Li Ding

List of Publications by Year
in descending order

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187 papers	86,383 citations	3874 91 h-index	5347 170 g-index
201 all docs	201 docs citations	201 times ranked	101334 citing authors

#	Article	IF	Citations
1	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	7.7	120
2	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, .	3.3	36
3	Cancer proteogenomics: current impact and future prospects. Nature Reviews Cancer, 2022, 22, 298-313.	12.8	79
4	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.	3.3	15
5	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
6	PDXNet portal: patient-derived Xenograft model, data, workflow and tool discovery. NAR Cancer, 2022, 4, zcac014.	1.6	7
7	frDriver: A Functional Region Driver Identification for Protein Sequence. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1773-1783.	1.9	13
8	Clinical characteristics associated with the properties of gut microbiota in peritoneal dialysis patients. Peritoneal Dialysis International, 2021, 41, 298-306.	1.1	14
9	MSIsensor-ct: microsatellite instability detection using cfDNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	17
10	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. Nature Genetics, 2021, 53, 86-99.	9.4	118
11	Precision Embolism: Biocompatible Temperatureâ€Sensitive Hydrogels as Novel Embolic Materials for Both Mainstream and Peripheral Vessels. Advanced Functional Materials, 2021, 31, 2011170.	7.8	10
12	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	7.7	189
13	Genomic and neoantigen evolution from primary tumor to first metastases in head and neck squamous cell carcinoma. Oncotarget, 2021, 12, 534-548.	0.8	6
14	Chromosome 8 gain is associated with high-grade transformation in MPNST. JCI Insight, 2021, 6, .	2.3	23
15	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	7.7	327
16	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, 2313.	5.8	12
17	Co-evolution of tumor and immune cells during progression of multiple myeloma. Nature Communications, 2021, 12, 2559.	5.8	68
18	Single-cell manifold-preserving feature selection for detecting rare cell populations. Nature Computational Science, 2021, 1, 374-384.	3.8	20

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19	Tracking minimal residual disease with urine tumor DNA in muscle-invasive bladder cancer after neoadjuvant chemotherapy.. Journal of Clinical Oncology, 2021, 39, e16514-e16514.	0.8	0
20	Isotope tracing in adult zebrafish reveals alanine cycling between melanoma and liver. Cell Metabolism, 2021, 33, 1493-1504.e5.	7.2	29
21	The clear cell sarcoma functional genomic landscape. Journal of Clinical Investigation, 2021, 131, .	3.9	15
22	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.	3.9	38
23	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
24	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.	3.9	35
25	Precise Targeting Therapy of Orthotopic Gastric Carcinoma by siRNA and Chemotherapeutic Drug Codelivered in pHâ€Sensitive Nano Platform. Advanced Healthcare Materials, 2021, 10, e2100966.	3.9	8
26	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. Nature Communications, 2021, 12, 5086.	5.8	58
27	KIF11 as a potential cancer prognostic marker promotes tumorigenesis in children with Wilms tumor. Pediatric Hematology and Oncology, 2021, , 1-13.	0.3	1
28	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
29	Genomic Determinants of Homologous Recombination Deficiency across Human Cancers. Cancers, 2021, 13, 4572.	1.7	3
30	Moving pan-cancer studies from basic research toward the clinic. Nature Cancer, 2021, 2, 879-890.	5.7	40
31	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. Journal of Clinical Oncology, 2021, 39, 3747-3758.	0.8	38
32	RNA Splicing and Immune-Checkpoint Inhibition. New England Journal of Medicine, 2021, 385, 1807-1809.	13.9	3
33	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
34	Understand the difference between clinical measured ultrafiltrationand real ultrafiltration in peritoneal dialysis. BMC Nephrology, 2021, 22, 382.	0.8	0
35	Characterization of T-Cell Exhaustion in Rapid Progressing Multiple Myeloma Using Cross Center Scrna-Seq Study. Blood, 2021, 138, 401-401.	0.6	1
36	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0

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37	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.	0.6	0
38	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
39	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
40	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
41	Tumor-on-a-chip platform to interrogate the role of macrophages in tumor progression. Integrative Biology (United Kingdom), 2020, 12, 221-232.	0.6	37
42	Proteomic Resistance Biomarkers for PI3K Inhibitor in Triple Negative Breast Cancer Patient-Derived Xenograft Models. Cancers, 2020, 12, 3857.	1.7	8
43	Discovery of driver non-coding splice-site-creating mutations in cancer. Nature Communications, 2020, 11, 5573.	5.8	26
44	Ancestry-specific predisposing germline variants in cancer. Genome Medicine, 2020, 12, 51.	3.6	35
45	Evolution and structure of clinically relevant gene fusions in multiple myeloma. Nature Communications, 2020, 11, 2666.	5.8	31
46	Temperature sensitive hydrogel for preoperative treatment of renal carcinoma. Materials Science and Engineering C, 2020, 111, 110798.	3.8	11
47	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
48	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
49	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
50	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. Cell Reports Medicine, 2020, 1, 100004.	3.3	46
51	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	7.7	151
52	Integrated Cytof, Scrna-Seq and Cite-Seq Analysis of Bone Marrow Immune Microenvironment in the Mmrf Commpass Study. Blood, 2020, 136, 28-29.	0.6	2
53	AeQTL: eQTL analysis using region-based aggregation of rare genomic variants. , 2020, , .		0
54	Myeloma Cell Associated Therapeutic Protein Discovery Using Single Cell RNA-Seq Data. Blood, 2020, 136, 4-5.	0.6	0

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55	Identification and Validation of CD138- Multiple Myeloma Immune and Tumor Subpopulations Using Cross Center Scrna-Seq Data. Blood, 2020, 136, 15-15.	0.6	0
56	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.	0.6	0
57	CharGer: clinical Characterization of Germline variants. Bioinformatics, 2019, 35, 865-867.	1.8	39
58	Multiple BACE1 inhibitors abnormally increase the BACE1 protein level in neurons by prolonging its halfâ€life. Alzheimer's and Dementia, 2019, 15, 1183-1194.	0.4	17
59	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	2.9	103
60	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
61	Local delivery of arsenic trioxide nanoparticles for hepatocellular carcinoma treatment. Signal Transduction and Targeted Therapy, 2019, 4, 28.	7.1	75
62	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. Cell, 2019, 179, 561-577.e22.	13.5	629
63	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. Molecular and Cellular Proteomics, 2019, 18, 1630-1650.	2.5	14
64	Gold-caged copolymer nanoparticles as multimodal synergistic photodynamic/photothermal/chemotherapy platform against lethality androgen-resistant prostate cancer. Biomaterials, 2019, 212, 73-86.	5.7	66
65	GENE-19. DEEP PROTEOMIC SURVEY ACROSS SEVEN CHILDHOOD BRAIN TUMORS. Neuro-Oncology, 2019, 21, ii85-ii85.	0.6	0
66	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	13.5	498
67	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
68	Dynamic host immune response in virus-associated cancers. Communications Biology, 2019, 2, 109.	2.0	34
69	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	9.0	7
70	Functional analysis of BARD1 missense variants in homology-directed repair and damage sensitivity. PLoS Genetics, 2019, 15, e1008049.	1.5	23
71	A cellular complex of BACE1 and Î³-secretase sequentially generates AÎ² from its full-length precursor. Journal of Cell Biology, 2019, 218, 644-663.	2.3	57
72	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	1.1	18

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73	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. Blood, 2019, 134, 5531-5531.	0.6	1
74	Single-Cell Pathway Enrichment and Regulatory Profiling of Multiple Myeloma across Disease Stages. Blood, 2019, 134, 364-364.	0.6	0
75	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.	0.4	52
76	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
77	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
78	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
79	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
80	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
81	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
82	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
83	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
84	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
85	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
86	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
87	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
88	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
89	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
90	Multifunctional Shellâ€"Core Nanoparticles for Treatment of Multidrug Resistance Hepatocellular Carcinoma. Advanced Functional Materials, 2018, 28, 1706124.	7.8	51

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91	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
92	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
93	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
94	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
95	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	7.7	213
96	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
97	Discriminating a common somatic ASXL1 mutation (c.1934dup; p.G646Wfs*12) from artifact in myeloid malignancies using NGS. Leukemia, 2018, 32, 1874-1878.	3.3	18
98	Database of evidence for precision oncology portal. Bioinformatics, 2018, 34, 4315-4317.	1.8	28
99	Integrative omics analyses broaden treatment targets in human cancer. Genome Medicine, 2018, 10, 60.	3.6	17
100	Abstract 5359: Regulatory germline variants in 10,389 adult cancers. Cancer Research, 2018, 78, 5359-5359.	0.4	13
101	Characterization of Germline Variants in Multiple Myeloma. Blood, 2018, 132, 4499-4499.	0.6	0
102	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	2.4	15
103	Thermoresponsive nanocomposite gel for local drug delivery to suppress the growth of glioma by inducing autophagy. Autophagy, 2017, 13, 1176-1190.	4.3	63
104	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. Nature Communications, 2017, 8, 14864.	5.8	112
105	MIRMMR: binary classification of microsatellite instability using methylation and mutations. Bioinformatics, 2017, 33, 3799-3801.	1.8	16
106	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
107	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	9.0	93
108	Temperature-Sensitive Gold Nanoparticle-Coated Pluronic-PLL Nanoparticles for Drug Delivery and Chemo-Photothermal Therapy. Theranostics, 2017, 7, 4424-4444.	4.6	46

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109	Visualizing tumor evolution with the fishplot package for R. BMC Genomics, 2016, 17, 880.	1.2	131
110	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.	0.8	9
111	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294.	1.6	60
112	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	13.7	1,384
113	Oncolytic Adenovirus Complexes Coated with Lipids and Calcium Phosphate for Cancer Gene Therapy. ACS Nano, 2016, 10, 11548-11560.	7.3	88
114	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	9.4	231
115	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	9.4	215
116	Protein-structure-guided discovery of functional mutations across 19 cancer types. Nature Genetics, 2016, 48, 827-837.	9.4	128
117	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
118	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	15.2	93
119	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.	2.5	104
120	Uncovering Clonal and Subclonal Druggable Targets in Multiple Myeloma Using Omic Data. Blood, 2016, 128, 2084-2084.	0.6	0
121	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	2.9	174
122	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
123	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	1.5	57
124	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	13.9	949
125	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	5.8	243
126	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.3	148

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127	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
128	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
129	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	13.7	685
130	Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS ONE, 2014, 9, e111153.	1.1	69
131	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	1.5	400
132	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	1.5	115
133	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	2.4	81
134	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	5.8	342
135	C11orf95â€“RELA fusions drive oncogenic NF-ÎºB signalling in ependymoma. Nature, 2014, 506, 451-455.	13.7	559
136	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
137	MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. Bioinformatics, 2014, 30, 1015-1016.	1.8	599
138	Clinical Significance of CTNNB1 Mutation and Wnt Pathway Activation in Endometrioid Endometrial Carcinoma. Journal of the National Cancer Institute, 2014, 106, .	3.0	182
139	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
140	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	15.2	1,533
141	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
142	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	13.9	1,161
143	Expanding the computational toolbox for mining cancer genomes. Nature Reviews Genetics, 2014, 15, 556-570.	7.7	166
144	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	2.9	583

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145	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
146	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
147	Differences that matter in cancer genomics. Nature Biotechnology, 2013, 31, 892-893.	9.4	3
148	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	9.0	443
149	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
150	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	13.7	3,695
151	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. Cancer Discovery, 2013, 3, 224-237.	7.7	697
152	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	2.9	539
153	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	7.7	252
154	Advances for studying clonal evolution in cancer. Cancer Letters, 2013, 340, 212-219.	3.2	76
155	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
156	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
157	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	1.6	437
158	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	9.4	588
159	Thread 1: Mutational drivers. Nature Genetics, 2013, , .	9.4	0
160	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	1.8	566
161	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	2.4	586
162	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	13.5	1,038

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163	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	13.7	1,430
164	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	13.7	1,795
165	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	13.7	442
166	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	2.4	4,086
167	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	13.5	1,365
168	Whole genome sequencing to characterize luminal-type breast cancer.. Journal of Clinical Oncology, 2012, 30, 503-503.	0.8	1
169	Use of whole genome sequencing to identify novel mutations in distinct subgroups of medulloblastoma.. Journal of Clinical Oncology, 2012, 30, 9518-9518.	0.8	0
170	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	0.6	0
171	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	9.0	451
172	PathScan: a tool for discerning mutational significance in groups of putative cancer genes. Bioinformatics, 2011, 27, 1595-1602.	1.8	87
173	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.	0.6	1
174	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.	0.6	7
175	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	7.7	6,138
176	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	13.7	1,077
177	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	13.9	1,777
178	DNA Sequence of the Cancer Genome of a Patient with Therapy-Related Acute Myeloid Leukemia. Blood, 2010, 116, 580-580.	0.6	0
179	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.	0.6	9
180	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.	0.6	0

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181	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	1.8	1,193
182	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	9.0	1,322
183	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	0.6	0
184	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
185	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	13.7	1,275
186	EAnnot: A genome annotation tool using experimental evidence. Genome Research, 2004, 14, 2503-2509.	2.4	18
187	Pollock: Fishing for Cell States. Bioinformatics Advances, 0, , .	0.9	0