

W Richard McCombie

List of Publications by Year in descending order

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129
papers

82,808
citations

8755

77
h-index

16791

127
g-index

140
all docs

140
docs citations

140
times ranked

89473
citing authors

#	ARTICLE	IF	CITATIONS
1	SLC5A3-Dependent Myo-inositol Auxotrophy in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 450-467.	7.7	14
2	Transcriptional Silencing of <i>ALDH2</i> Confers a Dependency on Fanconi Anemia Proteins in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2300-2315.	7.7	13
3	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020, 30, 1258-1273.	2.4	72
4	SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. <i>Plant Physiology</i> , 2020, 182, 215-227.	2.3	30
5	Future Promises and Concerns of Ubiquitous Next-Generation Sequencing. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a025783.	2.9	10
6	Next-Generation Sequencing Technologies. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a036798.	2.9	143
7	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. <i>Genome Research</i> , 2018, 28, 921-932.	2.4	76
8	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.	3.3	150
9	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.	2.4	142
10	Solution-Phase Exome Capture. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot094680.	0.2	0
11	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527.	13.7	1,113
12	1D Genome Sequencing on the Oxford Nanopore MinION. <i>Current Protocols in Human Genetics</i> , 2017, 94, 18.11.1-18.11.14.	3.5	7
13	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
14	Coming of age: ten years of next-generation sequencing technologies. <i>Nature Reviews Genetics</i> , 2016, 17, 333-351.	7.7	3,160
15	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. <i>Genome Biology</i> , 2015, 16, 79.	3.8	91
16	A trimming-and-retrieving alignment scheme for reduced representation bisulfite sequencing: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2040-2042.	1.8	3
17	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , 2015, 12, 780-786.	9.0	465
18	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. <i>Genome Research</i> , 2015, 25, 1750-1756.	2.4	331

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19	DISC1 as a genetic risk factor for schizophrenia and related major mental illness: response to Sullivan. <i>Molecular Psychiatry</i> , 2014, 19, 141-143.	4.1	62
20	Next-generation sequencing of endoscopic biopsies identifies ARID1A as a tumor-suppressor gene in Barrett's esophagus. <i>Oncogene</i> , 2014, 33, 347-357.	2.6	84
21	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.	3.8	228
22	Unlocking the Treasure Trove: From Genes to Schizophrenia Biology. <i>Schizophrenia Bulletin</i> , 2014, 40, 492-496.	2.3	19
23	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , 2014, 515, 216-221.	13.7	2,188
24	FamAnn: an automated variant annotation pipeline to facilitate target discovery for family-based sequencing studies. <i>Bioinformatics</i> , 2014, 30, 1175-1176.	1.8	7
25	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.	4.1	332
26	Two waves of de novo methylation during mouse germ cell development. <i>Genes and Development</i> , 2014, 28, 1544-1549.	2.7	123
27	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.	2.8	40
28	708 Common and 2010 rare DISC1 locus variants identified in 1542 subjects: analysis for association with psychiatric disorder and cognitive traits. <i>Molecular Psychiatry</i> , 2014, 19, 668-675.	4.1	59
29	Validation and assessment of variant calling pipelines for next-generation sequencing. <i>Human Genomics</i> , 2014, 8, 14.	1.4	121
30	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. <i>BMC Bioinformatics</i> , 2013, 14, S1.	1.2	88
31	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , 2013, 6, 4.	1.7	1,777
32	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , 2013, 6, 1.	1.7	186
33	The effects of carbon dioxide and temperature on microRNA expression in <i>Arabidopsis</i> development. <i>Nature Communications</i> , 2013, 4, 2145.	5.8	122
34	Translating next generation sequencing to practice: Opportunities and necessary steps. <i>Molecular Oncology</i> , 2013, 7, 743-755.	2.1	34
35	Chd5 Requires PHD-Mediated Histone 3 Binding for Tumor Suppression. <i>Cell Reports</i> , 2013, 3, 92-102.	2.9	47
36	A Hybrid Likelihood Model for Sequence-Based Disease Association Studies. <i>PLoS Genetics</i> , 2013, 9, e1003224.	1.5	19

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37	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.	2.4	260
38	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.	3.3	214
39	Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in <i>Arabidopsis thaliana</i> roots. <i>BMC Genomics</i> , 2013, 14, 701.	1.2	76
40	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	157
41	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , 2012, 491, 705-710.	13.7	983
42	De Novo Gene Disruptions in Children on the Autistic Spectrum. <i>Neuron</i> , 2012, 74, 285-299.	3.8	1,311
43	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.	9.4	788
44	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
45	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
46	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
47	Phylogenomic analysis of transcriptome data elucidates co-occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	0.8	94
48	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.	1.0	24
49	High-Throughput Sequencing. , 2011, , 461-478.		8
50	Sperm Methylation Profiles Reveal Features of Epigenetic Inheritance and Evolution in Primates. <i>Cell</i> , 2011, 146, 1029-1041.	13.5	368
51	Directional DNA Methylation Changes and Complex Intermediate States Accompany Lineage Specificity in the Adult Hematopoietic Compartment. <i>Molecular Cell</i> , 2011, 44, 17-28.	4.5	261
52	A comparative analysis of exome capture. <i>Genome Biology</i> , 2011, 12, R97.	13.9	110
53	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.	1.1	29
54	Transpositional landscape of the rice genome revealed by paired-end mapping of high-throughput resequencing data. <i>Plant Journal</i> , 2011, 66, 241-246.	2.8	62

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55	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	9.4	656
56	Tumour evolution inferred by single-cell sequencing. <i>Nature</i> , 2011, 472, 90-94.	13.7	2,313
57	Establishing the baseline level of repetitive element expression in the human cortex. <i>BMC Genomics</i> , 2011, 12, 495.	1.2	11
58	SpliceTrap: a method to quantify alternative splicing under single cellular conditions. <i>Bioinformatics</i> , 2011, 27, 3010-3016.	1.8	86
59	Distinct p53 genomic binding patterns in normal and cancer-derived human cells. <i>Cell Cycle</i> , 2011, 10, 4237-4249.	1.3	80
60	A Functional Phylogenomic View of the Seed Plants. <i>PLoS Genetics</i> , 2011, 7, e1002411.	1.5	134
61	Small RNA-based silencing strategies for transposons in the process of invading <i>Drosophila</i> species. <i>Rna</i> , 2010, 16, 1634-1645.	1.6	75
62	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
63	Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. <i>Genome Research</i> , 2009, 19, 1077-1083.	2.4	44
64	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , 2009, 19, 1593-1605.	2.4	198
65	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.	7.7	155
66	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
67	Hybrid selection of discrete genomic intervals on custom-designed microarrays for massively parallel sequencing. <i>Nature Protocols</i> , 2009, 4, 960-974.	5.5	171
68	Specialized piRNA Pathways Act in Germline and Somatic Tissues of the <i>Drosophila</i> Ovary. <i>Cell</i> , 2009, 137, 522-535.	13.5	774
69	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
70	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.	2.4	114
71	Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. <i>Nature Methods</i> , 2008, 5, 679-682.	9.0	166
72	Genome-wide transposon tagging reveals location-dependent effects on transcription and chromatin organization in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 55, 514-525.	2.8	80

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73	High-content analysis of cancer genome DNA alterations. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 68-72.	1.5	14
74	An Oncogenomics-Based In Vivo RNAi Screen Identifies Tumor Suppressors in Liver Cancer. <i>Cell</i> , 2008, 135, 852-864.	13.5	404
75	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.	3.3	261
76	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
77	Genome-wide in situ exon capture for selective resequencing. <i>Nature Genetics</i> , 2007, 39, 1522-1527.	9.4	635
78	Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2007, 5, e174.	2.6	400
79	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.	2.8	29
80	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.	3.3	121
81	Second-generation shRNA libraries covering the mouse and human genomes. <i>Nature Genetics</i> , 2005, 37, 1281-1288.	9.4	582
82	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.	1.8	25
83	Sorghum Genome Sequencing by Methylation Filtration. <i>PLoS Biology</i> , 2005, 3, e13.	2.6	138
84	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	73
85	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.	2.4	27
86	Differential methylation of genes and repeats in land plants. <i>Genome Research</i> , 2005, 15, 1431-1440.	2.4	145
87	Comparative analysis of a <i>Brassica</i> BAC clone containing several major aliphatic glucosinolate genes with its corresponding <i>Arabidopsis</i> sequence. <i>Genome</i> , 2004, 47, 666-679.	0.9	61
88	The mouse genome: Experimental examination of gene predictions and transcriptional start sites. <i>Genome Research</i> , 2004, 14, 2424-2429.	2.4	11
89	Production of complex nucleic acid libraries using highly parallel in situ oligonucleotide synthesis. <i>Nature Methods</i> , 2004, 1, 241-248.	9.0	96
90	A resource for large-scale RNA-interference-based screens in mammals. <i>Nature</i> , 2004, 428, 427-431.	13.7	620

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91	Role of transposable elements in heterochromatin and epigenetic control. <i>Nature</i> , 2004, 430, 471-476.	13.7	1,103
92	Sequencing the maize genome. <i>Current Opinion in Plant Biology</i> , 2004, 7, 102-107.	3.5	51
93	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. <i>Functional and Integrative Genomics</i> , 2004, 4, 102-117.	1.4	44
94	Gene enrichment in plant genomic shotgun libraries. <i>Current Opinion in Plant Biology</i> , 2003, 6, 150-156.	3.5	37
95	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. <i>Cancer Cell</i> , 2003, 3, 297-302.	7.7	229
96	Maize Genome Sequencing by Methylation Filtration. <i>Science</i> , 2003, 302, 2115-2117.	6.0	206
97	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	6.0	245
98	A Survey of Canine Expressed Sequence Tags and a Display of Their Annotations Through a Flexible Web-Based Interface. , 2003, 94, 15-22.		4
99	Genes and Transposons Are Differentially Methylated in Plants, but Not in Mammals. <i>Genome Research</i> , 2003, 13, 2658-2664.	2.4	122
100	Syntenic Relationships between <i>Medicago truncatula</i> and <i>Arabidopsis</i> Reveal Extensive Divergence of Genome Organization. , <i>Plant Physiology</i> , 2003, 131, 1018-1026.	2.3	67
101	Secretion Trap Tagging of Secreted and Membrane-Spanning Proteins Using <i>Arabidopsis</i> Gene Traps. <i>Plant Physiology</i> , 2003, 132, 698-708.	2.3	22
102	What is Finished, and Why Does it Matter. <i>Genome Research</i> , 2002, 12, 669-671.	2.4	57
103	<tt>GFScan</tt>: A Gene Family Search Tool at Genomic DNA Level. <i>Genome Research</i> , 2002, 12, 1142-1149.	2.4	8
104	On the importance of being finished. <i>Genome Biology</i> , 2002, 3, comment2010.1.	13.9	7
105	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
106	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , 2002, 415, 871-880.	13.7	1,508
107	GFScan: A Gene Family Search Tool at Genomic DNA Level. <i>Genome Research</i> , 2002, 12, 1142-1149.	2.4	1
108	Identification of Mesoderm Development (mesd) Candidate Genes by Comparative Mapping and Genome Sequence Analysis. <i>Genomics</i> , 2001, 72, 88-98.	1.3	17

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109	The First Plant Genome. <i>Cell</i> , 2001, 105, 571-574.	13.5	15
110	Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. <i>Nature</i> , 2001, 409, 207-211.	13.7	901
111	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
112	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	13.7	175
113	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
114	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.	3.3	184
115	A map for sequence analysis of the <i>Arabidopsis thaliana</i> genome. <i>Nature Genetics</i> , 1999, 22, 265-270.	9.4	134
116	Differential methylation of genes and retrotransposons facilitates shotgun sequencing of the maize genome. <i>Nature Genetics</i> , 1999, 23, 305-308.	9.4	237
117	Genetic Definition and Sequence Analysis of <i>Arabidopsis</i> Centromeres. <i>Science</i> , 1999, 286, 2468-2474.	6.0	417
118	Genetic analysis using genomic representations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 4487-4492.	3.3	83
119	Rapid isolation of cDNA by hybridization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 3764-3769.	3.3	5
120	PTEN, a Putative Protein Tyrosine Phosphatase Gene Mutated in Human Brain, Breast, and Prostate Cancer. <i>Science</i> , 1997, 275, 1943-1947.	6.0	4,506
121	Fluorescence-Based Sequencing of Double-Stranded DNA by Hexamer String Priming. <i>Analytical Biochemistry</i> , 1996, 241, 228-237.	1.1	7
122	Rapid and reliable fluorescent cycle sequencing of double-stranded templates. <i>DNA Sequence</i> , 1992, 2, 289-296.	0.7	97
123	Sequencing and analysis of genomic fragments from the <i>NF1</i> locus. <i>DNA Sequence</i> , 1992, 3, 237-243.	0.7	11
124	An insert mutation in the chromosome 20 amyloid precursor gene in a Gerstmann-StrÄussler-Scheinker family. <i>Journal of the Neurological Sciences</i> , 1992, 111, 189-194.	0.3	60
125	<i>Caenorhabditis elegans</i> expressed sequence tags identify gene families and potential disease gene homologues. <i>Nature Genetics</i> , 1992, 1, 124-131.	9.4	199
126	Creutzfeldt-Jakob disease cosegregates with the codon 178AsnPRNP mutation in families of European origin. <i>Annals of Neurology</i> , 1992, 31, 274-281.	2.8	105

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127	New mutation in scrapie amyloid precursor gene (at codon 178) in Finnish Creutzfeldt-Jakob kindred. Lancet, The, 1991, 337, 425.	6.3	212
128	Complementary DNA sequencing: expressed sequence tags and human genome project. Science, 1991, 252, 1651-1656.	6.0	2,165
129	Genome Sequencing Conference I: Summary. Genomics, 1990, 8, 186-188.	1.3	1