Marco A Marra

List of Publications by Year
in descending order

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513	222,497	97	21
papers	citations	166 h-index	447 g-index

533	533	533	191014
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
3	Circos: An information aesthetic for comparative genomics. Genome Research, 2009, 19, 1639-1645.	5.5	9,003
4	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
5	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
6	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
7	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
8	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
9	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
10	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
11	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
12	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
13	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
14	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
15	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
16	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
17	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
18	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496

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19	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
20	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
21	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
22	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
23	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
24	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
25	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
26	The Genome Sequence of the SARS-Associated Coronavirus. Science, 2003, 300, 1399-1404.	12.6	1,842
27	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
28	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
29	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
30	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
31	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
32	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
33	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
34	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
35	Conserved role of intragenic DNA methylation in regulating alternative promoters. Nature, 2010, 466, 253-257.	27.8	1,568
36	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504

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37	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
38	ARID1AMutations in Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2010, 363, 1532-1543.	27.0	1,460
39	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	27.8	1,448
40	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
41	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
42	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
43	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
44	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	19.0	1,254
45	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
46	The Genome of the Kinetoplastid Parasite, Leishmania major. Science, 2005, 309, 436-442.	12.6	1,237
47	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	27.8	1,158
48	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	12.6	1,147
49	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	12.6	1,124
50	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
51	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
52	The Genome of the Sea Urchin Strongylocentrotus purpuratus. Science, 2006, 314, 941-952.	12.6	1,018
53	Applications of next-generation sequencing technologies in functional genomics. Genomics, 2008, 92, 255-264.	2.9	1,013
54	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990

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55	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	27.8	984
56	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. Genome Research, 2008, 18, 610-621.	5.5	964
57	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	21.4	933
58	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886
59	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812
60	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
61	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
62	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
63	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
64	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
65	Mutation ofFOXL2in Granulosa-Cell Tumors of the Ovary. New England Journal of Medicine, 2009, 360, 2719-2729.	27.0	706
66	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
67	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
68	The Genome of the Basidiomycetous Yeast and Human Pathogen Cryptococcus neoformans. Science, 2005, 307, 1321-1324.	12.6	664
69	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
70	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	17.5	647
71	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
72	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623

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73	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
74	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
75	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
76	A tiling resolution DNA microarray with complete coverage of the human genome. Nature Genetics, 2004, 36, 299-303.	21.4	597
77	Identification of miR-145 and miR-146a as mediators of the 5qâ€“ syndrome phenotype. Nature Medicine, 2010, 16, 49-58.	30.7	588
78	The complete genome of Rhodococcus sp. RHA1 provides insights into a catabolic powerhouse. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15582-15587.	7.1	586
79	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	1.4	556
80	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. Nature, 2011, 471, 377-381.	27.8	551
81	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	27.8	545
82	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
83	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. Nature Medicine, 2018, 24, 103-112.	30.7	525
84	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
85	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
86	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
87	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
88	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
89	Applications of New Sequencing Technologies for Transcriptome Analysis. Annual Review of Genomics and Human Genetics, 2009, 10, 135-151.	6.2	457
90	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422

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91	Genetic Definition and Sequence Analysis of Arabidopsis Centromeres. Science, 1999, 286, 2468-2474.	12.6	417
92	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
93	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
94	High-throughput microfluidic single-cell RT-qPCR. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13999-14004.	7.1	406
95	High Throughput Fingerprint Analysis of Large-Insertâ€‰Clones. Genome Research, 1997, 7, 1072-1084.	5.5	405
96	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
97	Recurrent SomaticDICER1Mutations in Nonepithelial Ovarian Cancers. New England Journal of Medicine, 2012, 366, 234-242.	27.0	401
98	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
99	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
100	De novo transcriptome assembly with ABySS. Bioinformatics, 2009, 25, 2872-2877.	4.1	371
101	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. Cell, 2010, 143, 367-378.	28.9	365
102	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. Nature Genetics, 2020, 52, 231-240.	21.4	365
103	The Release 6 reference sequence of the Drosophila melanogaster genome. Genome Research, 2015, 25, 445-458.	5.5	359
104	Distinct evolutionary trajectories of primary highâ€grade serous ovarian cancers revealed through spatial mutational profiling. Journal of Pathology, 2013, 231, 21-34.	4.5	357
105	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. BioTechniques, 2008, 45, 81-94.	1.8	355
106	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
107	High-Throughput In Vivo Analysis of Gene Expression in Caenorhabditis elegans. PLoS Biology, 2007, 5, e237.	5.6	346
108	Analysis of the Genome and Transcriptome of Cryptococcus neoformans var. grubii Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	3.5	336

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109	SKPs Derive from Hair Follicle Precursors and Exhibit Properties of Adult Dermal Stem Cells. Cell Stem Cell, 2009, 5, 610-623.	11.1	335
110	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
111	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
112	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
113	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. Genome Research, 2014, 24, 1881-1893.	5.5	322
114	Rapid, reliable, and reproducible molecular sub-grouping of clinical medulloblastoma samples. Acta Neuropathologica, 2012, 123, 615-626.	7.7	318
115	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
116	A physical map of the mouse genome. Nature, 2002, 418, 743-750.	27.8	316
117	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. Blood, 2012, 119, 1963-1971.	1.4	313
118	Transcriptome Analysis of the Normal Human Mammary Cell Commitment and Differentiation Process. Cell Stem Cell, 2008, 3, 109-118.	11.1	310
119	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
120	Massively Parallel Sequencing: The Next Big Thing in Genetic Medicine. American Journal of Human Genetics, 2009, 85, 142-154.	6.2	308
121	Next-generation tag sequencing for cancer gene expression profiling. Genome Research, 2009, 19, 1825-1835.	5.5	306
122	Prospective isolation and molecular characterization of hematopoietic stem cells with durable self-renewal potential. Blood, 2009, 113, 6342-6350.	1.4	300
123	Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. Nature Genetics, 2014, 46, 427-429.	21.4	298
124	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. Nature, 2019, 572, 67-73.	27.8	293
125	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767.	21.4	287
126	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

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127	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	19.0	283
128	Development and Application of a Salmonid EST Database and cDNA Microarray: Data Mining and Interspecific Hybridization Characteristics. Genome Research, 2004, 14, 478-490.	5.5	279
129	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
130	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
131	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
132	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
133	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
134	Oligonucleotide Microarray Analysis of Genomic Imbalance in Children with Mental Retardation. American Journal of Human Genetics, 2006, 79, 500-513.	6.2	261
135	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201.	1.6	257
136	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	21.4	255
137	Mutations in EZH2 Cause Weaver Syndrome. American Journal of Human Genetics, 2012, 90, 110-118.	6.2	253
138	Functional Genomics of the Cilium, a Sensory Organelle. Current Biology, 2005, 15, 935-941.	3.9	245
139	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
140	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	16.8	244
141	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. Cancer Cell, 2014, 26, 33-47.	16.8	241
142	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 929-934.	7.1	239
143	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007.	5.5	237
144	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	27.8	236

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145	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
146	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
147	Conifer defence against insects: microarray gene expression profiling of Sitka spruce (Picea) Tj ETQq1 1 0.784314 rgBT /Overlock 10 transcriptome. Plant, Cell and Environment, 2006, 29, 1545-1570.	5.7	221
148	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	21.4	220
149	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont Grosmannia clavigera , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509.	7.1	218
150	Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. Nature Communications, 2016, 7, 13331.	12.8	218
151	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. Cancer Discovery, 2019, 9, 546-563.	9.4	213
152	Deep annotation of Drosophila melanogaster microRNAs yields insights into their processing, modification, and emergence. Genome Research, 2011, 21, 203-215.	5.5	207
153	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	21.4	207
154	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
155	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
156	Changes in Gene Expression Associated with Developmental Arrest and Longevity in Caenorhabditis elegans. Genome Research, 2001, 11, 1346-1352.	5.5	202
157	A SAGE Approach to Discovery of Genes Involved in Autophagic Cell Death. Current Biology, 2003, 13, 358-363.	3.9	198
158	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. Bioinformatics, 2010, 26, 730-736.	4.1	192
159	Hive plots--rational approach to visualizing networks. Briefings in Bioinformatics, 2012, 13, 627-644.	6.5	187
160	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
161	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
162	Genomics of hybrid poplar (Populus trichocarpaÃ— deltoides) interacting with forest tent caterpillars (Malacosoma disstria): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences. Molecular Ecology, 2006, 15, 1275-1297.	3.9	183

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163	ADAR1 Activation Drives Leukemia Stem Cell Self-Renewal by Impairing Let-7 Biogenesis. Cell Stem Cell, 2016, 19, 177-191.	11.1	182
164	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. Emerging Infectious Diseases, 2004, 10, 2192-2195.	4.3	182
165	Analysis of long-lived C. elegans daf-2 mutants using serial analysis of gene expression. Genome Research, 2005, 15, 603-615.	5.5	180
166	Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma. Nature Genetics, 2014, 46, 329-335.	21.4	180
167	Gene Discovery by EST Sequencing inToxoplasma gondiiReveals Sequences Restricted to theâ€‰Apicomplexa. Genome Research, 1998, 8, 18-28.	5.5	179
168	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
169	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246.	2.8	173
170	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	1.4	172
171	Massively parallel sequencing of the polyadenylated transcriptome of C. elegans. Genome Research, 2009, 19, 657-666.	5.5	169
172	Aberrant patterns of H3K4 and H3K27 histone lysine methylation occur across subgroups in medulloblastoma. Acta Neuropathologica, 2013, 125, 373-384.	7.7	169
173	A Pan-BCL2 Inhibitor Renders Bone-Marrow-Resident Human Leukemia Stem Cells Sensitive to Tyrosine Kinase Inhibition. Cell Stem Cell, 2013, 12, 316-328.	11.1	167
174	The ELT-2 GATA-factor and the global regulation of transcription in the C. elegans intestine. Developmental Biology, 2007, 302, 627-645.	2.0	165
175	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. Genome Research, 2008, 18, 1906-1917.	5.5	163
176	In-depth characterization of the microRNA transcriptome in a leukemia progression model. Genome Research, 2008, 18, 1787-1797.	5.5	162
177	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. Genome Research, 2013, 23, 1522-1540.	5.5	162
178	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	28.9	162
179	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. Journal of Pathology, 2012, 227, 286-297.	4.5	161
180	Acquired TNFRSF14 Mutations in Follicular Lymphoma Are Associated with Worse Prognosis. Cancer Research, 2010, 70, 9166-9174.	0.9	160

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181	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
182	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. Bioinformatics, 2012, 28, 907-913.	4.1	159
183	The molecular signature and cis-regulatory architecture of a C. elegans gustatory neuron. Genes and Development, 2007, 21, 1653-1674.	5.9	151
184	ADAR1 promotes malignant progenitor reprogramming in chronic myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1041-1046.	7.1	148
185	Identification of GPC2 as an Oncoprotein and Candidate Immunotherapeutic Target in High-Risk Neuroblastoma. Cancer Cell, 2017, 32, 295-309.e12.	16.8	148
186	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. Nature Cancer, 2021, 2, 157-173.	13.2	147
187	Notch Initiates the Endothelial-to-Mesenchymal Transition in the Atrioventricular Canal through Autocrine Activation of Soluble Guanylyl Cyclase. Developmental Cell, 2011, 21, 288-300.	7.0	144
188	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. Clinical Cancer Research, 2017, 23, 7521-7530.	7.0	144
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