Elaine R Mardis

List of Publications by Year
in descending order

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		3264	1518
244	107,533	94	224
papers	citations	h-index	g-index

276	276	276	126152
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>EGFR</scp> internal tandem duplications in fusionâ€negative congenital and neonatal spindle cell tumors. Genes Chromosomes and Cancer, 2023, 62, 17-26.	1.5	3
2	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. Cancer Discovery, 2022, 12, 154-171.	7.7	34
3	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.	1.8	13
4	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.	1.1	19
5	Clinical outcomes and efficacy of stereotactic body radiation therapy in children, adolescents, and young adults with metastatic solid tumors. British Journal of Radiology, 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. Clinical Cancer Research, 2022, 28, 498-506.	3.2	12
7	Expanding the Clinical Phenotype of FGFR1 Internal Tandem Duplication. Journal of Physical Education and Sports Management, 2022, , mcs.a006174.	0.5	4
8	LINC00355 regulates p27KIP expression by binding to MENIN to induce proliferation in late-stage relapse breast cancer. Npj Breast Cancer, 2022, 8, 49.	2.3	4
9	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.2	3
10	Acute lymphoblastic leukemia displays a distinct highly methylated genome. Nature Cancer, 2022, 3, 768-782.	5.7	15
11	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 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). Neuro-Oncology, 2022, 24, i36-i36.	0.6	0
13	LGG-47. Single-cell RNA Sequencing Reveals Immunosuppressive Myeloid Cell Diversity During Malignant Progression in Glioma. Neuro-Oncology, 2022, 24, i99-i99.	0.6	0
14	Leveraging gene therapy to achieve long-term continuous or controllable expression of biotherapeutics. Science Advances, 2022, 8, .	4.7	7
15	High early death rates, treatment resistance, and short survival ofÂBlack adolescents and young adults with AML. Blood Advances, 2022, 6, 5570-5581.	2.5	8
16	Frontiers in cancer immunotherapyâ€"a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	1.8	39
17	Clinical response to dabrafenib plus trametinib in a pediatric ganglioglioma with BRAF p.T599dup mutation. Journal of Physical Education and Sports Management, 2021, 7, a006023.	0.5	7
18	Novel morphologic findings in <scp>PLAG1â€rearranged</scp> soft tissue tumors. Genes Chromosomes and Cancer, 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. Acta Neuropathologica Communications, 2021, 9, 61.	2.4	5
20	Genomic prediction of neoantigens: immunogenomics before NGS. Nature Reviews Genetics, 2021, 22, 550-551.	7.7	4
21	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. Brain, 2021, 144, 2971-2978.	3.7	23
22	Gastroblastoma with a novel <scp>EWSR1â€CTBP1</scp> fusion presenting in adolescence. Genes Chromosomes and Cancer, 2021, 60, 640-646.	1.5	12
23	Endogenous retrovirus envelope as a tumor-associated immunotherapeutic target in murine osteosarcoma. IScience, 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. Frontiers in Oncology, 2021, 11, 721712.	1.3	6
25	Defining the AHR-regulated transcriptome in NK cells reveals gene expression programs relevant to development and function. Blood Advances, 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. Journal of Physical Education and Sports Management, 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. JCO Precision Oncology, 2021, 5, 1777-1787.	1.5	5
29	Discovery of clinically relevant fusions in pediatric cancer. BMC Genomics, 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. Acta Neuropathologica Communications, 2021, 9, 192.	2.4	5
31	The emergence of cancer genomics in diagnosis and precision medicine. Nature Cancer, 2021, 2, 1263-1264.	5.7	7
32	Envisioning the next human genome reference. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	5
33	Targeted Therapy in a Young Adult With a Novel Epithelioid Tumor Driven by a PRRC2B-ALK Fusion. Journal of the National Comprehensive Cancer Network: JNCCN, 2021, 19, 1116-1121.	2.3	2
34	Research-based PAM50 signature and long-term breast cancer survival. Breast Cancer Research and Treatment, 2020, 179, 197-206.	1.1	53
35	A roadmap for the next decade in cancer research. Nature Cancer, 2020, 1, 12-17.	5.7	17
36	Infantile fibrosarcomaâ€“like tumor driven by novel RBPMS-MET fusion consolidated with cabozantinib. Journal of Physical Education and Sports Management, 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. Nature Communications, 2020, 11, 3644.	5.8	55
38	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. Journal of Molecular Diagnostics, 2020, 22, 1238-1245.	1.2	9
39	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. Nature Communications, 2020, 11, 2156.	5.8	83
40	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.	0.5	15
41	Integrating Genetic and Genomic Testing Into Oncology Practice. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2020, 40, e259-e263.	1.8	6
42	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	4.7	41
43	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. Neurology: Genetics, 2020, 6, e460.	0.9	26
44	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	5.8	66
45	De novo primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) NFIA/CBFA2T3 translocation. Haematologica, 2020, 105, e194-e197.	1.7	9
46	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	1.6	132
47	An evaluation of MGMT promoter methylation within the methylation subclasses of glioblastoma. Neuro-Oncology Advances, 2020, 2, vdaa117.	0.4	1
48	Precision oncogenomics. Journal of Physical Education and Sports Management, 2019, 5, a004150.	0.5	2
49	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. IScience, 2019, 18, 1-10.	1.9	6
50	Immunotherapeutic Challenges for Pediatric Cancers. Molecular Therapy - Oncolytics, 2019, 15, 38-48.	2.0	26
51	Detection of neoantigen-specific T cells following a personalized vaccine in a patient with glioblastoma. OncoImmunology, 2019, 8, e1561106.	2.1	50
52	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. European Journal of Medical Genetics, 2019, 62, 103701.	0.7	12
53	miRNAs and Long-term Breast Cancer Survival: Evidence from the WHEL Study. Cancer Epidemiology Biomarkers and Prevention, 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. Pediatric Blood and Cancer, 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. Acta Neuropathologica Communications, 2019, 7, 20.	2.4	124
56	Neoantigens and genome instability: impact on immunogenomic phenotypes and immunotherapy response. Genome Medicine, 2019, 11, 71.	3.6	78
57	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.	3.3	40
58	Pediatric cancer: case studies illustrate mechanisms to address significant challenges. Journal of Physical Education and Sports Management, 2019, 5, a004788.	0.5	0
59	Next-Generation Sequencing Technologies. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036798.	2.9	143
60	The Impact of Next-Generation Sequencing on Cancer Genomics: From Discovery to Clinic. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a036269.	2.9	43
61	Accounting for proximal variants improves neoantigen prediction. Nature Genetics, 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. Journal of Physical Education and Sports Management, 2018, 4, a002618.	0.5	7
63	Insights from Large-Scale Cancer Genome Sequencing. Annual Review of Cancer Biology, 2018, 2, 429-444.	2.3	5
64	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 33, 937-948.e8.	7.7	142
65	The era of precision oncogenomics. Journal of Physical Education and Sports Management, 2018, 4, a002915.	0.5	3
66	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.	0.5	16
67	Clinical and Genomic Insights from Metastatic Cancers. Clinical Chemistry, 2018, 64, 766-768.	1.5	0
68	New additions to the cancer precision medicine toolkit. Genome Medicine, 2018, 10, 28.	3.6	2
69	The emerging clinical relevance of genomics in cancer medicine. Nature Reviews Clinical Oncology, 2018, 15, 353-365.	12.5	351
70	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	9.4	62
71	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	5.8	112
72	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 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. Clinical Cancer Research, 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. Blood Cancer Journal, 2018, 8, 35.	2.8	41
75	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	7.7	106
76	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. Cell Reports, 2018, 24, 2167-2178.	2.9	26
77	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. Journal of Clinical Investigation, 2018, 128, 1371-1383.	3.9	126
78	Advances in Cancer Research and Translational Medicine. Oncology & Hematology Review, 2018, 14, 14.	0.2	0
79	INTEGRATE-neo: a pipeline for personalized gene fusion neoantigen discovery. Bioinformatics, 2017, 33, 555-557.	1.8	105
80	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	9.4	460
81	Temporally Distinct PD-L1 Expression by Tumor and Host Cells Contributes to Immune Escape. Cancer Immunology Research, 2017, 5, 106-117.	1.6	236
82	Applications of Immunogenomics to Cancer. Cell, 2017, 168, 600-612.	13.5	198
83	Neoantigen Discovery in Human Cancers. Cancer Journal (Sudbury, Mass), 2017, 23, 97-101.	1.0	7
84	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. Bone, 2017, 101, 145-155.	1.4	37
85	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	3.8	222
86	Breast Cancer Neoantigens Can Induce CD8+ T-Cell Responses and Antitumor Immunity. Cancer Immunology Research, 2017, 5, 516-523.	1.6	74
87	DNA sequencing technologies: 2006â€“2016. Nature Protocols, 2017, 12, 213-218.	5.5	266
88	An mRNA Gene Expressionâ€“Based Signature to Identify FGFR1-Amplified Estrogen Receptorâ€“Positive Breast Tumors. Journal of Molecular Diagnostics, 2017, 19, 147-161.	1.2	11
89	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 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 IIIPIK3CA-Mutant ER-Positive and HER2-Negative Breast Cancer. Clinical Cancer Research, 2017, 23, 6823-6832.	3.2	66

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91	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.2	9
92	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.	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. PLoS Medicine, 2017, 14, e1002309.	3.9	256
94	California Dreamin': the Future of Genomic Medicine. Journal of Physical Education and Sports Management, 2016, 2, a000976.	0.5	0
95	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. PLoS Medicine, 2016, 13, e1002174.	3.9	86
96	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	1.2	131
97	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.	1.2	25
98	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 105-111.	2.0	22
99	The challenges of big data. DMM Disease Models and Mechanisms, 2016, 9, 483-485.	1.2	17
100	DGIdb 2.0: mining clinically relevant drugâ€“gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	6.5	359
101	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. Blood, 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. Blood, 2016, 127, 558-564.	0.6	56
103	DoCM: a database of curated mutations in cancer. Nature Methods, 2016, 13, 806-807.	9.0	96
104	Immunogenomics of Hypermutated Glioblastoma: A Patient with Germline POLE Deficiency Treated with Checkpoint Blockade Immunotherapy. Cancer Discovery, 2016, 6, 1230-1236.	7.7	242
105	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.	2.9	21
106	Impact of mutational profiles on response of primary oestrogen receptor-positive breast cancers to oestrogen deprivation. Nature Communications, 2016, 7, 13294.	5.8	34
107	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	9.4	231
108	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 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. Experimental Hematology, 2016, 44, 603-613.	0.2	44
110	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. Genome Medicine, 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. Acta Neuropathologica, 2016, 131, 833-845.	3.9	288
112	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.	3.2	86
113	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	2.9	174
114	From â€œNof 1â€•toNof more. Journal of Physical Education and Sports Management, 2015, 1, a000521.	0.5	2
115	Caenorhabditis elegans glp-4Encodes a Valyl Aminoacyl tRNA Synthetase. G3: Genes, Genomes, Genetics, 2015, 5, 2719-2728.	0.8	25
116	Tumor neoantigens: building a framework for personalized cancer immunotherapy. Journal of Clinical Investigation, 2015, 125, 3413-3421.	3.9	502
117	Where Next for Genetics and Genomics?. PLoS Biology, 2015, 13, e1002216.	2.6	9
118	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
119	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	1.5	57
120	Xenografts as Models of Clonal Selection and Acquired Resistance to Therapy. Clinical Chemistry, 2015, 61, 769-770.	1.5	2
121	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 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. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.3	148
124	RNAâ€sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	2.5	44
125	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	5.8	166
126	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. Nature Communications, 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. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 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. Scientific Reports, 2015, 5, 9124.	1.6	53
129	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.	0.8	84
130	A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. Science, 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. Lancet Oncology, The, 2015, 16, 1659-1666.	5.1	161
132	Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741 (Alliance). Journal of the National Cancer Institute, 2015, 107, .	3.0	52
133	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. BMC Medical Genomics, 2015, 8, 54.	0.7	352
134	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 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. Neoplasia, 2015, 17, 776-788.	2.3	75
136	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	13.7	685
137	Convergent loss of PTEN leads to clinical resistance to a PI(3)KÎ± inhibitor. Nature, 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. Blood, 2015, 126, 574-574.	0.6	2
139	Cancer Genomics. F1000Research, 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. PLoS ONE, 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. Blood, 2015, 126, 4207-4207.	0.6	0
142	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. Blood, 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. PLoS ONE, 2014, 9, e87645.	1.1	34
144	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	1.5	400

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145	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	1.5	115
146	Revolutionizing cancer care with next-generation sequencing: an interview with Elaine Mardis. DMM Disease Models and Mechanisms, 2014, 7, 313-317.	1.2	5
147	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. Nature, 2014, 515, 577-581.	13.7	1,705
148	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	7.7	330
149	Ancestry estimation and control of population stratification for sequence-based association studies. Nature Genetics, 2014, 46, 409-415.	9.4	136
150	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
151	C11orf95â€“RELA fusions drive oncogenic NF-ÎºB signalling in ependymoma. Nature, 2014, 506, 451-455.	13.7	559
152	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
153	Clinical Significance of CTNNB1 Mutation and Wnt Pathway Activation in Endometrioid Endometrial Carcinoma. Journal of the National Cancer Institute, 2014, 106, .	3.0	182
154	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	7.7	418
155	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	15.2	1,533
156	The translation of cancer genomics: time for a revolution in clinical cancer care. Genome Medicine, 2014, 6, 22.	3.6	13
157	Sequencing the AML Genome, Transcriptome, and Epigenome. Seminars in Hematology, 2014, 51, 250-258.	1.8	13
158	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	13.9	1,161
159	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.	3.2	84
160	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	2.9	583
161	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	1.2	40
162	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. Blood, 2014, 124, 3887-3895.	0.6	20

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163	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	9.0	443
164	The Next-Generation Sequencing Revolution and Its Impact on Genomics. Cell, 2013, 155, 27-38.	13.5	856
165	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. Cancer Discovery, 2013, 3, 224-237.	7.7	697
166	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	2.9	539
167	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	7.7	252
168	Next-Generation Sequencing Platforms. Annual Review of Analytical Chemistry, 2013, 6, 287-303.	2.8	519
169	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	9.4	704
170	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
171	Whole-Genome Sequencing. , 2013, , 87-93.		2
172	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	9.4	588
173	Abstract IA04: Genomic studies of breast cancer progression. , 2013, , .		0
174	A 50-Gene Intrinsic Subtype Classifier for Prognosis and Prediction of Benefit from Adjuvant Tamoxifen. Clinical Cancer Research, 2012, 18, 4465-4472.	3.2	258
175	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	1.8	566
176	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	2.4	586
177	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	13.7	922
178	Applying next-generation sequencing to pancreatic cancer treatment. Nature Reviews Gastroenterology and Hepatology, 2012, 9, 477-486.	8.2	41
179	Genome sequencing and cancer. Current Opinion in Genetics and Development, 2012, 22, 245-250.	1.5	62
180	The Pediatric Cancer Genome Project. Nature Genetics, 2012, 44, 619-622.	9.4	315

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