

Elaine R Mardis

List of Publications by Year in descending order

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Version: 2024-02-01

244
papers

107,533
citations

2797

94
h-index

1314

224
g-index

276
all docs

276
docs citations

276
times ranked

115215
citing authors

#	ARTICLE	IF	CITATIONS
1	<sc><i>EGFR</i></sc> internal tandem duplications in fusion-negative congenital and neonatal spindle cell tumors. <i>Genes Chromosomes and Cancer</i> , 2023, 62, 17-26.	1.5	3
2	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. <i>Cancer Discovery</i> , 2022, 12, 154-171.	7.7	34
3	Causal and Candidate Gene Variants in a Large Cohort of Women With Primary Ovarian Insufficiency. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 685-714.	1.8	13
4	Molecular and Pathology Features of Colorectal Tumors and Patient Outcomes Are Associated with <i>Fusobacterium nucleatum</i> and Its Subspecies <i>animalis</i>. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 210-220.	1.1	19
5	Clinical outcomes and efficacy of stereotactic body radiation therapy in children, adolescents, and young adults with metastatic solid tumors. <i>British Journal of Radiology</i> , 2022, 95, 20211088.	1.0	1
6	Immune Activity and Response Differences of Oncolytic Viral Therapy in Recurrent Glioblastoma: Gene Expression Analyses of a Phase IB Study. <i>Clinical Cancer Research</i> , 2022, 28, 498-506.	3.2	12
7	Expanding the Clinical Phenotype of FGFR1 Internal Tandem Duplication. <i>Journal of Physical Education and Sports Management</i> , 2022, , mcs.a006174.	0.5	4
8	LINC00355 regulates p27KIP expression by binding to MENIN to induce proliferation in late-stage relapse breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 49.	2.3	4
9	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.2	3
10	Acute lymphoblastic leukemia displays a distinct highly methylated genome. <i>Nature Cancer</i> , 2022, 3, 768-782.	5.7	15
11	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	5.7	3
12	EPCT-05. Phase Ib study of unesbulin (PTC596) in children with newly diagnosed diffuse intrinsic pontine glioma (DIPG) and high-grade glioma (HGG): A report from the COllaborative Network for NEuro-Oncology Clinical Trials (CONNECT). <i>Neuro-Oncology</i> , 2022, 24, i36-i36.	0.6	0
13	LGG-47. Single-cell RNA Sequencing Reveals Immunosuppressive Myeloid Cell Diversity During Malignant Progression in Glioma. <i>Neuro-Oncology</i> , 2022, 24, i99-i99.	0.6	0
14	Leveraging gene therapy to achieve long-term continuous or controllable expression of biotherapeutics. <i>Science Advances</i> , 2022, 8, .	4.7	7
15	High early death rates, treatment resistance, and short survival of Black adolescents and young adults with AML. <i>Blood Advances</i> , 2022, 6, 5570-5581.	2.5	8
16	Frontiers in cancer immunotherapy—a symposium report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1489, 30-47.	1.8	39
17	Clinical response to dabrafenib plus trametinib in a pediatric ganglioglioma with <i>BRAF</i> p.T599dup mutation. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a006023.	0.5	7
18	Novel morphologic findings in <sc>PLAG1</sc>-rearranged soft tissue tumors. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 577-585.	1.5	9

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19	Molecular classification of a complex structural rearrangement of the RB1 locus in an infant with sporadic, isolated, intracranial, sellar region retinoblastoma. <i>Acta Neuropathologica Communications</i> , 2021, 9, 61.	2.4	5
20	Genomic prediction of neoantigens: immunogenomics before NGS. <i>Nature Reviews Genetics</i> , 2021, 22, 550-551.	7.7	4
21	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	3.7	23
22	Gastroblastoma with a novel <i>EWSR1</i> – <i>CTBP1</i> fusion presenting in adolescence. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 640-646.	1.5	12
23	Endogenous retrovirus envelope as a tumor-associated immunotherapeutic target in murine osteosarcoma. <i>IScience</i> , 2021, 24, 102759.	1.9	1
24	Germline BAP1 Mutation in a Family With Multi-Generational Meningioma With Rhabdoid Features: A Case Series and Literature Review. <i>Frontiers in Oncology</i> , 2021, 11, 721712.	1.3	6
25	Defining the AHR-regulated transcriptome in NK cells reveals gene expression programs relevant to development and function. <i>Blood Advances</i> , 2021, 5, 4605-4618.	2.5	10
26	Eliciting an immune-mediated antitumor response through oncolytic herpes simplex virus-based shared antigen expression in tumors resistant to viroimmunotherapy. , 2021, 9, e002939.		1
27	Somatic variation as an incidental finding in the pediatric next-generation sequencing era. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a006135.	0.5	3
28	Association of 17q22 Amplicon Via Cell-Free DNA With Platinum Chemotherapy Response in Metastatic Triple-Negative Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 1777-1787.	1.5	5
29	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021, 22, 872.	1.2	13
30	Clinically aggressive pediatric spinal ependymoma with novel MYC amplification demonstrates molecular and histopathologic similarity to newly described MYCN-amplified spinal ependymomas. <i>Acta Neuropathologica Communications</i> , 2021, 9, 192.	2.4	5
31	The emergence of cancer genomics in diagnosis and precision medicine. <i>Nature Cancer</i> , 2021, 2, 1263-1264.	5.7	7
32	Envisioning the next human genome reference. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	5
33	Targeted Therapy in a Young Adult With a Novel Epithelioid Tumor Driven by a PRRC2B-ALK Fusion. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2021, 19, 1116-1121.	2.3	2
34	Research-based PAM50 signature and long-term breast cancer survival. <i>Breast Cancer Research and Treatment</i> , 2020, 179, 197-206.	1.1	53
35	A roadmap for the next decade in cancer research. <i>Nature Cancer</i> , 2020, 1, 12-17.	5.7	17
36	Infantile fibrosarcoma-like tumor driven by novel <i>RBPMS-MET</i> fusion consolidated with cabozantinib. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005645.	0.5	17

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37	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , 2020, 11, 3644.	5.8	55
38	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 1238-1245.	1.2	9
39	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020, 11, 2156.	5.8	83
40	Disease-associated mosaic variation in clinical exome sequencing: a two-year pediatric tertiary care experience. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005231.	0.5	15
41	Integrating Genetic and Genomic Testing Into Oncology Practice. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2020, 40, e259-e263.	1.8	6
42	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	4.7	41
43	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. <i>Neurology: Genetics</i> , 2020, 6, e460.	0.9	26
44	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, 913.	5.8	66
45	<i>De novo</i> primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) NFIA/CBFA2T3 translocation. <i>Haematologica</i> , 2020, 105, e194-e197.	1.7	9
46	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. <i>Cancer Immunology Research</i> , 2020, 8, 409-420.	1.6	132
47	An evaluation of MGMT promoter methylation within the methylation subclasses of glioblastoma. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa117.	0.4	1
48	Precision oncogenomics. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004150.	0.5	2
49	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019, 18, 1-10.	1.9	6
50	Immunotherapeutic Challenges for Pediatric Cancers. <i>Molecular Therapy - Oncolytics</i> , 2019, 15, 38-48.	2.0	26
51	Detection of neoantigen-specific T cells following a personalized vaccine in a patient with glioblastoma. <i>Oncolimmunology</i> , 2019, 8, e1561106.	2.1	50
52	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. <i>European Journal of Medical Genetics</i> , 2019, 62, 103701.	0.7	12
53	miRNAs and Long-term Breast Cancer Survival: Evidence from the WHEL Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1525-1533.	1.1	14
54	No evidence that G6PD deficiency affects the efficacy or safety of daunorubicin in acute lymphoblastic leukemia induction therapy. <i>Pediatric Blood and Cancer</i> , 2019, 66, e27681.	0.8	8

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55	Comprehensive gene expression meta-analysis identifies signature genes that distinguish microglia from peripheral monocytes/macrophages in health and glioma. <i>Acta Neuropathologica Communications</i> , 2019, 7, 20.	2.4	124
56	Neoantigens and genome instability: impact on immunogenomic phenotypes and immunotherapy response. <i>Genome Medicine</i> , 2019, 11, 71.	3.6	78
57	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23662-23670.	3.3	40
58	Pediatric cancer: case studies illustrate mechanisms to address significant challenges. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004788.	0.5	0
59	Next-Generation Sequencing Technologies. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a036798.	2.9	143
60	The Impact of Next-Generation Sequencing on Cancer Genomics: From Discovery to Clinic. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a036269.	2.9	43
61	Accounting for proximal variants improves neoantigen prediction. <i>Nature Genetics</i> , 2019, 51, 175-179.	9.4	43
62	Genome sequencing identifies somatic BRAF duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002618.	0.5	7
63	Insights from Large-Scale Cancer Genome Sequencing. <i>Annual Review of Cancer Biology</i> , 2018, 2, 429-444.	2.3	5
64	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2018, 33, 937-948.e8.	7.7	142
65	The era of precision oncogenomics. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002915.	0.5	3
66	Resistance-promoting effects of ependymoma treatment revealed through genomic analysis of multiple recurrences in a single patient. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002444.	0.5	16
67	Clinical and Genomic Insights from Metastatic Cancers. <i>Clinical Chemistry</i> , 2018, 64, 766-768.	1.5	0
68	New additions to the cancer precision medicine toolkit. <i>Genome Medicine</i> , 2018, 10, 28.	3.6	2
69	The emerging clinical relevance of genomics in cancer medicine. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 353-365.	12.5	351
70	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. <i>Nature Genetics</i> , 2018, 50, 1735-1743.	9.4	62
71	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3787.	5.8	112
72	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	5.8	89

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73	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. <i>Clinical Cancer Research</i> , 2018, 24, 5292-5304.	3.2	73
74	A multiple myeloma-specific capture sequencing platform discovers novel translocations and frequent, risk-associated point mutations in IGLL5. <i>Blood Cancer Journal</i> , 2018, 8, 35.	2.8	41
75	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	7.7	106
76	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. <i>Cell Reports</i> , 2018, 24, 2167-2178.	2.9	26
77	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 1371-1383.	3.9	126
78	Advances in Cancer Research and Translational Medicine. <i>Oncology & Hematology Review</i> , 2018, 14, 14.	0.2	0
79	INTEGRATE-neo: a pipeline for personalized gene fusion neoantigen discovery. <i>Bioinformatics</i> , 2017, 33, 555-557.	1.8	105
80	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	9.4	460
81	Temporally Distinct PD-L1 Expression by Tumor and Host Cells Contributes to Immune Escape. <i>Cancer Immunology Research</i> , 2017, 5, 106-117.	1.6	236
82	Applications of Immunogenomics to Cancer. <i>Cell</i> , 2017, 168, 600-612.	13.5	198
83	Neoantigen Discovery in Human Cancers. <i>Cancer Journal (Sudbury, Mass)</i> , 2017, 23, 97-101.	1.0	7
84	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. <i>Bone</i> , 2017, 101, 145-155.	1.4	37
85	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017, 94, 550-568.e10.	3.8	222
86	Breast Cancer Neoantigens Can Induce CD8+ T-Cell Responses and Antitumor Immunity. <i>Cancer Immunology Research</i> , 2017, 5, 516-523.	1.6	74
87	DNA sequencing technologies: 2006â€“2016. <i>Nature Protocols</i> , 2017, 12, 213-218.	5.5	266
88	An mRNA Gene Expressionâ€“Based Signature to Identify FGFR1-Amplified Estrogen Receptorâ€“Positive Breast Tumors. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 147-161.	1.2	11
89	Orthotopic patient-derived xenografts of paediatric solid tumours. <i>Nature</i> , 2017, 549, 96-100.	13.7	223
90	A Phase II Trial of Neoadjuvant MK-2206, an AKT Inhibitor, with Anastrozole in Clinical Stage II or III<i>PIK3CA</i>-Mutant ER-Positive and HER2-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6823-6832.	3.2	66

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91	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.2	9
92	Brief Report: The Role of Rare Protein-Coding Variants in Anti-Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 735-741.	2.9	8
93	Contribution of systemic and somatic factors to clinical response and resistance to PD-L1 blockade in urothelial cancer: An exploratory multi-omic analysis. <i>PLoS Medicine</i> , 2017, 14, e1002309.	3.9	256
94	California Dreamin': the Future of Genomic Medicine. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000976.	0.5	0
95	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. <i>PLoS Medicine</i> , 2016, 13, e1002174.	3.9	86
96	Visualizing tumor evolution with the fishplot package for R. <i>BMC Genomics</i> , 2016, 17, 880.	1.2	131
97	Genomic profiling of murine mammary tumors identifies potential personalized drug targets for p53 deficient mammary cancers. <i>DMM Disease Models and Mechanisms</i> , 2016, 9, 749-57.	1.2	25
98	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2016, 81, 105-111.	2.0	22
99	The challenges of big data. <i>DMM Disease Models and Mechanisms</i> , 2016, 9, 483-485.	1.2	17
100	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	6.5	359
101	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. <i>Blood</i> , 2016, 127, 893-897.	0.6	94
102	Genetic risk factors for the development of osteonecrosis in children under age 10 treated for acute lymphoblastic leukemia. <i>Blood</i> , 2016, 127, 558-564.	0.6	56
103	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016, 13, 806-807.	9.0	96
104	Immunogenomics of Hypermutated Glioblastoma: A Patient with Germline <i>POLE</i> Deficiency Treated with Checkpoint Blockade Immunotherapy. <i>Cancer Discovery</i> , 2016, 6, 1230-1236.	7.7	242
105	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	2.9	21
106	Impact of mutational profiles on response of primary oestrogen receptor-positive breast cancers to oestrogen deprivation. <i>Nature Communications</i> , 2016, 7, 13294.	5.8	34
107	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	9.4	231
108	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016, 7, 12498.	5.8	69

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109	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.2	44
110	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. <i>Genome Medicine</i> , 2016, 8, 11.	3.6	350
111	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016, 131, 833-845.	3.9	288
112	A Phase I Trial of BKM120 (Buparlisib) in Combination with Fulvestrant in Postmenopausal Women with Estrogen Receptor-Positive Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 1583-1591.	3.2	86
113	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	2.9	174
114	From "NoF" to "NoF" more. <i>Journal of Physical Education and Sports Management</i> , 2015, 1, a000521.	0.5	2
115	<i>Caenorhabditis elegans glp-4</i> Encodes a Valyl Aminoacyl tRNA Synthetase. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2719-2728.	0.8	25
116	Tumor neoantigens: building a framework for personalized cancer immunotherapy. <i>Journal of Clinical Investigation</i> , 2015, 125, 3413-3421.	3.9	502
117	Where Next for Genetics and Genomics?. <i>PLoS Biology</i> , 2015, 13, e1002216.	2.6	9
118	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	1.5	83
119	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . <i>PLoS Genetics</i> , 2015, 11, e1005493.	1.5	57
120	Xenografts as Models of Clonal Selection and Acquired Resistance to Therapy. <i>Clinical Chemistry</i> , 2015, 61, 769-770.	1.5	2
121	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015, 373, 2336-2346.	13.9	949
122	The Technology of Analyzing Nucleic Acids in Cancer. , 2015, , 347-356.e1.		0
123	The Genomic Landscape of Childhood and Adolescent Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 816-823.	0.3	148
124	RNA-sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. <i>Glia</i> , 2015, 63, 531-548.	2.5	44
125	Genomic landscape of paediatric adrenocortical tumours. <i>Nature Communications</i> , 2015, 6, 6302.	5.8	166
126	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. <i>Nature Communications</i> , 2015, 6, 7553.	5.8	72

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127	Whole genome analyses reveal no pathogenetic single nucleotide or structural differences between monozygotic twins discordant for amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2015, 16, 385-392.	1.1	27
128	Exome sequencing of case-unaffected-parents trios reveals recessive and de novo genetic variants in sporadic ALS. <i>Scientific Reports</i> , 2015, 5, 9124.	1.6	53
129	<i>Drosophila</i> Muller F Elements Maintain a Distinct Set of Genomic Properties Over 40 Million Years of Evolution. <i>C3: Genes, Genomes, Genetics</i> , 2015, 5, 719-740.	0.8	84
130	A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. <i>Science</i> , 2015, 348, 803-808.	6.0	1,139
131	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. <i>Lancet Oncology</i> , The, 2015, 16, 1659-1666.	5.1	161
132	Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741 (Alliance). <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	52
133	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. <i>BMC Medical Genomics</i> , 2015, 8, 54.	0.7	352
134	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 811.	3.8	302
135	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. <i>Neoplasia</i> , 2015, 17, 776-788.	2.3	75
136	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. <i>Nature</i> , 2015, 518, 552-555.	13.7	685
137	Convergent loss of PTEN leads to clinical resistance to a PI(3)K inhibitor. <i>Nature</i> , 2015, 518, 240-244.	13.7	486
138	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. <i>Blood</i> , 2015, 126, 574-574.	0.6	2
139	Cancer Genomics. <i>F1000Research</i> , 2015, 4, 1162.	0.8	2
140	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. <i>PLoS ONE</i> , 2015, 10, e0122271.	1.1	120
141	A Second Generation, Multiple Myeloma-Specific, Targeted Sequencing Platform for Detecting Translocations, Copy Number Alterations, and Single Nucleotide Variants. <i>Blood</i> , 2015, 126, 4207-4207.	0.6	0
142	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. <i>Blood</i> , 2015, 126, 686-686.	0.6	0
143	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. <i>PLoS ONE</i> , 2014, 9, e87645.	1.1	34
144	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. <i>PLoS Computational Biology</i> , 2014, 10, e1003665.	1.5	400

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145	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. <i>PLoS Genetics</i> , 2014, 10, e1004462.	1.5	115
146	Revolutionizing cancer care with next-generation sequencing: an interview with Elaine Mardis. <i>DMM Disease Models and Mechanisms</i> , 2014, 7, 313-317.	1.2	5
147	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. <i>Nature</i> , 2014, 515, 577-581.	13.7	1,705
148	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2014, 25, 379-392.	7.7	330
149	Ancestry estimation and control of population stratification for sequence-based association studies. <i>Nature Genetics</i> , 2014, 46, 409-415.	9.4	136
150	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. <i>Nature Communications</i> , 2014, 5, 3630.	5.8	342
151	C11orf95-RELA fusions drive oncogenic NF- κ B signalling in ependymoma. <i>Nature</i> , 2014, 506, 451-455.	13.7	559
152	Integrated analysis of germline and somatic variants in ovarian cancer. <i>Nature Communications</i> , 2014, 5, 3156.	5.8	253
153	Clinical Significance of CTNNB1 Mutation and Wnt Pathway Activation in Endometrioid Endometrial Carcinoma. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	182
154	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of <i>STAG2</i> and <i>TP53</i> Mutations. <i>Cancer Discovery</i> , 2014, 4, 1342-1353.	7.7	418
155	Age-related mutations associated with clonal hematopoietic expansion and malignancies. <i>Nature Medicine</i> , 2014, 20, 1472-1478.	15.2	1,533
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