

Richard K Wilson

List of PR Articles by Year in descending order

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379

PR articles

140,505

PR citations

110

142

PR h-index

41

357

g-index

434

documents

187500

doc citations

71

170

h-index

191692

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Cerebral organoids containing an <i>AUTS2</i> missense variant model microcephaly. <i>Brain</i> , 2023, 146, 387-404.	8.5	50
2	Long-read whole genome sequencing reveals HOXD13 alterations in synpolydactyly. <i>Human Mutation</i> , 2022, 43, 189-199.	3.9	12
3	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> , 2022, 102, 115631.	1.7	15
4	Case report and review of the literature: immune dysregulation in a large familial cohort due to a novel pathogenic <i>RELA</i> variant. <i>Rheumatology</i> , 2022, 62, 347-359.	2.0	16
5	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.6	11
6	Acute lymphoblastic leukemia displays a distinct highly methylated genome. <i>Nature Cancer</i> , 2022, 3, 768-782.	22.8	42
7	De novo missense variant in <i>GRIA2</i> in a patient with global developmental delay, autism spectrum disorder, and epileptic encephalopathy. <i>Journal of Physical Education and Sports Management</i> , 2022, 8, a006172.	1.5	8
8	Detection of brain somatic variation in epilepsy-associated developmental lesions. <i>Epilepsia</i> , 2022, 63, 1981-1997.	4.6	45
9	Molecular Heterogeneity in Pediatric Malignant Rhabdoid Tumors in Patients With Multi-Organ Involvement. <i>Frontiers in Oncology</i> , 2022, 12, .	2.7	7
10	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, .	4.0	31
11	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, .	5.0	11
12	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	8.5	37
13	Hypomorphic alleles pose challenges in rare disease genomic variant interpretation. <i>Clinical Genetics</i> , 2021, 100, 775-776.	2.1	5
14	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. <i>Journal of Clinical Oncology</i> , 2021, 39, 3747-3758.	21.6	98
15	A novel sialic acid-binding adhesin present in multiple species contributes to the pathogenesis of Infective endocarditis. <i>PLoS Pathogens</i> , 2021, 17, e1009222.	4.4	17
16	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. <i>American Journal of Surgical Pathology</i> , 2021, 45, 329-340.	3.6	26
17	Maternal mosaicism for a missense variant in the <i>SMS</i> gene that causes Snyder-Robinson syndrome. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a006122.	1.5	1
18	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021, 22, .	3.3	24

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19	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, .	5.0	15
20	Infantile fibrosarcoma-like tumor driven by novel <i>RBPMS-MET</i> fusion consolidated with cabozantinib. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005645.	1.5	23
21	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 1238-1245.	2.6	16
22	Sequence analysis in <i>Bos taurus</i> reveals pervasiveness of X ₁ arms races in mammalian lineages. <i>Genome Research</i> , 2020, 30, 1716-1726.	4.6	42
23	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020, 11, .	13.9	110
24	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, a005231.	1.5	27
25	Early-onset Wilson disease caused by <i>ATP7B</i> exon skipping associated with intronic variant. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005306.	1.5	7
26	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, .	11.0	71
27	Somatic <i>SLC35A2</i> mosaicism correlates with clinical findings in epilepsy brain tissue. <i>Neurology: Genetics</i> , 2020, 6, .	2.9	36
28	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, .	13.9	98
29	The Genotypic and Phenotypic Spectrum of <i>BICD2</i> Variants in Spinal Muscular Atrophy. <i>Annals of Neurology</i> , 2020, 87, 487-496.	6.3	29
30	<i>De novo</i> primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) <i>NFIA/CBFA2T3</i> translocation. <i>Haematologica</i> , 2020, 105, e194-e197.	4.1	15
31	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.	1.2	13
32	Mutations in <i>PLS1</i> , encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. <i>Human Mutation</i> , 2019, 40, 2286-2295.	3.9	27
33	<i>Streptococcus oralis</i> subsp. <i>dentisani</i> Produces Monolateral Serine-Rich Repeat Protein Fibrils, One of Which Contributes to Saliva Binding via Sialic Acid. <i>Infection and Immunity</i> , 2019, 87, .	2.7	20
34	Expansion of <i>B4GALT7</i> linkeropathy phenotype to include perinatal lethal skeletal dysplasia. <i>European Journal of Human Genetics</i> , 2019, 27, 1569-1577.	3.2	18
35	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	38.7	189
36	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>Science</i> , 2019, 18, 1-10.	3.6	9

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37	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, .	8.2	92
38	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. <i>Molecular Cancer Research</i> , 2019, 17, 895-906.	3.2	54
39	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.	1.6	14
40	Novel in-frame <i>FLNB</i> deletion causes Larsen syndrome in a three-generation pedigree. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004176.	1.5	2
41	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.	4.2	57
42	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	34.1	440
43	Genome sequencing identifies somatic <i>BRAF</i> duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002618.	1.5	9
44	Recurrent structural variation, clustered sites of selection, and disease risk for the complement factor H () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 467 Td (<i>CFH</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 457 Td () gene	7.6	59
45	2018, 115, . An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	34.1	3,192
46	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.	34.1	2,264
47	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	34.1	290
48	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	34.1	359
49	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	34.1	1,951
50	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	423
51	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	567
52	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.	6.4	238
53	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.4	907
54	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	145

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55	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	6.4	102
56	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	1,025
57	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	6.4	281
58	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	222
59	A de novo nonsense mutation in <i>ASXL3</i> shared by siblings with Bainbridge-Ropers syndrome. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002410.	1.5	40
60	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , 2018, 19, .	3.3	20
61	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	5.8	789
62	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.	5.8	392
63	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.	38.5	449
64	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	38.5	1,015
65	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	38.5	507
66	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	6.4	469
67	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. <i>New England Journal of Medicine</i> , 2018, 379, 2330-2341.	43.7	433
68	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018, 9, .	13.9	151
69	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, .	13.9	119
70	In-frame de novo mutation in <i>BICD2</i> in two patients with muscular atrophy and arthrogryposis. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003160.	1.5	18
71	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	38.5	856
72	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, .	5.1	43

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73	Cleavage-Independent HIV-1 Trimers From CHO Cell Lines Elicit Robust Autologous Tier 2 Neutralizing Antibodies. <i>Frontiers in Immunology</i> , 2018, 9, .	5.1	29
74	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	38.5	138
75	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	36.4	364
76	Long-read sequence and assembly of segmental duplications. <i>Nature Methods</i> , 2018, 16, 88-94.	25.9	203
77	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2018, 25, 1859-1875.	8.4	227
78	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017, 49, 387-394.	26.1	179
79	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017, , 1-14.	9.6	7
80	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. <i>Cell</i> , 2017, 168, 801-816.e13.	34.1	209
81	The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017, 1, .	10.3	155
82	Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. <i>Blood</i> , 2017, 129, 1397-1401.	4.2	28
83	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.	4.1	73
84	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.	4.6	1,103
85	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017, 94, 550-568.e10.	11.1	278
86	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 2017, 8, .	13.9	253
87	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	26.1	125
88	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	26.1	65
89	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.4	10
90	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	34.1	957

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91	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017, 27, 677-685.	4.6	378
92	Glutaraldehyde Cross-linking of HIV-1 Env Trimers Skews the Antibody Subclass Response in Mice. <i>Frontiers in Immunology</i> , 2017, 8, .	5.1	9
93	Acute Illness Among Surfers After Exposure to Seawater in Dry- and Wet-Weather Conditions. <i>American Journal of Epidemiology</i> , 2017, 186, 866-875.	3.4	64
94	The Contribution of GWAS Loci in Familial Dyslipidemias. <i>PLoS Genetics</i> , 2016, 12, e1006078.	3.3	54
95	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. <i>PLoS Medicine</i> , 2016, 13, e1002174.	8.5	98
96	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , 2016, 6, .	3.5	28
97	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, .	36.4	392
98	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, 1571-1589.	2.4	55
99	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	15.7	431
100	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	6.4	29
101	Interchromosomal core duplicons drive both evolutionary instability and disease susceptibility of the Chromosome 8p23.1 region. <i>Genome Research</i> , 2016, 26, 1453-1467.	4.6	41
102	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	4.6	118
103	Rare Variation in <i>TET2</i> Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1456-1463.	1.2	26
104	<i>TP53</i> and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.	43.7	762
105	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	26.1	286
106	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, .	13.9	38
107	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016, 7, .	13.9	75
108	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, .	11.0	80

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109	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.	2.0	51
110	Research note: Natural environments and prescribing in England. <i>Landscape and Urban Planning</i> , 2016, 151, 103-108.	9.0	12
111	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, 603-613.	0.4	48
112	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, 833-845.	9.3	358
113	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016, 26, 108-118.	4.6	131
114	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2016, 8, 109-125.	2.4	96
115	Thermostability of Well-Ordered HIV Spikes Correlates with the Elicitation of Autologous Tier 2 Neutralizing Antibodies. <i>PLoS Pathogens</i> , 2016, 12, e1005767.	4.4	79
116	Inactivation of RASA1 promotes melanoma tumorigenesis via R-Ras activation. <i>Oncotarget</i> , 2016, 7, 23885-23896.	1.7	24
117	Rare Pre-Existing MDS Subclones Contribute to Secondary AML Progression. <i>Blood</i> , 2016, 128, 959-959.	4.2	12
118	Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. <i>Blood</i> , 2016, 128, 5506-5506.	4.2	0
119	Clonal Evolution of Acute Myeloid Leukemia Following Allogeneic Stem Cell Transplantation. <i>Blood</i> , 2016, 128, 1528-1528.	4.2	5
120	DNMT3A-Dependent DNA Methylation May Act As a Tumor Suppressor-Not a Tumor Promoter-during AML Progression. <i>Blood</i> , 2016, 128, 1050-1050.	4.2	3
121	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	5.8	191
122	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. <i>Blood</i> , 2015, 126, 2484-2490.	4.2	228
123	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.	2.4	13
124	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	3.1	84
125	Whole Body Melanoma Transcriptome Response in Medaka. <i>PLoS ONE</i> , 2015, 10, e0143057.	2.4	14
126	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, 6413-6418.	7.6	86

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127	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, 14936-14941.	7.6	376
128	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015, 373, 2336-2346.	43.7	1,184
129	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015, 6, .	13.9	277
130	The Genomic Landscape of Childhood and Adolescent Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 816-823.	2.3	169
131	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.	6.5	172
132	Genomic landscape of paediatric adrenocortical tumours. <i>Nature Communications</i> , 2015, 6, .	13.9	194
133	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015, 33, 980-991.	11.9	24
134	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. <i>Nature Genetics</i> , 2015, 47, 330-337.	26.1	464
135	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	38.7	17,885
136	Genome Sequence of Enterovirus D68 from St. Louis, Missouri, USA. <i>Emerging Infectious Diseases</i> , 2015, 21, 184-186.	3.9	35
137	Genetic variation and the de novo assembly of human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 627-640.	47.6	337
138	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015, 13, .	4.0	46
139	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	34.1	1,758
140	Alzheimer's disease: rare variants with large effect sizes. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 49-55.	3.2	39
141	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.	17.1	322
142	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	4.6	125
143	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. <i>Blood</i> , 2015, 126, 574-574.	4.2	3
144	Dynamic Changes in the Clonal Structure of MDS and AML in Response to Epigenetic Therapy. <i>Blood</i> , 2015, 126, 610-610.	4.2	3

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145	Dynamic Changes in Clonal Clearance with Decitabine Therapy in AML and MDS Patients. <i>Blood</i> , 2015, 126, 689-689.	4.2	1
146	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 693-693.	4.2	1
147	Abstract 959: Aromatase inhibition shapes the clonal architecture of estrogen receptor-positive breast cancers. , 2015, , .		0
148	Detection of Clonal Hematopoiesis in Cytopenic Patients Using Targeted Sequencing. <i>Blood</i> , 2015, 126, 1654-1654.	4.2	0
149	Non-Malignant Oligoclonal Hematopoiesis Commonly Follows Cytoreductive Chemotherapy in Adult De Novo AML Patients. <i>Blood</i> , 2015, 126, 686-686.	4.2	0
150	Clonal Architectures and Driver Mutations in Metastatic Melanomas. <i>PLoS ONE</i> , 2014, 9, e111153.	2.4	79
151	Abnormal B cell memory subsets dominate HIV-specific responses in infected individuals. <i>Journal of Clinical Investigation</i> , 2014, 124, 3252-3262.	10.7	140
152	Genome of the house fly, <i>Musca domestica</i> L., a global vector of diseases with adaptations to a septic environment. <i>Genome Biology</i> , 2014, 15, .	8.2	295
153	A Dominant Mutation in Hexokinase 1 (<i>HK1</i>) Causes Retinitis Pigmentosa. , 2014, 55, 7147.		59
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