353.	5.5	138
108	Highly Conserved RNA Sequences That Are Sensors of Environmental Stress. <i>Molecular and Cellular Biology</i> , 1998, 18, 7371-7382.	2.3	59

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109	Searching for regulatory elements in human noncoding sequences. <i>Current Opinion in Structural Biology</i> , 1997, 7, 399-406.	5.7	208
110	Cloning and characterization of a gene encoding a novel immunodominant antigen of <i>Trypanosoma cruzi</i> 1Note: Nucleotide Sequence data reported in this paper are available in the GenBankâ„¢ data base under the accession number U24190 and U96914.1. <i>Molecular and Biochemical Parasitology</i> , 1997, 87, 193-204.	1.1	3
111	Evolutionary Affinities of the Order Perissodactyla and the Phylogenetic Status of the Superordinal Taxa Ungulata and Altungulata. <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 195-200.	2.7	29
112	Phylogenetic position of the order Lagomorpha (rabbits, hares and allies). <i>Nature</i> , 1996, 379, 333-335.	27.8	261
113	LALNVIEW: a graphical viewer for pairwise sequence alignments. <i>Bioinformatics</i> , 1996, 12, 507-510.	4.1	39
114	Statistical analysis of vertebrate sequences reveals that long genes are scarce in GC-rich isochores. <i>Journal of Molecular Evolution</i> , 1995, 40, 308-317.	1.8	232
115	Isolation and characterization of a cDNA encoding a chicken actin-like protein. <i>Gene</i> , 1995, 154, 205-209.	2.2	13
116	HOVERGEN: a database of homologous vertebrate genes. <i>Nucleic Acids Research</i> , 1994, 22, 2360-2365.	14.5	216
117	Strong conservation of non-coding sequences during vertebrates evolution; potential involvement in post-transcriptional regulation of gene expression. <i>Nucleic Acids Research</i> , 1993, 21, 2315-2322.	14.5	156