

# W Richard McCombie

## 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.

133  
papers

67,556  
citations

73  
h-index

140  
g-index

140  
ext. papers

76,811  
ext. citations

18.5  
avg, IF

7.73  
L-index

#	Paper	IF	Citations
133	Transcriptional Silencing of Confers a Dependency on Fanconi Anemia Proteins in Acute Myeloid Leukemia. <i>Cancer Discovery</i> , <b>2021</b> , 11, 2300-2315	24.4	5
132	SLC5A3-dependent myo-inositol auxotrophy in acute myeloid leukemia. <i>Cancer Discovery</i> , <b>2021</b> ,	24.4	6
131	SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. <i>Plant Physiology</i> , <b>2020</b> , 182, 215-227	6.6	10
130	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , <b>2020</b> , 30, 1258-1273	9.7	25
129	Future Promises and Concerns of Ubiquitous Next-Generation Sequencing. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2019</b> , 9,	5.4	1
128	Next-Generation Sequencing Technologies. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2019</b> , 9,	5.4	57
127	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. <i>Genome Research</i> , <b>2018</b> , 28, 921-932	9.7	54
126	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> , <b>2018</b> , 115, 6494-6499	11.5	83
125	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line. <i>Genome Research</i> , <b>2018</b> , 28, 1126-1135	9.7	74
124	Solution-Phase Exome Capture. <i>Cold Spring Harbor Protocols</i> , <b>2017</b> , 2017, pdb.prot094680	1.2	
123	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , <b>2017</b> , 546, 524-527	50.4	643
122	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , <b>2017</b> , 18, 541	4.5	33
121	1D Genome Sequencing on the Oxford Nanopore MinION. <i>Current Protocols in Human Genetics</i> , <b>2017</b> , 94, 18.11.1-18.11.14	3.2	3
120	Coming of age: ten years of next-generation sequencing technologies. <i>Nature Reviews Genetics</i> , <b>2016</b> , 17, 333-51	30.1	2189
119	A trimming-and-retrieving alignment scheme for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , <b>2015</b> , 31, 2040-2	7.2	3
118	Assembly and diploid architecture of an individual human genome via single-molecule technologies. <i>Nature Methods</i> , <b>2015</b> , 12, 780-6	21.6	383
117	Oxford Nanopore sequencing, hybrid error correction, and de novo assembly of a eukaryotic genome. <i>Genome Research</i> , <b>2015</b> , 25, 1750-6	9.7	257

116	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. <i>Genome Biology</i> , <b>2015</b> , 16, 79	18.3	62
115	Unlocking the treasure trove: from genes to schizophrenia biology. <i>Schizophrenia Bulletin</i> , <b>2014</b> , 40, 492-63		13
114	The contribution of de novo coding mutations to autism spectrum disorder. <i>Nature</i> , <b>2014</b> , 515, 216-21	50.4	1470
113	FamAnn: an automated variant annotation pipeline to facilitate target discovery for family-based sequencing studies. <i>Bioinformatics</i> , <b>2014</b> , 30, 1175-1176	7.2	7
112	De novo mutations in schizophrenia implicate chromatin remodeling and support a genetic overlap with autism and intellectual disability. <i>Molecular Psychiatry</i> , <b>2014</b> , 19, 652-8	15.1	263
111	Two waves of de novo methylation during mouse germ cell development. <i>Genes and Development</i> , <b>2014</b> , 28, 1544-9	12.6	89
110	Sugarcane genome sequencing by methylation filtration provides tools for genomic research in the genus <i>Saccharum</i> . <i>Plant Journal</i> , <b>2014</b> , 79, 162-72	6.9	30
109	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> , <b>2014</b> , 19, 668-75	15.1	48
108	Validation and assessment of variant calling pipelines for next-generation sequencing. <i>Human Genomics</i> , <b>2014</b> , 8, 14	6.8	79
107	Error correction and assembly complexity of single molecule sequencing reads. <b>2014</b> ,		59
106	Next-generation sequencing of endoscopic biopsies identifies ARID1A as a tumor-suppressor gene in Barrett's esophagus. <i>Oncogene</i> , <b>2014</b> , 33, 347-57	9.2	71
105	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> , <b>2014</b> , 15, 506	18.3	168
104	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> , <b>2013</b> , 14 Suppl 9, S1	3.6	69
103	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , <b>2013</b> , 6, 4	5.8	1110
102	Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. <i>Rice</i> , <b>2013</b> , 6, 1	5.8	93
101	The effects of carbon dioxide and temperature on microRNA expression in Arabidopsis development. <i>Nature Communications</i> , <b>2013</b> , 4, 2145	17.4	92
100	Translating next generation sequencing to practice: opportunities and necessary steps. <i>Molecular Oncology</i> , <b>2013</b> , 7, 743-55	7.9	28
99	Chd5 requires PHD-mediated histone 3 binding for tumor suppression. <i>Cell Reports</i> , <b>2013</b> , 3, 92-102	10.6	36

98	A hybrid likelihood model for sequence-based disease association studies. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003324	16
97	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <i>Genome Research</i> , <b>2013</b> , 23, 1651-62	9.7 199
96	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> , <b>2013</b> , 110, 7940-5	11.5 173
95	Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in <i>Arabidopsis thaliana</i> roots. <i>BMC Genomics</i> , <b>2013</b> , 14, 701	4.5 69
94	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , <b>2012</b> , 13, 243	18.3 131
93	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <i>Nature</i> , <b>2012</b> , 491, 705-10	10.4 821
92	De novo gene disruptions in children on the autistic spectrum. <i>Neuron</i> , <b>2012</b> , 74, 285-99	13.9 1052
91	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , <b>2012</b> , 44, 803-7	36.3 470
90	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , <b>2012</b> , 485, 635-41	50.4 2138
89	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 693-700	44.5 758
88	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> , <b>2012</b> , 99, 397-406	2.7 68
87	Draft genome sequence of pigeonpea ( <i>Cajanus cajan</i> ), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , <b>2011</b> , 30, 83-9	44.5 587
86	High-Throughput Sequencing <b>2011</b> , 461-478	2
85	Sperm methylation profiles reveal features of epigenetic inheritance and evolution in primates. <i>Cell</i> , <b>2011</b> , 146, 1029-41	56.2 280
84	Directional DNA methylation changes and complex intermediate states accompany lineage specificity in the adult hematopoietic compartment. <i>Molecular Cell</i> , <b>2011</b> , 44, 17-28	17.6 228
83	A comparative analysis of exome capture. <i>Genome Biology</i> , <b>2011</b> , 12, R97	18.3 99
82	Discovery of novel human breast cancer microRNAs from deep sequencing data by analysis of pri-microRNA secondary structures. <i>PLoS ONE</i> , <b>2011</b> , 6, e16403	3.7 29
81	Transpositional landscape of the rice genome revealed by paired-end mapping of high-throughput re-sequencing data. <i>Plant Journal</i> , <b>2011</b> , 66, 241-6	6.9 52

80	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , <b>2011</b> , 43, 101-8	36.3	502
79	Tumour evolution inferred by single-cell sequencing. <i>Nature</i> , <b>2011</b> , 472, 90-4	50.4	1834
78	Establishing the baseline level of repetitive element expression in the human cortex. <i>BMC Genomics</i> , <b>2011</b> , 12, 495	4.5	11
77	Whole transcriptome analysis of the fasting and fed Burmese python heart: insights into extreme physiological cardiac adaptation. <i>Physiological Genomics</i> , <b>2011</b> , 43, 69-76	3.6	21
76	SpliceTrap: a method to quantify alternative splicing under single cellular conditions. <i>Bioinformatics</i> , <b>2011</b> , 27, 3010-6	7.2	73
75	Distinct p53 genomic binding patterns in normal and cancer-derived human cells. <i>Cell Cycle</i> , <b>2011</b> , 10, 4237-49	4.7	73
74	A functional phylogenomic view of the seed plants. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002411	6	117
73	Small RNA-based silencing strategies for transposons in the process of invading <i>Drosophila</i> species. <i>Rna</i> , <b>2010</b> , 16, 1634-45	5.8	61
72	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000728	6	34
71	Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. <i>Genome Research</i> , <b>2009</b> , 19, 1077-83	9.7	40
70	High definition profiling of mammalian DNA methylation by array capture and single molecule bisulfite sequencing. <i>Genome Research</i> , <b>2009</b> , 19, 1593-605	9.7	183
69	Functional identification of tumor-suppressor genes through an in vivo RNA interference screen in a mouse lymphoma model. <i>Cancer Cell</i> , <b>2009</b> , 16, 324-35	24.3	143
68	Prepublication data sharing. <i>Nature</i> , <b>2009</b> , 461, 168-70	50.4	197
67	Hybrid selection of discrete genomic intervals on custom-designed microarrays for massively parallel sequencing. <i>Nature Protocols</i> , <b>2009</b> , 4, 960-74	18.8	153
66	Specialized piRNA pathways act in germline and somatic tissues of the <i>Drosophila</i> ovary. <i>Cell</i> , <b>2009</b> , 137, 522-35	56.2	627
65	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , <b>2009</b> , 326, 1112-5	33.3	2949
64	Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. <i>Nature Methods</i> , <b>2008</b> , 5, 679-82	1.6	136
63	Genome-wide transposon tagging reveals location-dependent effects on transcription and chromatin organization in <i>Arabidopsis</i> . <i>Plant Journal</i> , <b>2008</b> , 55, 514-25	6.9	47

62	High-content analysis of cancer genome DNA alterations. <i>Current Opinion in Genetics and Development</i> , <b>2008</b> , 18, 68-72	4.9	13
61	An oncogenomics-based in vivo RNAi screen identifies tumor suppressors in liver cancer. <i>Cell</i> , <b>2008</b> , 135, 852-64	56.2	366
60	Topoisomerase levels determine chemotherapy response in vitro and in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 9053-8	11.5	222
59	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> , <b>2008</b> , 18, 19-29	9.7	97
58	Genome-wide in situ exon capture for selective resequencing. <i>Nature Genetics</i> , <b>2007</b> , 39, 1522-7	36.3	565
57	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , <b>2007</b> , 17, 175-83	9.7	200
56	Epigenetic natural variation in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , <b>2007</b> , 5, e174	9.7	337
55	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> , <b>2006</b> , 103, 7444-9	11.5	112
54	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> , <b>2006</b> , 25, 592-8	5.1	26
53	Second-generation shRNA libraries covering the mouse and human genomes. <i>Nature Genetics</i> , <b>2005</b> , 37, 1281-8	36.3	522
52	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> , <b>2005</b> , 111, 949-55	6	22
51	Sorghum genome sequencing by methylation filtration. <i>PLoS Biology</i> , <b>2005</b> , 3, e13	9.7	126
50	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , <b>2005</b> , 15, 1284-91	9.7	66
49	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> , <b>2005</b> , 15, 496-504	9.7	25
48	Differential methylation of genes and repeats in land plants. <i>Genome Research</i> , <b>2005</b> , 15, 1431-40	9.7	119
47	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> , <b>2004</b> , 47, 666-79	2.4	51
46	The mouse genome: experimental examination of gene predictions and transcriptional start sites. <i>Genome Research</i> , <b>2004</b> , 14, 2424-9	9.7	11
45	Production of complex nucleic acid libraries using highly parallel in situ oligonucleotide synthesis. <i>Nature Methods</i> , <b>2004</b> , 1, 241-8	21.6	89

44	A resource for large-scale RNA-interference-based screens in mammals. <i>Nature</i> , <b>2004</b> , 428, 427-31	50.4	561
43	Role of transposable elements in heterochromatin and epigenetic control. <i>Nature</i> , <b>2004</b> , 430, 471-6	50.4	958
42	Sequencing the maize genome. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 102-7	9.9	48
41	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. <i>Functional and Integrative Genomics</i> , <b>2004</b> , 4, 102-17	3.8	40
40	Syntenic relationships between <i>Medicago truncatula</i> and <i>Arabidopsis</i> reveal extensive divergence of genome organization. <i>Plant Physiology</i> , <b>2003</b> , 131, 1018-26	6.6	59
39	Secretion trap tagging of secreted and membrane-spanning proteins using <i>Arabidopsis</i> gene traps. <i>Plant Physiology</i> , <b>2003</b> , 132, 698-708	6.6	21
38	Gene enrichment in plant genomic shotgun libraries. <i>Current Opinion in Plant Biology</i> , <b>2003</b> , 6, 150-6	9.9	31
37	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. <i>Cancer Cell</i> , <b>2003</b> , 3, 297-302	24.3	193
36	Maize genome sequencing by methylation filtration. <i>Science</i> , <b>2003</b> , 302, 2115-7	33.3	189
35	In-depth view of structure, activity, and evolution of rice chromosome 10. <i>Science</i> , <b>2003</b> , 300, 1566-9	33.3	234
34	A survey of canine expressed sequence tags and a display of their annotations through a flexible web-based interface. <i>Journal of Heredity</i> , <b>2003</b> , 94, 15-22	2.4	3
33	Genes and transposons are differentially methylated in plants, but not in mammals. <i>Genome Research</i> , <b>2003</b> , 13, 2658-64	9.7	108
32	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , <b>2002</b> , 420, 520-62	50.4	5376
31	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , <b>2002</b> , 415, 871-80	50.4	1281
30	What is finished, and why does it matter. <i>Genome Research</i> , <b>2002</b> , 12, 669-71	9.7	50
29	GFSan: a gene family search tool at genomic DNA level. <i>Genome Research</i> , <b>2002</b> , 12, 1142-9	9.7	7
28	On the importance of being finished. <i>Genome Biology</i> , <b>2002</b> , 3, COMMENT2010	18.3	7
27	Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. <i>Nature</i> , <b>2001</b> , 409, 207-11	50.4	831

26	Initial sequencing and analysis of the human genome. <i>Nature</i> , <b>2001</b> , 409, 860-921	50.4	17366
25	Identification of mesoderm development (mesd) candidate genes by comparative mapping and genome sequence analysis. <i>Genomics</i> , <b>2001</b> , 72, 88-98	4.3	16
24	The first plant genome. <i>Cell</i> , <b>2001</b> , 105, 571-4	56.2	12
23	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 823-6	50.4	137
22	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 796-815	50.4	7262
21	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> , <b>1999</b> , 96, 11416-21	11.5	164
20	zA map for sequence analysis of the <i>Arabidopsis thaliana</i> genome. <i>Nature Genetics</i> , <b>1999</b> , 22, 265-70	36.3	109
19	Differential methylation of genes and retrotransposons facilitates shotgun sequencing of the maize genome. <i>Nature Genetics</i> , <b>1999</b> , 23, 305-8	36.3	209
18	Genetic definition and sequence analysis of <i>Arabidopsis</i> centromeres. <i>Science</i> , <b>1999</b> , 286, 2468-74	33.3	381
17	Genetic analysis using genomic representations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 4487-92	11.5	74
16	Rapid isolation of cDNA by hybridization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 3764-9	11.5	5
15	PTEN, a putative protein tyrosine phosphatase gene mutated in human brain, breast, and prostate cancer. <i>Science</i> , <b>1997</b> , 275, 1943-7	33.3	4006
14	Fluorescence-based sequencing of double-stranded DNA by hexamer string priming. <i>Analytical Biochemistry</i> , <b>1996</b> , 241, 228-37	3.1	6
13	Rapid and reliable fluorescent cycle sequencing of double-stranded templates. <i>DNA Sequence</i> , <b>1992</b> , 2, 289-96		86
12	Sequencing and analysis of genomic fragments from the NF1 locus. <i>DNA Sequence</i> , <b>1992</b> , 3, 237-43		11
11	An insert mutation in the chromosome 20 amyloid precursor gene in a Gerstmann-Strüssler-Scheinker family. <i>Journal of the Neurological Sciences</i> , <b>1992</b> , 111, 189-94	3.2	54
10	<i>Caenorhabditis elegans</i> expressed sequence tags identify gene families and potential disease gene homologues. <i>Nature Genetics</i> , <b>1992</b> , 1, 124-31	36.3	170
9	Creutzfeldt-Jakob disease cosegregates with the codon 178Asn PRNP mutation in families of European origin. <i>Annals of Neurology</i> , <b>1992</b> , 31, 274-81	9.4	94



8	New mutation in scrapie amyloid precursor gene (at codon 178) in Finnish Creutzfeldt-Jakob kindred. <i>Lancet, The</i> , <b>1991</b> , 337, 425	40	179
7	Complementary DNA sequencing: expressed sequence tags and human genome project. <i>Science</i> , <b>1991</b> , 252, 1651-6	33-3	189-3
6	Long-read sequencing reveals rapid evolution of immunity- and cancer-related genes in bats		2
5	Third-generation sequencing and the future of genomics		55
4	Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line		6
3	Transcriptional silencing of ALDH2 in acute myeloid leukemia confers a dependency on Fanconi anemia proteins		2
2	In vivogenetic screen identifies a SLC5A3-dependent myo-inositol auxotrophy in acute myeloid leukemia		3
1	Comprehensive analysis of structural variants in breast cancer genomes using single molecule sequencing		3