

Richard K Wilson

List of Publications by Year in Descending Order

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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.

497
papers

224,206
citations

172
h-index

473
g-index

573
ext. papers

263,265
ext. citations

19.3
avg, IF

9.4
L-index

#	Paper	IF	Citations
497	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers.. <i>Cancer Genetics</i> , 2022 , 264-265, 90-99	2.3	1
496	A deletion in the N gene of SARS-CoV-2 may reduce test sensitivity for detection of SARS-CoV-2.. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021 , 102, 115631	2.9	0
495	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021 , 22, 872	4.5	2
494	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. <i>American Journal of Surgical Pathology</i> , 2021 , 45, 329-340	6.7	6
493	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021 , 19, 41	7.3	9
492	Novel morphologic findings in PLAG1-rearranged soft tissue tumors. <i>Genes Chromosomes and Cancer</i> , 2021 , 60, 577-585	5	0
491	Molecular classification of a complex structural rearrangement of the RB1 locus in an infant with sporadic, isolated, intracranial, sellar region retinoblastoma. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 61	7.3	1
490	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021 , 144, 2971-2978	11.2	5
489	Gastroblastoma with a novel EWSR1-CTBP1 fusion presenting in adolescence. <i>Genes Chromosomes and Cancer</i> , 2021 , 60, 640-646	5	1
488	Effects of TDP-43 overexpression on neuron proteome and morphology in vitro. <i>Molecular and Cellular Neurosciences</i> , 2021 , 114, 103627	4.8	1
487	Hypomorphic alleles pose challenges in rare disease genomic variant interpretation. <i>Clinical Genetics</i> , 2021 , 100, 775-776	4	0
486	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. <i>Journal of Clinical Oncology</i> , 2021 , 39, 3747-3758	2.2	4
485	Genome Assemblies across the Diverse Evolutionary Spectrum of Protozoan Parasites. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0054521	1.3	0
484	A novel sialic acid-binding adhesin present in multiple species contributes to the pathogenesis of Infective endocarditis. <i>PLoS Pathogens</i> , 2021 , 17, e1009222	7.6	3
483	Clinically aggressive pediatric spinal ependymoma with novel MYC amplification demonstrates molecular and histopathologic similarity to newly described MYCN-amplified spinal ependymomas.. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 192	7.3	0
482	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020 , 11, 2156	17.4	50
481	Disease-associated mosaic variation in clinical exome sequencing: a two-year pediatric tertiary care experience. <i>Journal of Physical Education and Sports Management</i> , 2020 , 6,	2.8	4

480	Early-onset Wilson disease caused by exon skipping associated with intronic variant. <i>Journal of Physical Education and Sports Management</i> , 2020 , 6,	2.8	2
479	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020 , 6, eaay9691	14.3	14
478	Somatic mosaicism correlates with clinical findings in epilepsy brain tissue. <i>Neurology: Genetics</i> , 2020 , 6, e460	3.8	7
477	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020 , 11, 913	17.4	32
476	HIV-1 gp120-CD4-Induced Antibody Complex Elicits CD4 Binding Site-Specific Antibody Response in Mice. <i>Journal of Immunology</i> , 2020 , 204, 1543-1561	5.3	1
475	The Genotypic and Phenotypic Spectrum of BICD2 Variants in Spinal Muscular Atrophy. <i>Annals of Neurology</i> , 2020 , 87, 487-496	9.4	9
474	primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) translocation. <i>Haematologica</i> , 2020 , 105, e194-e197	6.6	6
473	Infantile fibrosarcoma-like tumor driven by novel fusion consolidated with cabozantinib. <i>Journal of Physical Education and Sports Management</i> , 2020 , 6,	2.8	5
472	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. <i>Journal of Molecular Diagnostics</i> , 2020 , 22, 1238-1245	5.1	2
471	Sequence analysis in reveals pervasiveness of X-Y arms races in mammalian lineages. <i>Genome Research</i> , 2020 , 30, 1716-1726	9.7	6
470	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020 , 25, 1859-1875	15.1	106
469	Two of a kind: transmissible Schwann cell cancers in the endangered Tasmanian devil (<i>Sarcophilus harrisii</i>). <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 1847-1858	10.3	19
468	Whole Exome Sequencing of Highly Aggregated Lung Cancer Families Reveals Linked Loci for Increased Cancer Risk on Chromosomes 12q, 7p, and 4q. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 434-442	4	6
467	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019 , 20, 187	18.3	39
466	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. <i>Molecular Cancer Research</i> , 2019 , 17, 895-906	6.6	25
465	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. <i>European Journal of Medical Genetics</i> , 2019 , 62, 103701	2.6	6
464	Mutations in PLS1, encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. <i>Human Mutation</i> , 2019 , 40, 2286-2295	4.7	14
463	<i>Streptococcus oralis</i> subsp. Produces Monolateral Serine-Rich Repeat Protein Fibrils, One of Which Contributes to Saliva Binding via Sialic Acid. <i>Infection and Immunity</i> , 2019 , 87,	3.7	5

462	Expansion of B4GALT7 linkeropathy phenotype to include perinatal lethal skeletal dysplasia. <i>European Journal of Human Genetics</i> , 2019 , 27, 1569-1577	5.3	5
461	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019 , 572, 323-328.	38.4	69
460	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019 , 18, 1-10	6.1	1
459	Novel in-frame deletion causes Larsen syndrome in a three-generation pedigree. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	0
458	Long-read sequence and assembly of segmental duplications. <i>Nature Methods</i> , 2019 , 16, 88-94	21.6	86
457	Association of Tumor Microenvironment T-cell Repertoire and Mutational Load with Clinical Outcome after Sequential Checkpoint Blockade in Melanoma. <i>Cancer Immunology Research</i> , 2019 , 7, 458-465	12.5	23
456	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019 , 176, 663-675.e19	56.2	205
455	Genome sequencing identifies somatic duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	5
454	Recurrent structural variation, clustered sites of selection, and disease risk for the complement factor H () gene family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E4433-E4442	11.5	24
453	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
452	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
451	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e32	36.2	133
450	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
449	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
448	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
447	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
446	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
445	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

444	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
443	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	10.6	56
442	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
441	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
440	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
439	A de novo nonsense mutation in shared by siblings with Bainbridge-Ropers syndrome. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	14
438	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , 2018 , 19, 172	4.5	9
437	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
436	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
435	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
434	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
433	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
432	In-frame de novo mutation in in two patients with muscular atrophy and arthrogyriposis. <i>Journal of Physical Education and Sports Management</i> , 2018 , 4,	2.8	9
431	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
430	Structure-Guided Redesign Improves NFL HIV Env Trimer Integrity and Identifies an Inter-Protomer Disulfide Permitting Post-Expression Cleavage. <i>Frontiers in Immunology</i> , 2018 , 9, 1631	8.4	24
429	Cleavage-Independent HIV-1 Trimers From CHO Cell Lines Elicit Robust Autologous Tier 2 Neutralizing Antibodies. <i>Frontiers in Immunology</i> , 2018 , 9, 1116	8.4	19
428	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018 , 34, 411-426.e19	24.3	67
427	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018 , 360,	33.3	178

426	Transcriptome and proteome profiling reveals stress-induced expression signatures of imiquimod-treated Tasmanian devil facial tumor disease (DFTD) cells. <i>Oncotarget</i> , 2018 , 9, 15895-15914	3.3	10
425	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
424	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. <i>New England Journal of Medicine</i> , 2018 , 379, 2330-2341	59.2	165
423	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018 , 9, 3787	17.4	63
422	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018 , 9, 3476	17.4	51
421	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017 , 49, 387-394	36.3	92
420	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017 , 49, 170-174	36.3	308
419	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017 , 1-14	14.3	4
418	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. <i>Cell</i> , 2017 , 168, 801-816.e13	56.2	131
417	The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017 , 1, 69	12.3	81
416	Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. <i>Blood</i> , 2017 , 129, 1397-1401	2.2	17
415	Real-Time Electronic Tracking of Diarrheal Episodes and Laxative Therapy Enables Verification of Clostridium difficile Clinical Testing Criteria and Reduction of Clostridium difficile Infection Rates. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1276-1284	9.7	56
414	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017 , 27, 849-864	9.7	365
413	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017 , 94, 550-568.e10	13.9	133
412	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 2017 , 8, 15451	17.4	138
411	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017 , 49, 1705-1713	36.3	76
410	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017 , 49, 1714-1721	36.3	43
409	Acute Illness Among Surfers After Exposure to Seawater in Dry- and Wet-Weather Conditions. <i>American Journal of Epidemiology</i> , 2017 , 186, 866-875	3.8	36

408	Orthotopic patient-derived xenografts of paediatric solid tumours. <i>Nature</i> , 2017 , 549, 96-100	50.4	144
407	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017 , 55, 19-33	3.1	8
406	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
405	Dynamic changes in the clonal structure of MDS and AML in response to epigenetic therapy. <i>Leukemia</i> , 2017 , 31, 872-881	10.7	64
404	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017 , 27, 677-685	9.7	226
403	Glutaraldehyde Cross-linking of HIV-1 Env Trimers Skews the Antibody Subclass Response in Mice. <i>Frontiers in Immunology</i> , 2017 , 8, 1654	8.4	5
402	Targeted N-glycan deletion at the receptor-binding site retains HIV Env NFL trimer integrity and accelerates the elicited antibody response. <i>PLoS Pathogens</i> , 2017 , 13, e1006614	7.6	28
401	Targeted sequencing informs the evaluation of normal karyotype cytopenic patients for low-grade myelodysplastic syndrome. <i>Leukemia</i> , 2016 , 30, 2422-2426	10.7	4
400	Rare Variation in TET2 Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 1456-1463	4	14
399	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016 , 375, 2023-2036	59.2	493
398	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016 , 48, 1481-1489	36.3	145
397	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016 , 7, 12997	17.4	22
396	An HIV-1 Env-Antibody Complex Focuses Antibody Responses to Conserved Neutralizing Epitopes. <i>Journal of Immunology</i> , 2016 , 197, 3982-3998	5.3	12
395	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016 , 7, 12498	17.4	47
394	The genomic landscape of core-binding factor acute myeloid leukemias. <i>Nature Genetics</i> , 2016 , 48, 1551-1556	36.5	147
393	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016 , 2, e1600633	14.3	49
392	A High-Resolution SNP Array-Based Linkage Map Anchors a New Domestic Cat Draft Genome Assembly and Provides Detailed Patterns of Recombination. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1607-1616	3.2	32
391	Research note: Natural environments and prescribing in England. <i>Landscape and Urban Planning</i> , 2016 , 151, 103-108	7.7	9

390	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016 , 44, 603-13	3.1	33
389	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016 , 131, 833-45	14.3	209
388	High-Resolution Longitudinal Study of HIV-1 Env Vaccine-Elicited B Cell Responses to the Virus Primary Receptor Binding Site Reveals Affinity Maturation and Clonal Persistence. <i>Journal of Immunology</i> , 2016 , 196, 3729-43	5.3	24
387	The impact of chromosomal translocation locus and fusion oncogene coding sequence in synovial sarcomagenesis. <i>Oncogene</i> , 2016 , 35, 5021-32	9.2	27
386	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016 , 26, 108-18	9.7	81
385	Identification of a Novel Gene on 10q22.1 Causing Autosomal Dominant Retinitis Pigmentosa (adRP). <i>Advances in Experimental Medicine and Biology</i> , 2016 , 854, 193-200	3.6	6
384	Thermostability of Well-Ordered HIV Spikes Correlates with the Elicitation of Autologous Tier 2 Neutralizing Antibodies. <i>PLoS Pathogens</i> , 2016 , 12, e1005767	7.6	57
383	North Carolina macular dystrophy (MCDR1) caused by a novel tandem duplication of the gene. <i>Molecular Vision</i> , 2016 , 22, 1239-1247	2.3	21
382	Inactivation of RASA1 promotes melanoma tumorigenesis via R-Ras activation. <i>Oncotarget</i> , 2016 , 7, 23885-96	8.5	19
381	Rare Pre-Existing MDS Subclones Contribute to Secondary AML Progression. <i>Blood</i> , 2016 , 128, 959-959	2.2	1
380	Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. <i>Blood</i> , 2016 , 128, 5506-5506	2.2	
379	Clonal Evolution of Acute Myeloid Leukemia Following Allogeneic Stem Cell Transplantation. <i>Blood</i> , 2016 , 128, 1528-1528	2.2	
378	DNMT3A-Dependent DNA Methylation May Act As a Tumor Suppressor-Not a Tumor Promoter-during AML Progression. <i>Blood</i> , 2016 , 128, 1050-1050	2.2	1
377	The Contribution of GWAS Loci in Familial Dyslipidemias. <i>PLoS Genetics</i> , 2016 , 12, e1006078	6	38
376	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. <i>PLoS Medicine</i> , 2016 , 13, e1002174	11.6	62
375	IRF6 mutation screening in non-syndromic orofacial clefting: analysis of 1521 families. <i>Clinical Genetics</i> , 2016 , 90, 28-34	4	35
374	Visualizing tumor evolution with the fishplot package for R. <i>BMC Genomics</i> , 2016 , 17, 880	4.5	76
373	Dictyocaulus viviparus genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , 2016 , 6, 20316	4.9	17

372	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016 , 352, aae0344	33.3	282
371	Key gp120 Glycans Pose Roadblocks to the Rapid Development of VRC01-Class Antibodies in an HIV-1-Infected Chinese Donor. <i>Immunity</i> , 2016 , 44, 939-50	32.3	62
370	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of <i>Limulus polyphemus</i> (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016 , 8, 1571-89	3.9	33
369	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016 , 44, D1036-44	20.1	222
368	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. <i>Blood</i> , 2016 , 127, 893-7	2.2	80
367	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016 , 13, 806-7	21.6	63
366	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016 , 17, 249-260	10.6	14
365	Interchromosomal core duplicons drive both evolutionary instability and disease susceptibility of the Chromosome 8p23.1 region. <i>Genome Research</i> , 2016 , 26, 1453-1467	9.7	23
364	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322	9.7	54
363	The genomic landscape of childhood and adolescent melanoma. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 816-823	4.3	121
362	Identification of functional variants for cleft lip with or without cleft palate in or near PAX7, FGFR2, and NOG by targeted sequencing of GWAS loci. <i>American Journal of Human Genetics</i> , 2015 , 96, 397-411	11	106
361	Genomic landscape of paediatric adrenocortical tumours. <i>Nature Communications</i> , 2015 , 6, 6302	17.4	116
360	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015 , 33, 980-91	17.8	18
359	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. <i>Nature Genetics</i> , 2015 , 47, 330-7	36.3	303
358	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
357	Genome sequence of enterovirus D68 from St. Louis, Missouri, USA. <i>Emerging Infectious Diseases</i> , 2015 , 21, 184-6	10.2	33
356	Genetic variation and the de novo assembly of human genomes. <i>Nature Reviews Genetics</i> , 2015 , 16, 627-40.1	40.1	242
355	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015 , 13, 41	7.3	36

354	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
353	Alzheimer's disease: rare variants with large effect sizes. <i>Current Opinion in Genetics and Development</i> , 2015 , 33, 49-55	4.9	27
352	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 314, 811-22	27.4	242
351	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015 , 25, 1921-33	9.7	84
350	Clonal evolution revealed by whole genome sequencing in a case of primary myelofibrosis transformed to secondary acute myeloid leukemia. <i>Leukemia</i> , 2015 , 29, 869-76	10.7	38
349	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. <i>Nature</i> , 2015 , 518, 552-555	50.4	503
348	The Physarum polycephalum Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2015 , 8, 109-25	3.9	63
347	Optimizing cancer genome sequencing and analysis. <i>Cell Systems</i> , 2015 , 1, 210-223	10.6	135
346	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. <i>Blood</i> , 2015 , 126, 2484-90	2.2	150
345	Genetic heterogeneity of induced pluripotent stem cells: results from 24 clones derived from a single C57BL/6 mouse. <i>PLoS ONE</i> , 2015 , 10, e0120585	3.7	10
344	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015 , 11, e1004274	5	59
343	The Effects of the Endocannabinoids Anandamide and 2-Arachidonoylglycerol on Human Osteoblast Proliferation and Differentiation. <i>PLoS ONE</i> , 2015 , 10, e0136546	3.7	17
342	Whole Body Melanoma Transcriptome Response in Medaka. <i>PLoS ONE</i> , 2015 , 10, e0143057	3.7	13
341	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6413-8	11.5	52
340	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14936-41	11.5	220
339	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015 , 373, 2336-2346	59.2	641
338	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015 , 6, 10086	17.4	170
337	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. <i>Leukemia</i> , 2015 , 29, 1279-89	10.7	70

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5	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
4	Functional genomics of the stable fly, <i>Stomoxys calcitrans</i> , reveals mechanisms underlying reproduction, host interactions, and novel targets for pest control		8
3	The burden of deleterious variants in a non-human primate biomedical model		3
2	Cerebral Organoids Containing an AUTS2 Missense Variant Model Microcephaly		1
1	Detection of brain somatic variation in epilepsy-associated developmental lesions		1