Richard A Moore

List of Publications by Year
in descending order

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91 papers	45,416 citations	26630 56 h-index	39675 94 g-index
95 all docs	95 docs citations	95 times ranked	61044 citing authors

#	Article	IF	Citations
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
2	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
3	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
4	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
5	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
6	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
7	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
8	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
9	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
10	Fusobacterium nucleatum infection is prevalent in human colorectal carcinoma. Genome Research, 2012, 22, 299-306.	5.5	1,582
11	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
12	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
13	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
14	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	12.6	1,147
15	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
16	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
17	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886
18	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801

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19	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
20	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
21	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
22	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
23	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
24	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
25	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
26	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
27	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
28	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
29	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
30	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
31	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
32	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	27.8	321
33	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
34	Co-occurrence of anaerobic bacteria in colorectal carcinomas. Microbiome, 2013, 1, 16.	11.1	284
35	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
36	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270

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37	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
38	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	21.4	255
39	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	16.8	244
40	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. Cancer Cell, 2014, 26, 33-47.	16.8	241
41	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
42	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
43	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. Nature Cancer, 2021, 2, 157-173.	13.2	147
44	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. Clinical Cancer Research, 2017, 23, 7521-7530.	7.0	144
45	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
46	NRG1 Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in KRAS Wild-Type Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2019, 25, 4674-4681.	7.0	121
47	Altered Gene Expression along the Glycolysisâ€“Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 135-146.	7.0	121
48	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
49	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406.	16.8	105
50	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	13.2	103
51	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
52	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591.	7.0	82
53	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7.	6.4	74
54	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013.	12.8	64

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55	A somatic reference standard for cancer genome sequencing. Scientific Reports, 2016, 6, 24607.	3.3	64
56	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260.	4.5	57
57	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. PLoS ONE, 2011, 6, e19838.	2.5	55
58	Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 2019, 47, e12-e12.	14.5	50
59	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. Clinical Cancer Research, 2021, 27, 202-212.	7.0	50
60	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49
61	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	12.8	47
62	Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19098-19108.	7.1	42
63	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. Developmental Cell, 2018, 44, 709-724.e6.	7.0	35
64	Therapeutic immunisation with COPV early genes by epithelial DNA delivery. Virology, 2003, 314, 630-635.	2.4	32
65	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomicsâ€™ GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	2.5	31
66	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	2.8	29
67	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. Clinical Cancer Research, 2021, 27, 150-157.	7.0	24
68	Human papillomavirus type 16 E2- and L1-specific serological and T-cell responses in women with vulval intraepithelial neoplasia. Journal of General Virology, 2003, 84, 2089-2097.	2.9	22
69	MAVIS: merging, annotation, validation, and illustration of structural variants. Bioinformatics, 2019, 35, 515-517.	4.1	22
70	Diagnostic Value of Next-Generation Sequencing in an Unusual Sphenoid Tumor. Oncologist, 2014, 19, 623-630.	3.7	20
71	Intraepithelial DNA Immunisation with a Plasmid Encoding a Codon Optimised COPV E1 Gene Sequence, But Not the Wild-Type Gene Sequence Completely Protects against Mucosal Challenge with Infectious COPV in Beagles. Virology, 2002, 304, 451-459.	2.4	19
72	Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. Journal of Physical Education and Sports Management, 2018, 4, a002626.	1.2	18

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73	Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. PLoS ONE, 2017, 12, e0178706.	2.5	18
74	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. Journal of Physical Education and Sports Management, 2019, 5, a003814.	1.2	17
75	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. Clinical Cancer Research, 2021, 27, 246-254.	7.0	16
76	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. Clinical Cancer Research, 2021, 27, 522-531.	7.0	14
77	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92.	1.8	13
78	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	2.8	12
79	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. PLoS ONE, 2019, 14, e0224578.	2.5	12
80	Sample Tracking Using Unique Sequence Controls. Journal of Molecular Diagnostics, 2020, 22, 141-146.	2.8	10
81	Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. Cancer Medicine, 2021, 10, 1155-1165.	2.8	9
82	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline CHEK2:c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. Journal of Physical Education and Sports Management, 2017, 3, a001628.	1.2	8
83	Characterization of the human thyroid epigenome. Journal of Endocrinology, 2017, 235, 153-165.	2.6	8
84	Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. BMC Genomics, 2017, 18, 515.	2.8	8
85	Tumor microRNA profile and prognostic value for lymph node metastasis in oral squamous cell carcinoma patients. Oncotarget, 2020, 11, 2204-2215.	1.8	8
86	Complete Chloroplast Genome Sequence of a White Spruce (Picea glauca, Genotype WS77111) from Eastern Canada. Microbiology Resource Announcements, 2019, 8, .	0.6	7
87	Assessing Limit of Detection in Clinical Sequencing. Journal of Molecular Diagnostics, 2021, 23, 455-466.	2.8	7
88	A Distributed Whole Genome Sequencing Benchmark Study. Frontiers in Genetics, 2020, 11, 612515.	2.3	6
89	Complete Chloroplast Genome Sequence of an Engelmann Spruce (Picea engelmannii , Genotype) Tj ETQq1 1 0.784314 rgBT	0.6	4
90	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	2.3	2

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91	Use of Treatment-Focused Tumor Sequencing to Screen for Germline Cancer Predisposition. Journal of Molecular Diagnostics, 2021, 23, 1145-1158.	2.8	2