

Marco A Marra

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

510 papers	162,332 citations	152 h-index	402 g-index
533 ext. papers	198,899 ext. citations	15.5 avg, IF	9.33 L-index

#	Paper	IF	Citations
510	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
509	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012 , 490, 61-70	50.4	8025
508	Circos: an information aesthetic for comparative genomics. <i>Genome Research</i> , 2009 , 19, 1639-45	9.7	6014
507	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7	50.4	5640
506	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
505	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
504	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
503	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50	50.4	3310
502	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2013 , 368, 2059-74	59.2	3137
501	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
500	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012 , 489, 519-25	50.4	2820
499	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
498	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
497	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013 , 499, 43-9	50.4	2184
496	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
495	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
494	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807

493	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
492	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
491	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
490	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
489	The Genome sequence of the SARS-associated coronavirus. <i>Science</i> , 2003 , 300, 1399-404	33.3	1632
488	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
487	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16899-903	11.5	1457
486	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012 , 486, 395-9	50.4	1417
485	Conserved role of intragenic DNA methylation in regulating alternative promoters. <i>Nature</i> , 2010 , 466, 253-7	50.4	1298
484	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010 , 28, 1045-8	44.5	1284
483	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010 , 42, 181-5	36.3	1273
482	ARID1A mutations in endometriosis-associated ovarian carcinomas. <i>New England Journal of Medicine</i> , 2010 , 363, 1532-43	59.2	1208
481	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011 , 476, 298-303	50.4	1180
480	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
479	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
478	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
477	The genome of the kinetoplastid parasite, <i>Leishmania major</i> . <i>Science</i> , 2005 , 309, 436-42	33.3	1101
476	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007 , 4, 651-7	21.6	1077

475	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
474	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
473	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
472	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017 , 541, 169-175	50.4	965
471	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	56.2	961
470	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
469	Mutational analysis reveals the origin and therapy-driven evolution of recurrent glioma. <i>Science</i> , 2014 , 343, 189-193	33.3	912
468	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	56.2	13896
467	Identification of functional elements and regulatory circuits by Drosophila modENCODE. <i>Science</i> , 2010 , 330, 1787-97	33.3	892
466	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
465	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
464	Applications of next-generation sequencing technologies in functional genomics. <i>Genomics</i> , 2008 , 92, 255-64	4.3	885
463	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009 , 461, 809-13	50.4	879
462	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. <i>Genome Research</i> , 2008 , 18, 610-21	9.7	879
461	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
460	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
459	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
458	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755

457	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
456	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013 , 45, 279-84	36.3	717
455	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010 , 7, 909-12	21.6	701
454	The genome sequence of <i>Caenorhabditis briggsae</i> : a platform for comparative genomics. <i>PLoS Biology</i> , 2003 , 1, E45	9.7	677
453	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613
452	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012 , 488, 49-56	50.4	596
451	The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005 , 307, 1321-4	33.3	580
450	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
449	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010 , 28, 1097-105	44.5	570
448	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
447	Mutation of FOXL2 in granulosa-cell tumors of the ovary. <i>New England Journal of Medicine</i> , 2009 , 360, 2719-29	59.2	551
446	A tiling resolution DNA microarray with complete coverage of the human genome. <i>Nature Genetics</i> , 2004 , 36, 299-303	36.3	540
445	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
444	Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. <i>Cancer Cell</i> , 2012 , 22, 153-66	24.3	515
443	The complete genome of <i>Rhodococcus</i> sp. RHA1 provides insights into a catabolic powerhouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15582-7	11.5	515
442	Identification of miR-145 and miR-146a as mediators of the 5q- syndrome phenotype. <i>Nature Medicine</i> , 2010 , 16, 49-58	50.5	494
441	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
440	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. <i>Nature</i> , 2011 , 471, 377-81	50.4	467

439	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , 2011 , 117, 2451-9	2.2	458
438	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. <i>Nature</i> , 2015 , 518, 422-6	50.4	451
437	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
436	deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. <i>PLoS Computational Biology</i> , 2011 , 7, e1001138	5	409
435	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
434	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004 , 14, 2121-7	9.7	404
433	Applications of new sequencing technologies for transcriptome analysis. <i>Annual Review of Genomics and Human Genetics</i> , 2009 , 10, 135-51	9.7	392
432	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
431	Genetic definition and sequence analysis of Arabidopsis centromeres. <i>Science</i> , 1999 , 286, 2468-74	33.3	381
430	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
429	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
428	High-throughput microfluidic single-cell RT-qPCR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13999-4004	11.5	359
427	High throughput fingerprint analysis of large-insert clones. <i>Genome Research</i> , 1997 , 7, 1072-84	9.7	355
426	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
425	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018 , 173, 355-370.e14	56.2	342
424	Recurrent somatic DICER1 mutations in nonepithelial ovarian cancers. <i>New England Journal of Medicine</i> , 2012 , 366, 234-42	59.2	332
423	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
422	De novo transcriptome assembly with ABySS. <i>Bioinformatics</i> , 2009 , 25, 2872-7	7.2	326

421	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736.	24.3	324
420	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , 2008 , 45, 81-94	2.5	322
419	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
418	ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. <i>Cell</i> , 2010 , 143, 367-78	56.2	297
417	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
416	Distinct evolutionary trajectories of primary high-grade serous ovarian cancers revealed through spatial mutational profiling. <i>Journal of Pathology</i> , 2013 , 231, 21-34	9.4	292
415	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013 , 122, 1256-65	2.2	289
414	High-throughput in vivo analysis of gene expression in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , 2007 , 5, e237	9.7	285
413	A physical map of the mouse genome. <i>Nature</i> , 2002 , 418, 743-50	50.4	282
412	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
411	SKPs derive from hair follicle precursors and exhibit properties of adult dermal stem cells. <i>Cell Stem Cell</i> , 2009 , 5, 610-23	18	276
410	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018 , 33, 706-720.e9	24.3	275
409	Transcriptome analysis of the normal human mammary cell commitment and differentiation process. <i>Cell Stem Cell</i> , 2008 , 3, 109-18	18	274
408	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018 , 24, 103-112	50.5	272
407	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , 2009 , 19, 1825-35	35	271
406	Rapid, reliable, and reproducible molecular sub-grouping of clinical medulloblastoma samples. <i>Acta Neuropathologica</i> , 2012 , 123, 615-26	14.3	265
405	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. <i>Blood</i> , 2012 , 119, 1963-71	2.2	264
404	Analysis of the genome and transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> reveals complex RNA expression and microevolution leading to virulence attenuation. <i>PLoS Genetics</i> , 2014 , 10, e1004261	6	260

403	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
402	Massively parallel sequencing: the next big thing in genetic medicine. <i>American Journal of Human Genetics</i> , 2009 , 85, 142-54	11	257
401	Development and application of a salmonid EST database and cDNA microarray: data mining and interspecific hybridization characteristics. <i>Genome Research</i> , 2004 , 14, 478-90	9.7	251
400	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
399	Oligonucleotide microarray analysis of genomic imbalance in children with mental retardation. <i>American Journal of Human Genetics</i> , 2006 , 79, 500-13	11	247
398	Prospective isolation and molecular characterization of hematopoietic stem cells with durable self-renewal potential. <i>Blood</i> , 2009 , 113, 6342-50	2.2	237
397	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
396	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
395	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15544-9	11.5	229
394	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
393	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010 , 7, 843-7	21.6	227
392	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012 , 226, 7-16	9.4	226
391	Small cell carcinoma of the ovary, hypercalcemic type, displays frequent inactivating germline and somatic mutations in SMARCA4. <i>Nature Genetics</i> , 2014 , 46, 427-9	36.3	224
390	The Release 6 reference sequence of the Drosophila melanogaster genome. <i>Genome Research</i> , 2015 , 25, 445-58	9.7	222
389	TITAN: inference of copy number architectures in clonal cell populations from tumor whole-genome sequence data. <i>Genome Research</i> , 2014 , 24, 1881-93	9.7	218
388	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
387	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. <i>Nature Genetics</i> , 2016 , 48, 758-67	36.3	209
386	14-3-3 fusion oncogenes in high-grade endometrial stromal sarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 929-34	11.5	208

385	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016 , 529, 351-7	50.4	206
384	Functional genomics of the cilium, a sensory organelle. <i>Current Biology</i> , 2005 , 15, 935-41	6.3	206
383	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003 , 424, 157-64	50.4	202
382	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406	10.6	200
381	Conifer defence against insects: microarray gene expression profiling of Sitka spruce (<i>Picea sitchensis</i>) induced by mechanical wounding or feeding by spruce budworms (<i>Choristoneura occidentalis</i>) or white pine weevils (<i>Pissodes strobi</i>) reveals large-scale changes of the host transcriptome. <i>Plant, Cell and Environment</i> , 2006 , 29, 1545-70	8.4	197
380	Mutations in EZH2 cause Weaver syndrome. <i>American Journal of Human Genetics</i> , 2012 , 90, 110-8	11	190
379	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
378	Changes in gene expression associated with developmental arrest and longevity in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2001 , 11, 1346-52	9.7	186
377	Deep annotation of <i>Drosophila melanogaster</i> microRNAs yields insights into their processing, modification, and emergence. <i>Genome Research</i> , 2011 , 21, 203-15	9.7	185
376	Quiescent sox2(+) cells drive hierarchical growth and relapse in sonic hedgehog subgroup medulloblastoma. <i>Cancer Cell</i> , 2014 , 26, 33-47	24.3	181
375	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. <i>Genome Research</i> , 2012 , 22, 1995-2007	9.7	181
374	A SAGE approach to discovery of genes involved in autophagic cell death. <i>Current Biology</i> , 2003 , 13, 358-63		181
373	Recurrent DGCR8, DROSHA, and SIX homeodomain mutations in favorable histology Wilms tumors. <i>Cancer Cell</i> , 2015 , 27, 286-97	24.3	175
372	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. <i>Bioinformatics</i> , 2010 , 26, 730-6	7.2	174
371	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
370	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007 , 17, 760-74	9.7	163
369	Gene discovery by EST sequencing in <i>Toxoplasma gondii</i> reveals sequences restricted to the Apicomplexa. <i>Genome Research</i> , 1998 , 8, 18-28	9.7	162
368	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 2504-9	11.5	161

367	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. <i>Nature Genetics</i> , 2017 , 49, 1487-1494	36.3	160
366	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2	10.6	159
365	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , 2018 , 19, 785-798	21.7	159
364	Genomics of hybrid poplar (<i>Populus trichocarpax deltoides</i>) interacting with forest tent caterpillars (<i>Malacosoma disstria</i>): normalized and full-length cDNA libraries, expressed sequence tags, and a cDNA microarray for the study of insect-induced defences in poplar. <i>Molecular Ecology</i> , 2006 , 15, 1275-97	5.7	159
363	Analysis of long-lived <i>C. elegans</i> daf-2 mutants using serial analysis of gene expression. <i>Genome Research</i> , 2005 , 15, 603-15	9.7	158
362	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013 , 45, 836-41	36.3	154
361	Novel avian influenza H7N3 strain outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004 , 10, 2192-5	10.2	154
360	Massively parallel sequencing of the polyadenylated transcriptome of <i>C. elegans</i> . <i>Genome Research</i> , 2009 , 19, 657-66	9.7	152
359	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
358	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
357	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019 , 572, 67-73	50.4	149
356	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020 , 52, 231-240	36.3	148
355	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012 , 13, 627-44	13.4	148
354	In-depth characterization of the microRNA transcriptome in a leukemia progression model. <i>Genome Research</i> , 2008 , 18, 1787-97	9.7	148
353	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018 , 23, 297-312.e12	10.6	147
352	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008 , 18, 1906-17	9.7	147
351	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
350	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010 , 11, R82	18.3	144

349	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. <i>Journal of Pathology</i> , 2012 , 227, 286-97	9.4	142
348	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017 , 49, 856-865	36.3	141
347	Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma. <i>Nature Genetics</i> , 2014 , 46, 329-35	36.3	141
346	A Pan-BCL2 inhibitor renders bone-marrow-resident human leukemia stem cells sensitive to tyrosine kinase inhibition. <i>Cell Stem Cell</i> , 2013 , 12, 316-28	18	140
345	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018 , 562, 373-379	50.4	140
344	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006 , 7, 246	4.5	139
343	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2019 , 37, 190-201	2.2	137
342	JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data. <i>Bioinformatics</i> , 2012 , 28, 907-13	7.2	136
341	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	31.2	133
340	Acquired TNFRSF14 mutations in follicular lymphoma are associated with worse prognosis. <i>Cancer Research</i> , 2010 , 70, 9166-74	10.1	133
339	The ELT-2 GATA-factor and the global regulation of transcription in the C. elegans intestine. <i>Developmental Biology</i> , 2007 , 302, 627-45	3.1	131
338	Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2016 , 7, 13331	17.4	128
337	Global analysis of in vivo Foxa2-binding sites in mouse adult liver using massively parallel sequencing. <i>Nucleic Acids Research</i> , 2008 , 36, 4549-64	20.1	127
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