

Richard E Green

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97
papers

21,472
citations

50
h-index

109
g-index

109
ext. papers

26,287
ext. citations

16.2
avg, IF

5.85
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 97 | The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63 | 33.3 | 2807 |
| 96 | A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722 | 33.3 | 2599 |
| 95 | The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014 , 505, 43-9 | 50.4 | 1339 |
| 94 | A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , 2012 , 338, 222-6 | 33.3 | 1276 |
| 93 | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31 | 33.3 | 1182 |
| 92 | Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60 | 50.4 | 1169 |
| 91 | The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011 , 471, 473-9 | 50.4 | 1094 |
| 90 | 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, 189-92 | 11.5 | 768 |
| 89 | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20 | 33.3 | 628 |
| 88 | 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, 14616-21 | 11.5 | 610 |
| 87 | Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006 , 444, 330-6 | 50.4 | 511 |
| 86 | Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. <i>Nature</i> , 2007 , 446, 926-9 | 50.4 | 469 |
| 85 | Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016 , 26, 342-50 | 9.7 | 415 |
| 84 | A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26 | 56.2 | 405 |
| 83 | Targeted retrieval and analysis of five Neandertal mtDNA genomes. <i>Science</i> , 2009 , 325, 318-21 | 33.3 | 387 |
| 82 | The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , 2007 , 17, 1908-12 | 6.3 | 376 |
| 81 | Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41 | 9.7 | 364 |

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|----|--|------|-----|
| 80 | The shaping of modern human immune systems by multiregional admixture with archaic humans. <i>Science</i> , 2011 , 334, 89-94 | 33.3 | 353 |
| 79 | Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. <i>Science</i> , 2013 , 342, 871-4 | 33.3 | 328 |
| 78 | The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 273-82 | 8.1 | 263 |
| 77 | Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014 , 346, 1254449 | 33.3 | 231 |
| 76 | 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 | 18.3 | 227 |
| 75 | Targeted investigation of the Neandertal genome by array-based sequence capture. <i>Science</i> , 2010 , 328, 723-5 | 33.3 | 224 |
| 74 | Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746 | 36.4 | 161 |
| 73 | An unappreciated role for RNA surveillance. <i>Genome Biology</i> , 2004 , 5, R8 | 18.3 | 145 |
| 72 | Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 1044-1053 | 44.5 | 143 |
| 71 | Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i118-21 | 7.2 | 138 |
| 70 | Genomic DNA sequences from mastodon and woolly mammoth reveal deep speciation of forest and savanna elephants. <i>PLoS Biology</i> , 2010 , 8, e1000564 | 9.7 | 133 |
| 69 | Genomic evidence for island population conversion resolves conflicting theories of polar bear evolution. <i>PLoS Genetics</i> , 2013 , 9, e1003345 | 6 | 131 |
| 68 | Methylation of the protein phosphatase 2A catalytic subunit is essential for association of Balph regulatory subunit but not SG2NA, striatin, or polyomavirus middle tumor antigen. <i>Molecular Biology of the Cell</i> , 2001 , 12, 185-99 | 3.5 | 129 |
| 67 | The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009 , 28, 2494-502 | 13 | 118 |
| 66 | 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 | 11.5 | 109 |
| 65 | Genomic evidence of geographically widespread effect of gene flow from polar bears into brown bears. <i>Molecular Ecology</i> , 2015 , 24, 1205-17 | 5.7 | 104 |
| 64 | Global analysis of positive and negative pre-mRNA splicing regulators in <i>Drosophila</i> . <i>Genes and Development</i> , 2005 , 19, 1306-14 | 12.6 | 97 |
| 63 | Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016 , 48, 1089-93 | 36.3 | 95 |

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|----|--|------|----|
| 62 | Minimizing polymerase biases in metabarcoding. <i>Molecular Ecology Resources</i> , 2018 , 18, 927 | 8.4 | 95 |
| 61 | Sulfotransferases and sulfatases in mycobacteria. <i>Chemistry and Biology</i> , 2002 , 9, 767-76 | | 92 |
| 60 | Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020 , 4, 820-830 | 12.3 | 91 |
| 59 | Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010 , 11, R47 | 18.3 | 81 |
| 58 | 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, 2937-41 | 11.5 | 79 |
| 57 | Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018 , 1, 197 | 6.7 | 74 |
| 56 | 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, 438-49 | 17.6 | 70 |
| 55 | Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017 , 358, 951-954 | 33.3 | 68 |
| 54 | 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 | 6 | 68 |
| 53 | Functionality of intergenic transcription: an evolutionary comparison. <i>PLoS Genetics</i> , 2006 , 2, e171 | 6 | 59 |
| 52 | 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 | 8.3 | 58 |
| 51 | 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, 775-86 | 17.6 | 54 |
| 50 | Early mesozoic coexistence of amniotes and hepadnaviridae. <i>PLoS Genetics</i> , 2014 , 10, e1004559 | 6 | 51 |
| 49 | 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, 2373-81 | 4.9 | 50 |
| 48 | Multiple lineages of ancient CR1 retroposons shaped the early genome evolution of amniotes. <i>Genome Biology and Evolution</i> , 2014 , 7, 205-17 | 3.9 | 49 |
| 47 | Epigenetic maintenance of topological domains in the highly rearranged gibbon genome. <i>Genome Research</i> , 2018 , 28, 983-997 | 9.7 | 47 |
| 46 | New Approaches for Genome Assembly and Scaffolding. <i>Annual Review of Animal Biosciences</i> , 2019 , 7, 17-40 | 13.7 | 42 |
| 45 | Towards complete and error-free genome assemblies of all vertebrate species | | 38 |

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|----|---|------|----|
| 44 | Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. <i>Molecular Ecology</i> , 2016 , 25, 357-79 | 5.7 | 38 |
| 43 | Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018 , 361, 511-516 | 33.3 | 36 |
| 42 | Comparative population genomics of the ejaculate in humans and the great apes. <i>Molecular Biology and Evolution</i> , 2013 , 30, 964-76 | 8.3 | 34 |
| 41 | Analysis of human accelerated DNA regions using archaic hominin genomes. <i>PLoS ONE</i> , 2012 , 7, e32877 | 3.7 | 32 |
| 40 | Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit | | 29 |
| 39 | Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. <i>Genome Research</i> , 2017 , 27, 686-696 | 9.7 | 28 |
| 38 | Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1190-1209 | 8.3 | 28 |
| 37 | Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020 , 370, | 33.3 | 28 |
| 36 | Reintroduction of the archaic variant of in cortical organoids alters neurodevelopment. <i>Science</i> , 2021 , 371, | 33.3 | 28 |
| 35 | 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, | 5.8 | 26 |
| 34 | A phylogenetic approach for haplotype analysis of sequence data from complex mitochondrial mixtures. <i>Forensic Science International: Genetics</i> , 2017 , 30, 93-105 | 4.3 | 25 |
| 33 | A ligation-based single-stranded library preparation method to analyze cell-free DNA and synthetic oligos. <i>BMC Genomics</i> , 2019 , 20, 1023 | 4.5 | 25 |
| 32 | Detecting hybridization using ancient DNA. <i>Molecular Ecology</i> , 2016 , 25, 2398-412 | 5.7 | 24 |
| 31 | Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. <i>Nature Communications</i> , 2019 , 10, 4769 | 17.4 | 24 |
| 30 | The joint allele-frequency spectrum in closely related species. <i>Genetics</i> , 2007 , 177, 387-98 | 4 | 22 |
| 29 | Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. <i>Bioinformatics</i> , 2005 , 21, 3824-31 | 7.2 | 21 |
| 28 | Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020 , 9, | 7.6 | 18 |
| 27 | 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 | 7.6 | 16 |

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|----|---|------|----|
| 26 | A method for positive forensic identification of samples from extremely low-coverage sequence data. <i>BMC Genomics</i> , 2015 , 16, 1034 | 4.5 | 16 |
| 25 | Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. <i>Journal of Visualized Experiments</i> , 2009 , 1573 | 1.6 | 16 |
| 24 | An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021 , 7, | 14.3 | 15 |
| 23 | Evolution of a tissue-specific splicing network. <i>Genes and Development</i> , 2011 , 25, 608-20 | 12.6 | 14 |
| 22 | Human evolution: turning back the clock. <i>Current Biology</i> , 2013 , 23, R286-8 | 6.3 | 13 |
| 21 | Pairwise alignment incorporating dipeptide covariation. <i>Bioinformatics</i> , 2005 , 21, 3704-10 | 7.2 | 13 |
| 20 | 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 | 3.7 | 12 |
| 19 | Ancient DNA Resolves the History of Tetragnatha (Araneae, Tetragnathidae) Spiders on Rapa Nui. <i>Genes</i> , 2017 , 8, | 4.2 | 11 |
| 18 | EquCab3, an Updated Reference Genome for the Domestic Horse | | 11 |
| 17 | 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 | 3.9 | 11 |
| 16 | A Fast and Efficient Single-stranded Genomic Library Preparation Method Optimized for Ancient DNA. <i>Journal of Heredity</i> , 2021 , 112, 241-249 | 2.4 | 10 |
| 15 | A novel NGS library preparation method to characterize native termini of fragmented DNA. <i>Nucleic Acids Research</i> , 2020 , 48, e47 | 20.1 | 6 |
| 14 | One fly-one genome: chromosome-scale genome assembly of a single outbred <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2020 , 48, e75 | 20.1 | 5 |
| 13 | AD-LIBS: inferring ancestry across hybrid genomes using low-coverage sequence data. <i>BMC Bioinformatics</i> , 2017 , 18, 203 | 3.6 | 5 |
| 12 | Deeply conserved synteny and the evolution of metazoan chromosomes.. <i>Science Advances</i> , 2022 , 8, eabi5884 | 14.3 | 5 |
| 11 | Structural Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue. <i>Journal of Molecular Diagnostics</i> , 2019 , 21, 375-383 | 5.1 | 4 |
| 10 | A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021 , 112, 184-191 | 2.4 | 4 |
| 9 | Mountain lion genomes provide insights into genetic rescue of inbred populations | | 3 |

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| 8 | A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021 , 112, 174-183 | 2.4 | 3 |
| 7 | Development. Aneuploidy and mother's genes. <i>Science</i> , 2015 , 348, 180-1 | 33.3 | 2 |
| 6 | 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 | 1.9 | 1 |
| 5 | A high-quality reference genome assembly of the saltwater crocodile, <i>Crocodylus porosus</i> , reveals patterns of selection in Crocodylidae | | 1 |
| 4 | One fly - one genome : Chromosome-scale genome assembly of a single outbred <i>Drosophila melanogaster</i> | | 1 |
| 3 | An Annotated Draft Genome for the Andean Bear, <i>Tremarctos ornatus</i> . <i>Journal of Heredity</i> , 2021 , 112, 377-384 | 2.4 | 1 |
| 2 | The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 273-273 | 8.1 | 0 |
| 1 | A mouse following in the footsteps of human prehistory. <i>Cell</i> , 2013 , 152, 667-8 | 56.2 | |