

Richard E Green

List of Publications by Year in Descending Order

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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	Deeply conserved synteny and the evolution of metazoan chromosomes.. <i>Science Advances</i> , 2022 , 8, eabi5884	14.3	5
96	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
95	An Annotated Draft Genome for the Andean Bear, <i>Tremarctos ornatus</i> . <i>Journal of Heredity</i> , 2021 , 112, 377-384	2.4	1
94	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
93	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021 , 112, 184-191	2.4	4
92	Reintroduction of the archaic variant of in cortical organoids alters neurodevelopment. <i>Science</i> , 2021 , 371,	33.3	28
91	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021 , 112, 174-183	2.4	3
90	An ancestral recombination graph of human, Neanderthal, and Denisovan genomes. <i>Science Advances</i> , 2021 , 7,	14.3	15
89	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
88	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
87	A novel NGS library preparation method to characterize native termini of fragmented DNA. <i>Nucleic Acids Research</i> , 2020 , 48, e47	20.1	6
86	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020 , 9,	7.6	18
85	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
84	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020 , 370,	33.3	28
83	Deeply conserved synteny resolves early events in vertebrate evolution. <i>Nature Ecology and Evolution</i> , 2020 , 4, 820-830	12.3	91
82	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
81	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

80	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
79	New Approaches for Genome Assembly and Scaffolding. <i>Annual Review of Animal Biosciences</i> , 2019 , 7, 17-40	13.7	42
78	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
77	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
76	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018 , 361, 511-516	33.3	36
75	Epigenetic maintenance of topological domains in the highly rearranged gibbon genome. <i>Genome Research</i> , 2018 , 28, 983-997	9.7	47
74	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018 , 1, 197	6.7	74
73	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
72	Minimizing polymerase biases in metabarcoding. <i>Molecular Ecology Resources</i> , 2018 , 18, 927	8.4	95
71	Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. <i>Genome Research</i> , 2017 , 27, 686-696	9.7	28
70	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
69	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
68	Natural selection shaped the rise and fall of passenger pigeon genomic diversity. <i>Science</i> , 2017 , 358, 951-954	33.3	68
67	AD-LIBS: inferring ancestry across hybrid genomes using low-coverage sequence data. <i>BMC Bioinformatics</i> , 2017 , 18, 203	3.6	5
66	Ancient DNA Resolves the History of Tetragnatha (Araneae, Tetragnathidae) Spiders on Rapa Nui. <i>Genes</i> , 2017 , 8,	4.2	11
65	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
64	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
63	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

62	Detecting hybridization using ancient DNA. <i>Molecular Ecology</i> , 2016 , 25, 2398-412	5.7	24
61	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
60	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. <i>Genome Research</i> , 2016 , 26, 342-50	9.7	415
59	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
58	Development. Aneuploidy and mother's genes. <i>Science</i> , 2015 , 348, 180-1	33.3	2
57	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
56	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
55	A method for positive forensic identification of samples from extremely low-coverage sequence data. <i>BMC Genomics</i> , 2015 , 16, 1034	4.5	16
54	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
53	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014 , 505, 43-9	50.4	1339
52	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
51	Early mesozoic coexistence of amniotes and hepadnaviridae. <i>PLoS Genetics</i> , 2014 , 10, e1004559	6	51
50	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014 , 346, 1254449	33.3	231
49	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
48	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
47	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
46	Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. <i>Science</i> , 2013 , 342, 871-4	33.3	328
45	A mouse following in the footsteps of human prehistory. <i>Cell</i> , 2013 , 152, 667-8	56.2	

44	Human evolution: turning back the clock. <i>Current Biology</i> , 2013 , 23, R286-8	6.3	13
43	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
42	Genomic evidence for island population conversion resolves conflicting theories of polar bear evolution. <i>PLoS Genetics</i> , 2013 , 9, e1003345	6	131
41	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , 2012 , 338, 222-6	33.3	1276
40	Analysis of human accelerated DNA regions using archaic hominin genomes. <i>PLoS ONE</i> , 2012 , 7, e32877	3.7	32
39	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011 , 471, 473-9	50.4	1094
38	The shaping of modern human immune systems by multiregional admixture with archaic humans. <i>Science</i> , 2011 , 334, 89-94	33.3	353
37	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
36	Evolution of a tissue-specific splicing network. <i>Genes and Development</i> , 2011 , 25, 608-20	12.6	14
35	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
34	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
33	Computational challenges in the analysis of ancient DNA. <i>Genome Biology</i> , 2010 , 11, R47	18.3	81
32	Targeted investigation of the Neandertal genome by array-based sequence capture. <i>Science</i> , 2010 , 328, 723-5	33.3	224
31	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
30	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
29	The Neandertal genome and ancient DNA authenticity. <i>EMBO Journal</i> , 2009 , 28, 2494-502	13	118
28	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
27	Targeted retrieval and analysis of five Neandertal mtDNA genomes. <i>Science</i> , 2009 , 325, 318-21	33.3	387

26	Primer extension capture: targeted sequence retrieval from heavily degraded DNA sources. <i>Journal of Visualized Experiments</i> , 2009 , 1573	1.6	16
25	A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. <i>Cell</i> , 2008 , 134, 416-26	56.2	405
24	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
23	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. <i>Nature</i> , 2007 , 446, 926-9	50.4	469
22	The derived FOXP2 variant of modern humans was shared with Neandertals. <i>Current Biology</i> , 2007 , 17, 1908-12	6.3	376
21	The joint allele-frequency spectrum in closely related species. <i>Genetics</i> , 2007 , 177, 387-98	4	22
20	Functionality of intergenic transcription: an evolutionary comparison. <i>PLoS Genetics</i> , 2006 , 2, e171	6	59
19	Analysis of one million base pairs of Neanderthal DNA. <i>Nature</i> , 2006 , 444, 330-6	50.4	511
18	Pairwise alignment incorporating dipeptide covariation. <i>Bioinformatics</i> , 2005 , 21, 3704-10	7.2	13
17	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. <i>Bioinformatics</i> , 2005 , 21, 3824-31	7.2	21
16	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
15	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
14	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 273-82	8.1	263
13	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 273-273	8.1	0
12	An unappreciated role for RNA surveillance. <i>Genome Biology</i> , 2004 , 5, R8	18.3	145
11	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
10	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
9	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

8	Sulfotransferases and sulfatases in mycobacteria. <i>Chemistry and Biology</i> , 2002 , 9, 767-76		92
7	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
6	A high-quality reference genome assembly of the saltwater crocodile, <i>Crocodylus porosus</i> , reveals patterns of selection in Crocodylidae		1
5	One fly - one genome : Chromosome-scale genome assembly of a single outbred <i>Drosophila melanogaster</i>		1
4	Towards complete and error-free genome assemblies of all vertebrate species		38
3	EquCab3, an Updated Reference Genome for the Domestic Horse		11
2	Mountain lion genomes provide insights into genetic rescue of inbred populations		3
1	Efficient de novo assembly of eleven human genomes using PromethION sequencing and a novel nanopore toolkit		29