Elaine R Mardis

List of Publications by Year
in descending order

244 papers	107,533 citations	2802 94 h-index	1316 224 g-index
276 all docs	276 docs citations	276 times ranked	115215 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	An obesity-associated gut microbiome with increased capacity for energy harvest. Nature, 2006, 444, 1027-1031.	27.8	10,136
3	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
4	EGF receptor gene mutations are common in lung cancers from â€œnever smokersâ€• and are associated with sensitivity of tumors to gefitinib and erlotinib. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13306-13311.	7.1	4,106
5	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	5.5	4,086
6	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
7	Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes. Journal of Clinical Oncology, 2009, 27, 1160-1167.	1.6	3,730
8	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	27.8	2,694
9	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
10	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
11	Next-Generation DNA Sequencing Methods. Annual Review of Genomics and Human Genetics, 2008, 9, 387-402.	6.2	1,788
12	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
13	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. Nature, 2014, 515, 577-581.	27.8	1,705
14	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	30.7	1,533
15	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
16	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	19.0	1,322
17	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
18	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275

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19	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	4.1	1,193
20	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	27.0	1,161
21	A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. Science, 2015, 348, 803-808.	12.6	1,139
22	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
23	Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting. Nature, 2012, 482, 400-404.	27.8	1,075
24	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	27.8	1,020
25	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
26	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
27	The Next-Generation Sequencing Revolution and Its Impact on Genomics. Cell, 2013, 155, 27-38.	28.9	856
28	A decadeâ€™s perspective on DNA sequencing technology. Nature, 2011, 470, 198-203.	27.8	731
29	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
30	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. Cancer Discovery, 2013, 3, 224-237.	9.4	697
31	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
32	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
33	A Comparison of PAM50 Intrinsic Subtyping with Immunohistochemistry and Clinical Prognostic Factors in Tamoxifen-Treated Estrogen Receptorâ€“Positive Breast Cancer. Clinical Cancer Research, 2010, 16, 5222-5232.	7.0	676
34	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
35	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
36	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	5.5	586

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37	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
38	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
39	C11orf95â€“RELA fusions drive oncogenic NF-Î²B signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
40	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
41	Next-Generation Sequencing Platforms. Annual Review of Analytical Chemistry, 2013, 6, 287-303.	5.4	519
42	Tumor neoantigens: building a framework for personalized cancer immunotherapy. Journal of Clinical Investigation, 2015, 125, 3413-3421.	8.2	502
43	Convergent loss of PTEN leads to clinical resistance to a PI(3)KÎ± inhibitor. Nature, 2015, 518, 240-244.	27.8	486
44	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
45	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
46	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
47	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
48	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	9.4	418
49	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
50	Whole-genome sequencing and variant discovery in C. elegans. Nature Methods, 2008, 5, 183-188.	19.0	380
51	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. JAMA - Journal of the American Medical Association, 2012, 307, 1062.	7.4	379
52	DGIdb 2.0: mining clinically relevant drugâ€“gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359
53	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. BMC Medical Genomics, 2015, 8, 54.	1.5	352
54	The emerging clinical relevance of genomics in cancer medicine. Nature Reviews Clinical Oncology, 2018, 15, 353-365.	27.6	351

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55	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. Genome Medicine, 2016, 8, 11.	8.2	350
56	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
57	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
58	The Pediatric Cancer Genome Project. Nature Genetics, 2012, 44, 619-622.	21.4	315
59	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
60	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathologica, 2016, 131, 833-845.	7.7	288
61	DNA sequencing technologies: 2006â€“2016. Nature Protocols, 2017, 12, 213-218.	12.0	266
62	A 50-Gene Intrinsic Subtype Classifier for Prognosis and Prediction of Benefit from Adjuvant Tamoxifen. Clinical Cancer Research, 2012, 18, 4465-4472.	7.0	258
63	Contribution of systemic and somatic factors to clinical response and resistance to PD-L1 blockade in urothelial cancer: An exploratory multi-omic analysis. PLoS Medicine, 2017, 14, e1002309.	8.4	256
64	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
65	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252
66	Immunogenomics of Hypermutated Glioblastoma: A Patient with Germline POLE Deficiency Treated with Checkpoint Blockade Immunotherapy. Cancer Discovery, 2016, 6, 1230-1236.	9.4	242
67	Temporally Distinct PD-L1 Expression by Tumor and Host Cells Contributes to Immune Escape. Cancer Immunology Research, 2017, 5, 106-117.	3.4	236
68	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233
69	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
70	The $1,000 genome, the $100,000 analysis?. Genome Medicine, 2010, 2, 84.	8.2	229
71	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	27.8	223
72	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222

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73	Applications of Immunogenomics to Cancer. Cell, 2017, 168, 600-612.	28.9	198
74	Cancer genome sequencing: a review. Human Molecular Genetics, 2009, 18, R163-R168.	2.9	185
75	Clinical Significance of CTNNB1 Mutation and Wnt Pathway Activation in Endometrioid Endometrial Carcinoma. Journal of the National Cancer Institute, 2014, 106, .	6.3	182
76	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
77	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246.	2.8	173
78	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
79	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. Lancet Oncology, The, 2015, 16, 1659-1666.	10.7	161
80	Anticipating the 1,000 dollar genome. Genome Biology, 2006, 7, 112.	9.6	154
81	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
82	Next-generation sequencing identifies the natural killer cell microRNA transcriptome. Genome Research, 2010, 20, 1590-1604.	5.5	144
83	Next-Generation Sequencing Technologies. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036798.	6.2	143
84	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 33, 937-948.e8.	16.8	142
85	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	21.4	136
86	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	3.4	132
87	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	2.8	131
88	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. Journal of Clinical Investigation, 2018, 128, 1371-1383.	8.2	126
89	Comprehensive gene expression meta-analysis identifies signature genes that distinguish microglia from peripheral monocytes/macrophages in health and glioma. Acta Neuropathologica Communications, 2019, 7, 20.	5.2	124
90	Analysis of next-generation genomic data in cancer: accomplishments and challenges. Human Molecular Genetics, 2010, 19, R188-R196.	2.9	122

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91	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.	2.5	120
92	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	3.5	115
93	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	12.8	112
94	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
95	INTEGRATE-neo: a pipeline for personalized gene fusion neoantigen discovery. Bioinformatics, 2017, 33, 555-557.	4.1	105
96	DoCM: a database of curated mutations in cancer. Nature Methods, 2016, 13, 806-807.	19.0	96
97	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood, 2016, 127, 893-897.	1.4	94
98	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	8.2	91
99	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	12.8	89
100	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine, 2016, 13, e1002174.	8.4	86
101	A Phase I Trial of BKM120 (Buparlisib) in Combination with Fulvestrant in Postmenopausal Women with Estrogen Receptorâ€“Positive Metastatic Breast Cancer. Clinical Cancer Research, 2016, 22, 1583-1591.	7.0	86
102	A Surprising Cross-Species Conservation in the Genomic Landscape of Mouse and Human Oral Cancer Identifies a Transcriptional Signature Predicting Metastatic Disease. Clinical Cancer Research, 2014, 20, 2873-2884.	7.0	84
103	Drosophila Muller F Elements Maintain a Distinct Set of Genomic Properties Over 40 Million Years of Evolution. G3: Genes, Genomes, Genetics, 2015, 5, 719-740.	1.8	84
104	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
105	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. Nature Communications, 2020, 11, 2156.	12.8	83
106	Neoantigens and genome instability: impact on immunogenomic phenotypes and immunotherapy response. Genome Medicine, 2019, 11, 71.	8.2	78
107	New strategies and emerging technologies for massively parallel sequencing: applications in medical research. Genome Medicine, 2009, 1, 40.	8.2	75
108	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. Neoplasia, 2015, 17, 776-788.	5.3	75

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109	Breast Cancer Neoantigens Can Induce CD8+ T-Cell Responses and Antitumor Immunity. Cancer Immunology Research, 2017, 5, 516-523.	3.4	74
110	Integrated Analysis of RNA and DNA from the Phase III Trial CALGB 40601 Identifies Predictors of Response to Trastuzumab-Based Neoadjuvant Chemotherapy in HER2-Positive Breast Cancer. Clinical Cancer Research, 2018, 24, 5292-5304.	7.0	73
111	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. Nature Communications, 2015, 6, 7553.	12.8	72
112	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 2016, 7, 12498.	12.8	69
113	Quantitative Chromatographic Estimation of Î±-Amino-Acids. Nature, 1948, 161, 763-763.	27.8	66
114	A Phase II Trial of Neoadjuvant MK-2206, an AKT Inhibitor, with Anastrozole in Clinical Stage II or IIIPIK3CA-Mutant ER-Positive and HER2-Negative Breast Cancer. Clinical Cancer Research, 2017, 23, 6823-6832.	7.0	66
115	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66
116	Genome sequencing and cancer. Current Opinion in Genetics and Development, 2012, 22, 245-250.	3.3	62
117	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	21.4	62
118	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. Bioinformatics, 2010, 26, 464-469.	4.1	59
119	What is Finished, and Why Does it Matter. Genome Research, 2002, 12, 669-671.	5.5	57
120	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	3.5	57
121	Genetic risk factors for the development of osteonecrosis in children under age 10 treated for acute lymphoblastic leukemia. Blood, 2016, 127, 558-564.	1.4	56
122	A pilot study of high-throughput, sequence-based mutational profiling of primary human acute myeloid leukemia cell genomes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14275-14280.	7.1	55
123	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	12.8	55
124	Exome sequencing of case-unaffected-parents trios reveals recessive and de novo genetic variants in sporadic ALS. Scientific Reports, 2015, 5, 9124.	3.3	53
125	Research-based PAM50 signature and long-term breast cancer survival. Breast Cancer Research and Treatment, 2020, 179, 197-206.	2.5	53
126	Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741 (Alliance). Journal of the National Cancer Institute, 2015, 107, .	6.3	52

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127	Detection of neoantigen-specific T cells following a personalized vaccine in a patient with glioblastoma. OncoImmunology, 2019, 8, e1561106.	4.6	50
128	RNAâ€sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	4.9	44
129	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.4	44
130	The Impact of Next-Generation Sequencing on Cancer Genomics: From Discovery to Clinic. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036269.	6.2	43
131	Accounting for proximal variants improves neoantigen prediction. Nature Genetics, 2019, 51, 175-179.	21.4	43
132	Applying next-generation sequencing to pancreatic cancer treatment. Nature Reviews Gastroenterology and Hepatology, 2012, 9, 477-486.	17.8	41
133	A multiple myeloma-specific capture sequencing platform discovers novel translocations and frequent, risk-associated point mutations in IGLL5. Blood Cancer Journal, 2018, 8, 35.	6.2	41
134	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	10.3	41
135	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	2.8	40
136	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23662-23670.	7.1	40
137	Frontiers in cancer immunotherapyâ€"a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	3.8	39
138	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. Bone, 2017, 101, 145-155.	2.9	37
139	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. PLoS ONE, 2014, 9, e87645.	2.5	34
140	Impact of mutational profiles on response of primary oestrogen receptor-positive breast cancers to oestrogen deprivation. Nature Communications, 2016, 7, 13294.	12.8	34
141	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. Cancer Discovery, 2022, 12, 154-171.	9.4	34
142	A vertebrate case study of the quality of assemblies derived from next-generation sequences. Genome Biology, 2011, 12, R31.	9.6	32
143	Whole genome analyses reveal no pathogenetic single nucleotide or structural differences between monozygotic twins discordant for amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2015, 16, 385-392.	1.7	27
144	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. Cell Reports, 2018, 24, 2167-2178.	6.4	26

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145	Immunotherapeutic Challenges for Pediatric Cancers. Molecular Therapy - Oncolytics, 2019, 15, 38-48.	4.4	26
146	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. Neurology: Genetics, 2020, 6, e460.	1.9	26
147	Caenorhabditis elegans glp-4Encodes a Valyl Aminoacyl tRNA Synthetase. G3: Genes, Genomes, Genetics, 2015, 5, 2719-2728.	1.8	25
148	Genomic profiling of murine mammary tumors identifies potential personalized drug targets for p53 deficient mammary cancers. DMM Disease Models and Mechanisms, 2016, 9, 749-57.	2.4	25
149	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. Brain, 2021, 144, 2971-2978.	7.6	23
150	Cancer Genome Sequencing and Its Implications for Personalized Cancer Vaccines. Cancers, 2011, 3, 4191-4211.	3.7	22
151	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 105-111.	1.1	22
152	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.	6.4	21
153	Genomics of Acute Myeloid Leukemia. Cancer Journal (Sudbury, Mass), 2011, 17, 487-491.	2.0	20
154	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. Blood, 2014, 124, 3887-3895.	1.4	20
155	Molecular and Pathology Features of Colorectal Tumors and Patient Outcomes Are Associated with Fusobacterium nucleatum and Its Subspecies animalis. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 210-220.	2.5	19
156	Cancer genomics identifies determinants of tumor biology. Genome Biology, 2010, 11, 211.	9.6	17
157	The challenges of big data. DMM Disease Models and Mechanisms, 2016, 9, 483-485.	2.4	17
158	A roadmap for the next decade in cancer research. Nature Cancer, 2020, 1, 12-17.	13.2	17
159	Infantile fibrosarcomaâ€“like tumor driven by novel RBPMS-MET fusion consolidated with cabozantinib. Journal of Physical Education and Sports Management, 2020, 6, a005645.	1.2	17
160	Resistance-promoting effects of ependymoma treatment revealed through genomic analysis of multiple recurrences in a single patient. Journal of Physical Education and Sports Management, 2018, 4, a002444.	1.2	16
161	Disease-associated mosaic variation in clinical exome sequencing: a two-year pediatric tertiary care experience. Journal of Physical Education and Sports Management, 2020, 6, a005231.	1.2	15
162	Acute lymphoblastic leukemia displays a distinct highly methylated genome. Nature Cancer, 2022, 3, 768-782.	13.2	15

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163	miRNAs and Long-term Breast Cancer Survival: Evidence from the WHEL Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1525-1533.	2.5	14
164	The translation of cancer genomics: time for a revolution in clinical cancer care. Genome Medicine, 2014, 6, 22.	8.2	13
165	Sequencing the AML Genome, Transcriptome, and Epigenome. Seminars in Hematology, 2014, 51, 250-258.	3.4	13
166	Causal and Candidate Gene Variants in a Large Cohort of Women With Primary Ovarian Insufficiency. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 685-714.	3.6	13
167	Discovery of clinically relevant fusions in pediatric cancer. BMC Genomics, 2021, 22, 872.	2.8	13
168	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. European Journal of Medical Genetics, 2019, 62, 103701.	1.3	12
169	Gastroblastoma with a novel <scp>EWSR1â€CTBP1</scp> fusion presenting in adolescence. Genes Chromosomes and Cancer, 2021, 60, 640-646.	2.8	12
170	Immune Activity and Response Differences of Oncolytic Viral Therapy in Recurrent Glioblastoma: Gene Expression Analyses of a Phase IB Study. Clinical Cancer Research, 2022, 28, 498-506.	7.0	12
171	Comprehensive Genomic Studies. American Journal of Clinical Pathology, 2012, 138, 31-41.	0.7	11
172	An mRNA Gene Expressionâ€“Based Signature to Identify FGFR1-Amplified Estrogen Receptorâ€“Positive Breast Tumors. Journal of Molecular Diagnostics, 2017, 19, 147-161.	2.8	11
173	A Pneumatic Device for Rapid Loading of DNA Sequencingâ€‰Gels. Genome Research, 1998, 8, 543-548.	5.5	10
174	Defining the AHR-regulated transcriptome in NK cells reveals gene expression programs relevant to development and function. Blood Advances, 2021, 5, 4605-4618.	5.2	10
175	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	5.6	9
176	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
177	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. Journal of Molecular Diagnostics, 2020, 22, 1238-1245.	2.8	9
178	De novo primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) NFIA/CBFA2T3 translocation. Haematologica, 2020, 105, e194-e197.	3.5	9
179	Novel morphologic findings in <scp>PLAG1â€rearranged</scp> soft tissue tumors. Genes Chromosomes and Cancer, 2021, 60, 577-585.	2.8	9
180	Mutations In the DNA Methyltransferase Gene DNMT3A Are Highly Recurrent In Patients with Intermediate Risk Acute Myeloid Leukemia, and Predict Poor Outcomes. Blood, 2010, 116, 99-99.	1.4	9

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181	A focus on personal genomics. Personalized Medicine, 2009, 6, 603-606.	1.5	8
182	Brief Report: The Role of Rare Proteinâ€Coding Variants in Antiâ€“Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. Arthritis and Rheumatology, 2017, 69, 735-741.	5.6	8
183	No evidence that G6PD deficiency affects the efficacy or safety of daunorubicin in acute lymphoblastic leukemia induction therapy. Pediatric Blood and Cancer, 2019, 66, e27681.	1.5	8
184	High early death rates, treatment resistance, and short survival ofÂBlack adolescents and young adults with AML. Blood Advances, 2022, 6, 5570-5581.	5.2	8
185	Neoantigen Discovery in Human Cancers. Cancer Journal (Sudbury, Mass), 2017, 23, 97-101.	2.0	7
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