

W Richard Mccombie

List of Publications by Year in descending order

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129
papers

82,808
citations

7568

77
h-index

14759

127
g-index

140
all docs

140
docs citations

140
times ranked

80150
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. Nature, 2000, 408, 796-815.	27.8	8,336
3	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
4	<i>PTEN</i> , a Putative Protein Tyrosine Phosphatase Gene Mutated in Human Brain, Breast, and Prostate Cancer. Science, 1997, 275, 1943-1947.	12.6	4,506
5	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
6	Coming of age: ten years of next-generation sequencing technologies. Nature Reviews Genetics, 2016, 17, 333-351.	16.3	3,160
7	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
8	Tumour evolution inferred by single-cell sequencing. Nature, 2011, 472, 90-94.	27.8	2,313
9	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	27.8	2,188
10	Complementary DNA Sequencing: Expressed Sequence Tags and Human Genome Project. Science, 1991, 252, 1651-1656.	12.6	2,165
11	Improvement of the Oryza sativa Nipponbare reference genome using next generation sequence and optical map data. Rice, 2013, 6, 4.	4.0	1,777
12	The genome sequence of Schizosaccharomyces pombe. Nature, 2002, 415, 871-880.	27.8	1,508
13	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	8.1	1,311
14	Improved maize reference genome with single-molecule technologies. Nature, 2017, 546, 524-527.	27.8	1,113
15	Role of transposable elements in heterochromatin and epigenetic control. Nature, 2004, 430, 471-476.	27.8	1,103
16	Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature, 2012, 491, 705-710.	27.8	983
17	Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700.	17.5	946
18	Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. Nature, 2001, 409, 207-211.	27.8	901

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19	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	17.5	788
20	Specialized piRNA Pathways Act in Germline and Somatic Tissues of the <i>Drosophila</i> Ovary. <i>Cell</i> , 2009, 137, 522-535.	28.9	774
21	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	21.4	656
22	Genome-wide in situ exon capture for selective resequencing. <i>Nature Genetics</i> , 2007, 39, 1522-1527.	21.4	635
23	A resource for large-scale RNA-interference-based screens in mammals. <i>Nature</i> , 2004, 428, 427-431.	27.8	620
24	Second-generation shRNA libraries covering the mouse and human genomes. <i>Nature Genetics</i> , 2005, 37, 1281-1288.	21.4	582
25	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
26	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	19.0	465
27	Genetic Definition and Sequence Analysis of <i>Arabidopsis</i> Centromeres. <i>Science</i> , 1999, 286, 2468-2474.	12.6	417
28	An Oncogenomics-Based In Vivo RNAi Screen Identifies Tumor Suppressors in Liver Cancer. <i>Cell</i> , 2008, 135, 852-864.	28.9	404
29	Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2007, 5, e174.	5.6	400
30	Sperm Methylation Profiles Reveal Features of Epigenetic Inheritance and Evolution in Primates. <i>Cell</i> , 2011, 146, 1029-1041.	28.9	368
31	De novo mutations in schizophrenia implicate chromatin remodeling and support a genetic overlap with autism and intellectual disability. <i>Molecular Psychiatry</i> , 2014, 19, 652-658.	7.9	332
32	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. <i>Genome Research</i> , 2015, 25, 1750-1756.	5.5	331
33	Topoisomerase levels determine chemotherapy response <i>in vitro</i> and <i>in vivo</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9053-9058.	7.1	261
34	Directional DNA Methylation Changes and Complex Intermediate States Accompany Lineage Specificity in the Adult Hematopoietic Compartment. <i>Molecular Cell</i> , 2011, 44, 17-28.	9.7	261
35	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <i>Genome Research</i> , 2013, 23, 1651-1662.	5.5	260
36	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	12.6	245

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37	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
38	Differential methylation of genes and retrotransposons facilitates shotgun sequencing of the maize genome. <i>Nature Genetics</i> , 1999, 23, 305-308.	21.4	237
39	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. <i>Cancer Cell</i> , 2003, 3, 297-302.	16.8	229
40	Whole genome de novo assemblies of three divergent strains of rice, <i>Oryza sativa</i> , document novel gene space of aus and indica. <i>Genome Biology</i> , 2014, 15, 506.	8.8	228
41	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	5.5	218
42	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	7.1	214
43	New mutation in scrapie amyloid precursor gene (at codon 178) in Finnish Creutzfeldt-Jakob kindred. <i>Lancet</i> , The, 1991, 337, 425.	13.7	212
44	Maize Genome Sequencing by Methylation Filtration. <i>Science</i> , 2003, 302, 2115-2117.	12.6	206
45	<i>Caenorhabditis elegans</i> expressed sequence tags identify gene families and potential disease gene homologues. <i>Nature Genetics</i> , 1992, 1, 124-131.	21.4	199
46	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , 2009, 19, 1593-1605.	5.5	198
47	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , 2013, 6, 1.	4.0	186
48	The <i>Arabidopsis</i> SKP1-LIKE1 gene is essential for male meiosis and may control homologue separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11416-11421.	7.1	184
49	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	27.8	175
50	Hybrid selection of discrete genomic intervals on custom-designed microarrays for massively parallel sequencing. <i>Nature Protocols</i> , 2009, 4, 960-974.	12.0	171
51	Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. <i>Nature Methods</i> , 2008, 5, 679-682.	19.0	166
52	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	9.6	157
53	Functional Identification of Tumor-Suppressor Genes through an In Vivo RNA Interference Screen in a Mouse Lymphoma Model. <i>Cancer Cell</i> , 2009, 16, 324-335.	16.8	155
54	Temporal transcriptional logic of dynamic regulatory networks underlying nitrogen signaling and use in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6494-6499.	7.1	150

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55	Differential methylation of genes and repeats in land plants. <i>Genome Research</i> , 2005, 15, 1431-1440.	5.5	145
56	Next-Generation Sequencing Technologies. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a036798.	6.2	143
57	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. <i>Genome Research</i> , 2018, 28, 1126-1135.	5.5	142
58	Sorghum Genome Sequencing by Methylation Filtration. <i>PLoS Biology</i> , 2005, 3, e13.	5.6	138
59	A map for sequence analysis of the <i>Arabidopsis thaliana</i> genome. <i>Nature Genetics</i> , 1999, 22, 265-270.	21.4	134
60	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	3.5	134
61	Two waves of de novo methylation during mouse germ cell development. <i>Genes and Development</i> , 2014, 28, 1544-1549.	5.9	123
62	Genes and Transposons Are Differentially Methylated in Plants, but Not in Mammals. <i>Genome Research</i> , 2003, 13, 2658-2664.	5.5	122
63	The effects of carbon dioxide and temperature on microRNA expression in <i>Arabidopsis</i> development. <i>Nature Communications</i> , 2013, 4, 2145.	12.8	122
64	Loss of p53 impedes the antileukemic response to BCR-ABL inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7444-7449.	7.1	121
65	Validation and assessment of variant calling pipelines for next-generation sequencing. <i>Human Genomics</i> , 2014, 8, 14.	2.9	121
66	Massively parallel bisulphite pyrosequencing reveals the molecular complexity of breast cancer-associated cytosine-methylation patterns obtained from tissue and serum DNA. <i>Genome Research</i> , 2008, 18, 19-29.	5.5	114
67	A comparative analysis of exome capture. <i>Genome Biology</i> , 2011, 12, R97.	9.6	110
68	Creutzfeldtâ€”Jakob disease cosegregates with the codon 178^{Asn}<i>PRNP</i> mutation in families of European origin. <i>Annals of Neurology</i> , 1992, 31, 274-281.	5.3	105
69	Rapid and reliable fluorescent cycle sequencing of double-stranded templates. <i>DNA Sequence</i> , 1992, 2, 289-296.	0.7	97
70	Production of complex nucleic acid libraries using highly parallel in situ oligonucleotide synthesis. <i>Nature Methods</i> , 2004, 1, 241-248.	19.0	96
71	Phylogenomic analysis of transcriptome data elucidates coâ€”occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	1.7	94
72	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. <i>Genome Biology</i> , 2015, 16, 79.	8.8	91

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73	Parallel comparison of Illumina RNA-Seq and Affymetrix microarray platforms on transcriptomic profiles generated from 5-aza-deoxy-cytidine treated HT-29 colon cancer cells and simulated datasets. BMC Bioinformatics, 2013, 14, S1.	2.6	88
74	SpliceTrap: a method to quantify alternative splicing under single cellular conditions. Bioinformatics, 2011, 27, 3010-3016.	4.1	86
75	Next-generation sequencing of endoscopic biopsies identifies ARID1A as a tumor-suppressor gene in Barrett's esophagus. Oncogene, 2014, 33, 347-357.	5.9	84
76	Genetic analysis using genomic representations. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4487-4492.	7.1	83
77	Genome-wide transposon tagging reveals location-dependent effects on transcription and chromatin organization in Arabidopsis. Plant Journal, 2008, 55, 514-525.	5.7	80
78	Distinct p53 genomic binding patterns in normal and cancer-derived human cells. Cell Cycle, 2011, 10, 4237-4249.	2.6	80
79	Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in Arabidopsis thaliana roots. BMC Genomics, 2013, 14, 701.	2.8	76
80	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. Genome Research, 2018, 28, 921-932.	5.5	76
81	Small RNA-based silencing strategies for transposons in the process of invading <i>Drosophila</i> species. Rna, 2010, 16, 1634-1645.	3.5	75
82	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. Genome Research, 2005, 15, 1284-1291.	5.5	73
83	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. Genome Research, 2020, 30, 1258-1273.	5.5	72
84	Syntenic Relationships between Medicago truncatula and Arabidopsis Reveal Extensive Divergence of Genome Organization. Plant Physiology, 2003, 131, 1018-1026.	4.8	67
85	Transpositional landscape of the rice genome revealed by paired-end mapping of high-throughput resequencing data. Plant Journal, 2011, 66, 241-246.	5.7	62
86	DISC1 as a genetic risk factor for schizophrenia and related major mental illness: response to Sullivan. Molecular Psychiatry, 2014, 19, 141-143.	7.9	62
87	Comparative analysis of a Brassica BAC clone containing several major aliphatic glucosinolate genes with its corresponding Arabidopsis sequence. Genome, 2004, 47, 666-679.	2.0	61
88	An insert mutation in the chromosome 20 amyloid precursor gene in a Gerstmann-Sträussler-Scheinker family. Journal of the Neurological Sciences, 1992, 111, 189-194.	0.6	60
89	708 Common and 2010 rare DISC1 locus variants identified in 1542 subjects: analysis for association with psychiatric disorder and cognitive traits. Molecular Psychiatry, 2014, 19, 668-675.	7.9	59
90	What is Finished, and Why Does it Matter. Genome Research, 2002, 12, 669-671.	5.5	57

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91	Sequencing the maize genome. <i>Current Opinion in Plant Biology</i> , 2004, 7, 102-107.	7.1	51
92	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	2.8	51
93	Chd5 Requires PHD-Mediated Histone 3 Binding for Tumor Suppression. <i>Cell Reports</i> , 2013, 3, 92-102.	6.4	47
94	Sequence analysis of the long arm of rice chromosome 11 for rice?wheat synteny. <i>Functional and Integrative Genomics</i> , 2004, 4, 102-117.	3.5	44
95	Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. <i>Genome Research</i> , 2009, 19, 1077-1083.	5.5	44
96	Sugarcane genome sequencing by methylation filtration provides tools for genomic research in the genus <i>Saccharum</i> . <i>Plant Journal</i> , 2014, 79, 162-172.	5.7	40
97	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	3.5	39
98	Gene enrichment in plant genomic shotgun libraries. <i>Current Opinion in Plant Biology</i> , 2003, 6, 150-156.	7.1	37
99	Translating next generation sequencing to practice: Opportunities and necessary steps. <i>Molecular Oncology</i> , 2013, 7, 743-755.	4.6	34
100	SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. <i>Plant Physiology</i> , 2020, 182, 215-227.	4.8	30
101	Comparative analysis of methylthioalkylmalate synthase (MAM) gene family and flanking DNA sequences in <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> . <i>Plant Cell Reports</i> , 2006, 25, 592-598.	5.6	29
102	Discovery of Novel Human Breast Cancer MicroRNAs from Deep Sequencing Data by Analysis of Pri-MicroRNA Secondary Structures. <i>PLoS ONE</i> , 2011, 6, e16403.	2.5	29
103	Comparing low coverage random shotgun sequence data from <i>Brassica oleracea</i> and <i>Oryza sativa</i> genome sequence for their ability to add to the annotation of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2005, 15, 496-504.	5.5	27
104	Comparative analysis of a transposon-rich <i>Brassica oleracea</i> BAC clone with its corresponding sequence in <i>A. thaliana</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 949-955.	3.6	25
105	Whole transcriptome analysis of the fasting and fed Burmese python heart: insights into extreme physiological cardiac adaptation. <i>Physiological Genomics</i> , 2011, 43, 69-76.	2.3	24
106	Secretion Trap Tagging of Secreted and Membrane-Spanning Proteins Using <i>Arabidopsis</i> Gene Traps. <i>Plant Physiology</i> , 2003, 132, 698-708.	4.8	22
107	A Hybrid Likelihood Model for Sequence-Based Disease Association Studies. <i>PLoS Genetics</i> , 2013, 9, e1003224.	3.5	19
108	Unlocking the Treasure Trove: From Genes to Schizophrenia Biology. <i>Schizophrenia Bulletin</i> , 2014, 40, 492-496.	4.3	19

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109	Identification of Mesoderm Development (mesd) Candidate Genes by Comparative Mapping and Genome Sequence Analysis. Genomics, 2001, 72, 88-98.	2.9	17
110	The First Plant Genome. Cell, 2001, 105, 571-574.	28.9	15
111	High-content analysis of cancer genome DNA alterations. Current Opinion in Genetics and Development, 2008, 18, 68-72.	3.3	14
112	SLC5A3-Dependent Myo-inositol Auxotrophy in Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 450-467.	9.4	14
113	Transcriptional Silencing of <i>ALDH2</i> Confers a Dependency on Fanconi Anemia Proteins in Acute Myeloid Leukemia. Cancer Discovery, 2021, 11, 2300-2315.	9.4	13
114	Sequencing and analysis of genomic fragments from the <i>NF1</i> locus. DNA Sequence, 1992, 3, 237-243.	0.7	11
115	The mouse genome: Experimental examination of gene predictions and transcriptional start sites. Genome Research, 2004, 14, 2424-2429.	5.5	11
116	Establishing the baseline level of repetitive element expression in the human cortex. BMC Genomics, 2011, 12, 495.	2.8	11
117	Future Promises and Concerns of Ubiquitous Next-Generation Sequencing. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a025783.	6.2	10
118	<i>GFScan</i> : A Gene Family Search Tool at Genomic DNA Level. Genome Research, 2002, 12, 1142-1149.	5.5	8
119	High-Throughput Sequencing. , 2011, , 461-478.		8
120	Fluorescence-Based Sequencing of Double-Stranded DNA by Hexamer String Priming. Analytical Biochemistry, 1996, 241, 228-237.	2.4	7
121	On the importance of being finished. Genome Biology, 2002, 3, comment2010.1.	9.6	7
122	FamAnn: an automated variant annotation pipeline to facilitate target discovery for family-based sequencing studies. Bioinformatics, 2014, 30, 1175-1176.	4.1	7
123	1D Genome Sequencing on the Oxford Nanopore MinION. Current Protocols in Human Genetics, 2017, 94, 18.11.1-18.11.14.	3.5	7
124	Rapid isolation of cDNA by hybridization. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 3764-3769.	7.1	5
125	A Survey of Canine Expressed Sequence Tags and a Display of Their Annotations Through a Flexible Web-Based Interface. , 2003, 94, 15-22.		4
126	A trimming-and-retrieving alignment scheme for reduced representation bisulfite sequencing: Fig. 1.. Bioinformatics, 2015, 31, 2040-2042.	4.1	3

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127	Genome Sequencing Conference I: Summary. Genomics, 1990, 8, 186-188.	2.9	1
128	GFScan: A Gene Family Search Tool at Genomic DNA Level. Genome Research, 2002, 12, 1142-1149.	5.5	1
129	Solution-Phase Exome Capture. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot094680.	0.3	0