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	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. Clinical Cancer Research, 2021, 27, 522-531.	7.0	14
2	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. Clinical Cancer Research, 2021, 27, 246-254.	7.0	16
3	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. Clinical Cancer Research, 2021, 27, 202-212.	7.0	50
4	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. Clinical Cancer Research, 2021, 27, 150-157.	7.0	24
5	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. Nature Cancer, 2021, 2, 157-173.	13.2	147
6	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	12.8	47
7	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49
8	Assessing Limit of Detection in Clinical Sequencing. Journal of Molecular Diagnostics, 2021, 23, 455-466.	2.8	7
9	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	2.3	2
10	Use of Treatment-Focused Tumor Sequencing to Screen for Germline Cancer Predisposition. Journal of Molecular Diagnostics, 2021, 23, 1145-1158.	2.8	2
11	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
12	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
13	Sample Tracking Using Unique Sequence Controls. Journal of Molecular Diagnostics, 2020, 22, 141-146.	2.8	10
14	A Distributed Whole Genome Sequencing Benchmark Study. Frontiers in Genetics, 2020, 11, 612515.	2.3	6
15	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	13.2	103
16	Tumor microRNA profile and prognostic value for lymph node metastasis in oral squamous cell carcinoma patients. Oncotarget, 2020, 11, 2204-2215.	1.8	8
17	MAVIS: merging, annotation, validation, and illustration of structural variants. Bioinformatics, 2019, 35, 515-517.	4.1	22
18	Complete Chloroplast Genome Sequence of an Engelmann Spruce (Picea engelmannii , Genotype) Tj ETQq0 0 0 rgBT /Overlock 1	0.6	4

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19	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. PLoS ONE, 2019, 14, e0224578.	2.5	12
20	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
21	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
22	Complete Chloroplast Genome Sequence of a White Spruce (Picea glauca, Genotype WS77111) from Eastern Canada. Microbiology Resource Announcements, 2019, 8, .	0.6	7
23	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. Journal of Physical Education and Sports Management, 2019, 5, a003814.	1.2	17
24	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
25	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92.	1.8	13
26	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
27	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
28	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
29	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
30	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
31	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
32	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
33	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
34	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
35	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
36	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

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37	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
38	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
39	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
40	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
41	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
42	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
43	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
44	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
45	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
46	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
47	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
48	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
49	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
50	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
51	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
52	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	21.4	255
53	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	27.8	321
54	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787

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55	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
56	Characterization of the human thyroid epigenome. Journal of Endocrinology, 2017, 235, 153-165.	2.6	8
57	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
58	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. Clinical Cancer Research, 2017, 23, 7521-7530.	7.0	144
59	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
60	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
61	Increasing quality, throughput and speed of sample preparation for strand-specific messenger RNA sequencing. BMC Genomics, 2017, 18, 515.	2.8	8
62	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
63	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomicsâ€™ GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	2.5	31
64	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
65	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
66	A somatic reference standard for cancer genome sequencing. Scientific Reports, 2016, 6, 24607.	3.3	64
67	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
68	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
69	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406.	16.8	105
70	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
71	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013.	12.8	64
72	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	16.8	244

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73	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
74	Diagnostic Value of Next-Generation Sequencing in an Unusual Sphenoid Tumor. Oncologist, 2014, 19, 623-630.	3.7	20
75	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	12.6	1,147
76	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. Cancer Cell, 2014, 26, 33-47.	16.8	241
77	Co-occurrence of anaerobic bacteria in colorectal carcinomas. Microbiome, 2013, 1, 16.	11.1	284
78	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
79	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	2.8	12
80	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260.	4.5	57
81	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
82	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
83	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
84	Fusobacterium nucleatum infection is prevalent in human colorectal carcinoma. Genome Research, 2012, 22, 299-306.	5.5	1,582
85	The Sensitivity of Massively Parallel Sequencing for Detecting Candidate Infectious Agents Associated with Human Tissue. PLoS ONE, 2011, 6, e19838.	2.5	55
86	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886
87	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
88	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
89	Therapeutic immunisation with COPV early genes by epithelial DNA delivery. Virology, 2003, 314, 630-635.	2.4	32
90	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

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91	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