

Richard E Green

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

29,613
citations

31902

53
h-index

37111

96
g-index

109
all docs

109
docs citations

109
times ranked

31771
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
2	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
3	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	13.7	1,830
4	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	6.0	1,695
5	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
6	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	13.7	1,537
7	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	13.7	1,379
8	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
9	Evidence for the widespread coupling of alternative splicing and nonsense-mediated mRNA decay in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 189-192.	3.3	920
10	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
11	Patterns of damage in genomic DNA sequences from a Neandertal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14616-14621.	3.3	799
12	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016, 26, 342-350.	2.4	679
13	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006, 444, 330-336.	13.7	671
14	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. <i>Nature</i> , 2007, 446, 926-929.	13.7	593
15	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	13.5	503
16	The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. <i>Current Biology</i> , 2007, 17, 1908-1912.	1.8	487
17	Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.	6.0	456
18	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443

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19	The Shaping of Modern Human Immune Systems by Multiregional Admixture with Archaic Humans. <i>Science</i> , 2011, 334, 89-94.	6.0	441
20	Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs. <i>Science</i> , 2013, 342, 871-874.	6.0	438
21	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
22	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004, 14, 273-282.	2.6	304
23	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254-1259.	6.0	300
24	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
25	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	6.0	255
26	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020, 4, 820-830.	3.4	250
27	Genomic Evidence for Island Population Conversion Resolves Conflicting Theories of Polar Bear Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003345.	1.5	181
28	Improving nanopore read accuracy with the R2C2 method enables the sequencing of highly multiplexed full-length single-cell cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9726-9731.	3.3	180
29	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009, 28, 2494-2502.	3.5	170
30	Genomic DNA Sequences from Mastodon and Woolly Mammoth Reveal Deep Speciation of Forest and Savanna Elephants. <i>PLoS Biology</i> , 2010, 8, e1000564.	2.6	162
31	Minimizing polymerase biases in metabarcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 927-939.	2.2	160
32	An unappreciated role for RNA surveillance. <i>Genome Biology</i> , 2004, 5, R8.	13.9	159
33	Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. <i>Bioinformatics</i> , 2003, 19, i118-i121.	1.8	155
34	Methylation of the Protein Phosphatase 2A Catalytic Subunit Is Essential for Association of B1± Regulatory Subunit But Not SG2NA, Striatin, or Polyomavirus Middle Tumor Antigen. <i>Molecular Biology of the Cell</i> , 2001, 12, 185-199.	0.9	148
35	Genomic evidence of geographically widespread effect of gene flow from polar bears into brown bears. <i>Molecular Ecology</i> , 2015, 24, 1205-1217.	2.0	148
36	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018, 1, 197.	2.0	148

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37	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010, 11, R47.	13.9	135
38	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	9.4	122
39	Sulfotransferases and Sulfatases in Mycobacteria. <i>Chemistry and Biology</i> , 2002, 9, 767-776.	6.2	109
40	Transoceanic drift and the domestication of African bottle gourds in the Americas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2937-2941.	3.3	108
41	Global analysis of positive and negative pre-mRNA splicing regulators in <i>Drosophila</i> . <i>Genes and Development</i> , 2005, 19, 1306-1314.	2.7	106
42	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017, 358, 951-954.	6.0	105
43	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	6.0	105
44	Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment. <i>Science</i> , 2021, 371, .	6.0	96
45	Genomic Evidence of Widespread Admixture from Polar Bears into Brown Bears during the Last Ice Age. <i>Molecular Biology and Evolution</i> , 2018, 35, 1120-1129.	3.5	91
46	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2009, 5, e1000525.	1.5	87
47	Epigenetic maintenance of topological domains in the highly rearranged gibbon genome. <i>Genome Research</i> , 2018, 28, 983-997.	2.4	85
48	Deeply conserved synteny and the evolution of metazoan chromosomes. <i>Science Advances</i> , 2022, 8, eabi5884.	4.7	81
49	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the <i>Drosophila</i> hnRNP A/B Family Members. <i>Molecular Cell</i> , 2009, 33, 438-449.	4.5	79
50	New Approaches for Genome Assembly and Scaffolding. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 17-40.	3.6	79
51	Functionality of Intergenic Transcription: An Evolutionary Comparison. <i>PLoS Genetics</i> , 2006, 2, e171.	1.5	73
52	Genome-Directed Lead Discovery: Biosynthesis, Structure Elucidation, and Biological Evaluation of Two Families of Polyene Macrolactams against <i>Trypanosoma brucei</i> . <i>ACS Chemical Biology</i> , 2015, 10, 2373-2381.	1.6	69
53	A Fast and Efficient Single-stranded Genomic Library Preparation Method Optimized for Ancient DNA. <i>Journal of Heredity</i> , 2021, 112, 241-249.	1.0	68
54	Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. <i>Genome Biology and Evolution</i> , 2015, 7, 205-217.	1.1	62

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55	Early Mesozoic Coexistence of Amniotes and Hepadnaviridae. <i>PLoS Genetics</i> , 2014, 10, e1004559.	1.5	61
56	Genome-Wide Analysis Reveals an Unexpected Function for the <i>Drosophila</i> Splicing Factor U2AF50 in the Nuclear Export of Intronless mRNAs. <i>Molecular Cell</i> , 2004, 14, 775-786.	4.5	56
57	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018, 361, 511-516.	6.0	56
58	Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019, 10, 4769.	5.8	55
59	Inferring species divergence times using pairwise sequential Markovian coalescent modelling and low-coverage genomic data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150138.	1.8	54
60	A ligation-based single-stranded library preparation method to analyze cell-free DNA and synthetic oligos. <i>BMC Genomics</i> , 2019, 20, 1023.	1.2	49
61	Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. <i>Molecular Ecology</i> , 2016, 25, 357-379.	2.0	47
62	An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021, 7, .	4.7	47
63	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
64	Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. <i>Molecular Biology and Evolution</i> , 2018, 35, 1190-1209.	3.5	45
65	Comparative Population Genomics of the Ejaculate in Humans and the Great Apes. <i>Molecular Biology and Evolution</i> , 2013, 30, 964-976.	3.5	40
66	A phylogenetic approach for haplotype analysis of sequence data from complex mitochondrial mixtures. <i>Forensic Science International: Genetics</i> , 2017, 30, 93-105.	1.6	39
67	Analysis of Human Accelerated DNA Regions Using Archaic Hominin Genomes. <i>PLoS ONE</i> , 2012, 7, e32877.	1.1	38
68	Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. <i>Genome Research</i> , 2017, 27, 686-696.	2.4	38
69	Detecting hybridization using ancient <scp>DNA</scp>. <i>Molecular Ecology</i> , 2016, 25, 2398-2412.	2.0	37
70	The Joint Allele-Frequency Spectrum in Closely Related Species. <i>Genetics</i> , 2007, 177, 387-398.	1.2	28
71	Evolution of a tissue-specific splicing network. <i>Genes and Development</i> , 2011, 25, 608-620.	2.7	27
72	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i>. <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25

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73	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. <i>Bioinformatics</i> , 2005, 21, 3824-3831.	1.8	22
74	Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. <i>Journal of Visualized Experiments</i> , 2009, , 1573.	0.2	22
75	One flyâ€œone genome: chromosome-scale genome assembly of a single outbred <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2020, 48, e75.	6.5	20
76	A method for positive forensic identification of samples from extremely low-coverage sequence data. <i>BMC Genomics</i> , 2015, 16, 1034.	1.2	18
77	A chromosome-scale genome assembly and karyotype of the ctenophore <i>Hormiphora californensis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	18
78	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017, 6, 1-6.	3.3	17
79	Stable C and N isotope analysis of hair suggest undernourishment as a factor in the death of a mummified girl from late 19th century San Francisco, CA. <i>PLoS ONE</i> , 2017, 12, e0184921.	1.1	15
80	A High-Quality Reference Genome Assembly of the Saltwater Crocodile, <i>Crocodylus porosus</i> , Reveals Patterns of Selection in Crocodylidae. <i>Genome Biology and Evolution</i> , 2020, 12, 3635-3646.	1.1	15
81	Human Evolution: Turning Back the Clock. <i>Current Biology</i> , 2013, 23, R286-R288.	1.8	14
82	Ancient DNA Resolves the History of Tetragnatha (Araneae, Tetragnathidae) Spiders on Rapa Nui. <i>Genes</i> , 2017, 8, 403.	1.0	14
83	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
84	Pairwise alignment incorporating dipeptide covariation. <i>Bioinformatics</i> , 2005, 21, 3704-3710.	1.8	13
85	Structural Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 375-383.	1.2	10
86	A polar bear paleogenome reveals extensive ancient gene flow from polar bears into brown bears. <i>Nature Ecology and Evolution</i> , 2022, 6, 936-944.	3.4	10
87	A novel NGS library preparation method to characterize native termini of fragmented DNA. <i>Nucleic Acids Research</i> , 2020, 48, e47-e47.	6.5	8
88	AD-LIBS: inferring ancestry across hybrid genomes using low-coverage sequence data. <i>BMC Bioinformatics</i> , 2017, 18, 203.	1.2	7
89	An Annotated Draft Genome for the Andean Bear, <i>Tremarctos ornatus</i> . <i>Journal of Heredity</i> , 2021, 112, 377-384.	1.0	6
90	Genome Sequencing of a Gray Wolf from Peninsular India Provides New Insights into the Evolution and Hybridization of Gray Wolves. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	5

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91	The complete mitochondrial genome of the black surfperch, <i>Embiotoca jacksoni</i> : Selection and substitution rates among surfperches (Embiotocidae). <i>Marine Genomics</i> , 2016, 28, 107-112.	0.4	3
92	Aneuploidy and mother's genes. <i>Science</i> , 2015, 348, 180-181.	6.0	2
93	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004, 14, 273-273.	2.6	1
94	A Mouse Following in the Footsteps of Human Prehistory. <i>Cell</i> , 2013, 152, 667-668.	13.5	1