Li Ding

List of Publications by Year
in descending order

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187	86,383	3334 91	4645 170
papers	citations	h-index	g-index

201	201	201	93511
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	16.8	6,138
2	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
3	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	5.5	4,086
4	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
5	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
6	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
7	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	27.8	2,694
8	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
9	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
10	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
11	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
12	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
13	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
14	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
15	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	30.7	1,533
16	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
17	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
18	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	27.8	1,384

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19	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
20	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	19.0	1,322
21	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
22	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
23	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	4.1	1,193
24	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	27.0	1,161
25	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
26	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
27	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
28	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	21.4	830
29	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
30	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
31	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
32	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
33	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. Cancer Discovery, 2013, 3, 224-237.	9.4	697
34	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
35	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
36	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636

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37	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. Cell, 2019, 179, 561-577.e22.	28.9	629
38	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
39	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
40	MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. Bioinformatics, 2014, 30, 1015-1016.	4.1	599
41	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
42	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	5.5	586
43	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
44	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
45	C11orf95â€“RELA fusions drive oncogenic NF-ÎºB signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
46	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
47	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
48	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	28.9	498
49	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
50	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
51	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
52	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
53	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	3.3	437
54	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430

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55	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
56	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	28.9	410
57	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
58	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
59	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
60	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
61	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
62	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
63	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	16.8	327
64	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296
65	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
66	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	28.9	273
67	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
68	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
69	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252
70	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
71	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	28.9	236
72	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231

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73	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
74	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
75	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	16.8	213
76	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	189
77	Clinical Significance of CTNNB1 Mutation and Wnt Pathway Activation in Endometrioid Endometrial Carcinoma. Journal of the National Cancer Institute, 2014, 106, .	6.3	182
78	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
79	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	28.9	177
80	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
81	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	28.9	170
82	Expanding the computational toolbox for mining cancer genomes. Nature Reviews Genetics, 2014, 15, 556-570.	16.3	166
83	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	19.0	161
84	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
85	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
86	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	2.8	131
87	Protein-structure-guided discovery of functional mutations across 19 cancer types. Nature Genetics, 2016, 48, 827-837.	21.4	128
88	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	16.8	120
89	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. Nature Genetics, 2021, 53, 86-99.	21.4	118
90	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	3.5	115

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91	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. Nature Communications, 2017, 8, 14864.	12.8	112
92	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. Molecular and Cellular Proteomics, 2016, 15, 1060-1071.	3.8	104
93	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
94	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	30.7	93
95	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
96	Oncolytic Adenovirus Complexes Coated with Lipids and Calcium Phosphate for Cancer Gene Therapy. ACS Nano, 2016, 10, 11548-11560.	14.6	88
97	PathScan: a tool for discerning mutational significance in groups of putative cancer genes. Bioinformatics, 2011, 27, 1595-1602.	4.1	87
98	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
99	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	5.5	81
100	Cancer proteogenomics: current impact and future prospects. Nature Reviews Cancer, 2022, 22, 298-313.	28.4	79
101	Advances for studying clonal evolution in cancer. Cancer Letters, 2013, 340, 212-219.	7.2	76
102	Local delivery of arsenic trioxide nanoparticles for hepatocellular carcinoma treatment. Signal Transduction and Targeted Therapy, 2019, 4, 28.	17.1	75
103	Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS ONE, 2014, 9, e111153.	2.5	69
104	Co-evolution of tumor and immune cells during progression of multiple myeloma. Nature Communications, 2021, 12, 2559.	12.8	68
105	Gold-caged copolymer nanoparticles as multimodal synergistic photodynamic/photothermal/chemotherapy platform against lethality androgen-resistant prostate cancer. Biomaterials, 2019, 212, 73-86.	11.4	66
106	Thermoresponsive nanocomposite gel for local drug delivery to suppress the growth of glioma by inducing autophagy. Autophagy, 2017, 13, 1176-1190.	9.1	63
107	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294.	3.3	60
108	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. Nature Communications, 2021, 12, 5086.	12.8	58

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109	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	3.5	57
110	A cellular complex of BACE1 and Î³-secretase sequentially generates AÎ² from its full-length precursor. Journal of Cell Biology, 2019, 218, 644-663.	5.2	57
111	Mass Spectrometryâ€“Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. Cancer Research, 2018, 78, 2732-2746.	0.9	52
112	Multifunctional Shellâ€“Core Nanoparticles for Treatment of Multidrug Resistance Hepatocellular Carcinoma. Advanced Functional Materials, 2018, 28, 1706124.	14.9	51
113	Temperature-Sensitive Gold Nanoparticle-Coated Pluronic-PLL Nanoparticles for Drug Delivery and Chemo-Photothermal Therapy. Theranostics, 2017, 7, 4424-4444.	10.0	46
114	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. Cell Reports Medicine, 2020, 1, 100004.	6.5	46
115	Moving pan-cancer studies from basic research toward the clinic. Nature Cancer, 2021, 2, 879-890.	13.2	40
116	CharGer: clinical Characterization of Germline variants. Bioinformatics, 2019, 35, 865-867.	4.1	39
117	Urine tumor DNA detection of minimal residual disease in muscle-invasive bladder cancer treated with curative-intent radical cystectomy: A cohort study. PLoS Medicine, 2021, 18, e1003732.	8.4	38
118	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. Journal of Clinical Oncology, 2021, 39, 3747-3758.	1.6	38
119	Tumor-on-a-chip platform to interrogate the role of macrophages in tumor progression. Integrative Biology (United Kingdom), 2020, 12, 221-232.	1.3	37
120	LINE-1 expression in cancer correlates with p53 mutation, copy number alteration, and S phase checkpoint. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	36
121	Ancestry-specific predisposing germline variants in cancer. Genome Medicine, 2020, 12, 51.	8.2	35
122	Cell-free DNA ultra-low-pass whole genome sequencing to distinguish malignant peripheral nerve sheath tumor (MPNST) from its benign precursor lesion: A cross-sectional study. PLoS Medicine, 2021, 18, e1003734.	8.4	35
123	Dynamic host immune response in virus-associated cancers. Communications Biology, 2019, 2, 109.	4.4	34
124	Evolution and structure of clinically relevant gene fusions in multiple myeloma. Nature Communications, 2020, 11, 2666.	12.8	31
125	Isotope tracing in adult zebrafish reveals alanine cycling between melanoma and liver. Cell Metabolism, 2021, 33, 1493-1504.e5.	16.2	29
126	Database of evidence for precision oncology portal. Bioinformatics, 2018, 34, 4315-4317.	4.1	28

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127	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
128	Discovery of driver non-coding splice-site-creating mutations in cancer. Nature Communications, 2020, 11, 5573.	12.8	26
129	Functional analysis of BARD1 missense variants in homology-directed repair and damage sensitivity. PLoS Genetics, 2019, 15, e1008049.	3.5	23
130	Chromosome 8 gain is associated with high-grade transformation in MPNST. JCI Insight, 2021, 6, .	5.0	23
131	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
132	Single-cell manifold-preserving feature selection for detecting rare cell populations. Nature Computational Science, 2021, 1, 374-384.	8.0	20
133	EAnnot: A genome annotation tool using experimental evidence. Genome Research, 2004, 14, 2503-2509.	5.5	18
134	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. Leukemia, 2018, 32, 1874-1878.	7.2	18
135	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	2.5	18
136	Integrative omics analyses broaden treatment targets in human cancer. Genome Medicine, 2018, 10, 60.	8.2	17
137	Multiple BACE1 inhibitors abnormally increase the BACE1 protein level in neurons by prolonging its halfâ€life. Alzheimer's and Dementia, 2019, 15, 1183-1194.	0.8	17
138	MSIsensor-ct: microsatellite instability detection using cfDNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	6.5	17
139	MIRMMR: binary classification of microsatellite instability using methylation and mutations. Bioinformatics, 2017, 33, 3799-3801.	4.1	16
140	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	5.5	15
141	The clear cell sarcoma functional genomic landscape. Journal of Clinical Investigation, 2021, 131, .	8.2	15
142	CS1 CAR-T targeting the distal domain of CS1 (SLAMF7) shows efficacy in high tumor burden myeloma model despite fratricide of CD8+CS1 expressing CAR-T cells. Leukemia, 2022, 36, 1625-1634.	7.2	15
143	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. Molecular and Cellular Proteomics, 2019, 18, 1630-1650.	3.8	14
144	Clinical characteristics associated with the properties of gut microbiota in peritoneal dialysis patients. Peritoneal Dialysis International, 2021, 41, 298-306.	2.3	14

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145	frDriver: A Functional Region Driver Identification for Protein Sequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1773-1783.	3.0	13
146	Abstract 5359: Regulatory germline variants in 10,389 adult cancers. Cancer Research, 2018, 78, 5359-5359.	0.9	13
147	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, 2313.	12.8	12
148	Temperature sensitive hydrogel for preoperative treatment of renal carcinoma. Materials Science and Engineering C, 2020, 111, 110798.	7.3	11
149	Precision Embolism: Biocompatible Temperatureâ€Sensitive Hydrogels as Novel Embolic Materials for Both Mainstream and Peripheral Vessels. Advanced Functional Materials, 2021, 31, 2011170.	14.9	10
150	Possible role of IL-6 and TIE2 gene polymorphisms in predicting the initial high transport status in patients with peritoneal dialysis: an observational study. BMJ Open, 2016, 6, e012967.	1.9	9
151	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
152	Proteomic Resistance Biomarkers for PI3K Inhibitor in Triple Negative Breast Cancer Patient-Derived Xenograft Models. Cancers, 2020, 12, 3857.	3.7	8
153	Precise Targeting Therapy of Orthotopic Gastric Carcinoma by siRNA and Chemotherapeutic Drug Codelivered in pHâ€Sensitive Nano Platform. Advanced Healthcare Materials, 2021, 10, e2100966.	7.6	8
154	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	19.0	7
155	Transcriptome Sequence Analysis of Pediatric Acute Megakaryoblastic Leukemia Identifies An Inv(16)(p13.3;q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein As a Recurrent Lesion in 39% of Non-Infant Cases: A Report From the St. Jude Children's Research Hospital â€“ Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 757-757.	1.4	7
156	PDXNet portal: patient-derived Xenograft model, data, workflow and tool discovery. NAR Cancer, 2022, 4, zcac014.	3.1	7
157	Genomic and neoantigen evolution from primary tumor to first metastases in head and neck squamous cell carcinoma. Oncotarget, 2021, 12, 534-548.	1.8	6
158	LINC00355 regulates p27KIP expression by binding to MENIN to induce proliferation in late-stage relapse breast cancer. Npj Breast Cancer, 2022, 8, 49.	5.2	4
159	Differences that matter in cancer genomics. Nature Biotechnology, 2013, 31, 892-893.	17.5	3
160	Genomic Determinants of Homologous Recombination Deficiency across Human Cancers. Cancers, 2021, 13, 4572.	3.7	3
161	RNA Splicing and Immune-Checkpoint Inhibition. New England Journal of Medicine, 2021, 385, 1807-1809.	27.0	3
162	Integrated Cytof, Scrna-Seq and Cite-Seq Analysis of Bone Marrow Immune Microenvironment in the Mmrf Commpass Study. Blood, 2020, 136, 28-29.	1.4	2

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163	KIF11 as a potential cancer prognostic marker promotes tumorigenesis in children with Wilms tumor. Pediatric Hematology and Oncology, 2021, , 1-13.	0.8	1
164	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. Blood, 2019, 134, 5531-5531.	1.4	1
165	Complete Sequencing and Comparison of 12 Normal Karyotype M1 AML Genomes with 12 t(15;17) Positive M3-APL Genomes. Blood, 2011, 118, 404-404.	1.4	1
166	Whole genome sequencing to characterize luminal-type breast cancer.. Journal of Clinical Oncology, 2012, 30, 503-503.	1.6	1
167	Characterization of T-Cell Exhaustion in Rapid Progressing Multiple Myeloma Using Cross Center Scrna-Seq Study. Blood, 2021, 138, 401-401.	1.4	1
168	Thread 1: Mutational drivers. Nature Genetics, 2013, , .	21.4	0
169	GENE-19. DEEP PROTEOMIC SURVEY ACROSS SEVEN CHILDHOOD BRAIN TUMORS. Neuro-Oncology, 2019, 21, ii85-ii85.	1.2	0
170	Tracking minimal residual disease with urine tumor DNA in muscle-invasive bladder cancer after neoadjuvant chemotherapy.. Journal of Clinical Oncology, 2021, 39, e16514-e16514.	1.6	0
171	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	1.4	0
172	DNA Sequence of the Cancer Genome of a Patient with Therapy-Related Acute Myeloid Leukemia. Blood, 2010, 116, 580-580.	1.4	0
173	Resolution of a Clinical Dilemma with Whole Genome Sequencing, and Discovery of a New Mechanism for Generating PML-Rara: Insertional Fusion. Blood, 2010, 116, 2755-2755.	1.4	0
174	Use of whole genome sequencing to identify novel mutations in distinct subgroups of medulloblastoma.. Journal of Clinical Oncology, 2012, 30, 9518-9518.	1.6	0
175	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	1.4	0
176	Uncovering Clonal and Subclonal Druggable Targets in Multiple Myeloma Using Omic Data. Blood, 2016, 128, 2084-2084.	1.4	0
177	Characterization of Germline Variants in Multiple Myeloma. Blood, 2018, 132, 4499-4499.	1.4	0
178	Single-Cell Pathway Enrichment and Regulatory Profiling of Multiple Myeloma across Disease Stages. Blood, 2019, 134, 364-364.	1.4	0
179	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 172-183.	0.7	0
180	Understand the difference between clinical measured ultrafiltrationand real ultrafiltration in peritoneal dialysis. BMC Nephrology, 2021, 22, 382.	1.8	0

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181	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0
182	Single-Cell RNA-Seq Analysis of CD138-Depleted Bone Marrow Samples Reveals Genetic Alterations and Disease Progression Correlate with Tumor and Bone Marrow Immune Microenvironment in the Mmrf Commpass Study. Blood, 2021, 138, 2691-2691.	1.4	0
183	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. , 2020, , .		0
184	Myeloma Cell Associated Therapeutic Protein Discovery Using Single Cell RNA-Seq Data. Blood, 2020, 136, 4-5.	1.4	0
185	Identification and Validation of CD138- Multiple Myeloma Immune and Tumor Subpopulations Using Cross Center Scrna-Seq Data. Blood, 2020, 136, 15-15.	1.4	0
186	Characterization of Plasma and Immune Cells Molecular Landscape That Play a Role in Rapid Progression of Multiple Myeloma Using Cross Center Scrna-Seq Study. Blood, 2020, 136, 6-8.	1.4	0
187	Pollock: Fishing for Cell States. Bioinformatics Advances, 0, , .	2.4	0