

# Richard K Wilson

## List of Publications by Year in descending order

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538  
papers

287,283  
citations

43

188  
h-index

6

494  
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573  
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573  
docs citations

573  
times ranked

219454  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cerebral organoids containing an <i>AUTS2</i> missense variant model microcephaly. <i>Brain</i> , 2023, 146, 387-404.	3.7	11
2	Long-read whole genome sequencing reveals HOXD13 alterations in synpolydactyly. <i>Human Mutation</i> , 2022, 43, 189-199.	1.1	7
3	Biallelic SEPSECS variants in two siblings with pontocerebellar hypoplasia type 2D underscore the relevance of splice-disrupting synonymous variants in disease.. <i>Journal of Physical Education and Sports Management</i> , 2022, , mcs.a006165.	0.5	0
4	Inherited and de novo variants extend the etiology of TAOK1-associated neurodevelopmental disorder. <i>Journal of Physical Education and Sports Management</i> , 2022, , mcs.a006180.	0.5	6
5	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.	0.8	12
6	Expanding the Clinical Phenotype of FGFR1 Internal Tandem Duplication. <i>Journal of Physical Education and Sports Management</i> , 2022, , mcs.a006174.	0.5	4
7	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.	0.9	4
8	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.2	3
9	Acute lymphoblastic leukemia displays a distinct highly methylated genome. <i>Nature Cancer</i> , 2022, 3, 768-782.	5.7	15
10	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.	0.5	2
11	Detection of brain somatic variation in epilepsy-associated developmental lesions. <i>Epilepsia</i> , 2022, 63, 1981-1997.	2.6	29
12	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.	1.7	19
13	Novel morphologic findings in <i>PLAG1</i> rearranged soft tissue tumors. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 577-585.	1.5	9
14	Expanding the phenotypic spectrum of internal tandem duplications in somatic disease. <i>Molecular Genetics and Metabolism</i> , 2021, 132, S44.	0.5	0
15	Outcomes of in-house rapid genome sequencing at a Children's Hospital. <i>Molecular Genetics and Metabolism</i> , 2021, 132, S165-S166.	0.5	0
16	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.	2.4	5
17	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	3.7	23
18	Gastroblastoma with a novel <i>EWSR1</i> - <i>CTBP1</i> fusion presenting in adolescence. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 640-646.	1.5	12

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19	Effects of TDP-43 overexpression on neuron proteome and morphology in vitro. <i>Molecular and Cellular Neurosciences</i> , 2021, 114, 103627.	1.0	1
20	Hypomorphic alleles pose challenges in rare disease genomic variant interpretation. <i>Clinical Genetics</i> , 2021, 100, 775-776.	1.0	4
21	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. <i>Journal of Clinical Oncology</i> , 2021, 39, 3747-3758.	0.8	38
22	Genome Assemblies across the Diverse Evolutionary Spectrum of <i>Leishmania</i> Protozoan Parasites. <i>Microbiology Resource Announcements</i> , 2021, 10, e0054521.	0.3	8
23	A novel sialic acid-binding adhesin present in multiple species contributes to the pathogenesis of Infective endocarditis. <i>PLoS Pathogens</i> , 2021, 17, e1009222.	2.1	11
24	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. <i>American Journal of Surgical Pathology</i> , 2021, 45, 329-340.	2.1	14
25	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.	0.5	0
26	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021, 22, 872.	1.2	13
27	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.	2.4	5
28	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.	4.1	191
29	Two of a kind: transmissible Schwann cell cancers in the endangered Tasmanian devil ( <i>Sarcophilus</i> ). <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005645.	0.5	17
30	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.	0.5	17
31	Genetic Characterization of Pediatric Sarcomas by Targeted RNA Sequencing. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 1238-1245.	1.2	9
32	Sequence analysis in <i>Bos taurus</i> reveals pervasiveness of X-chromosome arms races in mammalian lineages. <i>Genome Research</i> , 2020, 30, 1716-1726.	2.4	29
33	Long non-coding RNA <i>RAMS11</i> promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020, 11, 2156.	5.8	83
34	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.	0.5	15
35	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.	0.5	4
36	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	4.7	41

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37	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. <i>Neurology: Genetics</i> , 2020, 6, e460.	0.9	26
38	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, 913.	5.8	66
39	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.	0.4	4
40	The Genotypic and Phenotypic Spectrum of <i>BICD2</i> Variants in Spinal Muscular Atrophy. <i>Annals of Neurology</i> , 2020, 87, 487-496.	2.8	18
41	<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.	1.7	9
42	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.	1.1	11
43	Mutations in <i>PLS1</i> , encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. <i>Human Mutation</i> , 2019, 40, 2286-2295.	1.1	23
44	<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, .	1.0	14
45	Expansion of B4GALT7 linkeropathy phenotype to include perinatal lethal skeletal dysplasia. <i>European Journal of Human Genetics</i> , 2019, 27, 1569-1577.	1.4	10
46	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	13.7	161
47	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019, 18, 1-10.	1.9	6
48	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	3.8	71
49	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. <i>Molecular Cancer Research</i> , 2019, 17, 895-906.	1.5	40
50	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.	0.7	12
51	Novel in-frame FLNB deletion causes Larsen syndrome in a three-generation pedigree. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004176.	0.5	1
52	Long-read sequence and assembly of segmental duplications. <i>Nature Methods</i> , 2019, 16, 88-94.	9.0	139
53	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.	1.6	43
54	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	13.5	364

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55	Genome sequencing identifies somatic BRAF duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. Journal of Physical Education and Sports Management, 2018, 4, a002618.	0.5	7
56	Recurrent structural variation, clustered sites of selection, and disease risk for the complement factor H ( <i>CFH</i> ) gene family. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4433-E4442.	3.3	43
57	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
58	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
59	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
60	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
61	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
62	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
63	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
64	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
65	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
66	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
67	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
68	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
69	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
70	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
71	A de novo nonsense mutation in <i>ASXL3</i> shared by siblings with Bainbridge-Ropers syndrome. Journal of Physical Education and Sports Management, 2018, 4, a002410.	0.5	29
72	Improving eukaryotic genome annotation using single molecule mRNA sequencing. BMC Genomics, 2018, 19, 172.	1.2	17

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73	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
74	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.	2.9	284
75	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.	7.7	400
76	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
77	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
78	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.	0.8	13
79	Patient stratification into robust cancer-cell intrinsic subtypes from colorectal cancer biopsies may inform prospective clinical trials. <i>European Journal of Surgical Oncology</i> , 2018, 44, S49.	0.5	0
80	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
81	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. <i>New England Journal of Medicine</i> , 2018, 379, 2330-2341.	13.9	322
82	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3787.	5.8	112
83	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	5.8	89
84	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.	0.5	14
85	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
86	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.	2.2	37
87	Cleavage-Independent HIV-1 Trimers From CHO Cell Lines Elicit Robust Autologous Tier 2 Neutralizing Antibodies. <i>Frontiers in Immunology</i> , 2018, 9, 1116.	2.2	27
88	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	7.7	106
89	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	6.0	304
90	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017, 49, 387-394.	9.4	147

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91	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	9.4	460
92	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017, , 1-14.	16.4	6
93	CpG Island Hypermethylation Mediated by DNMT3A Is a Consequence of AML Progression. <i>Cell</i> , 2017, 168, 801-816.e13.	13.5	177
94	The evolution and population diversity of human-specific segmental duplications. <i>Nature Ecology and Evolution</i> , 2017, 1, 69.	3.4	123
95	Mutational landscape and response are conserved in peripheral blood of AML and MDS patients during decitabine therapy. <i>Blood</i> , 2017, 129, 1397-1401.	0.6	24
96	Real-Time Electronic Tracking of Diarrheal Episodes and Laxative Therapy Enables Verification of <i>Clostridium difficile</i> Clinical Testing Criteria and Reduction of <i>Clostridium difficile</i> Infection Rates. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1276-1284.	1.8	69
97	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.	2.4	728
98	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017, 94, 550-568.e10.	3.8	222
99	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 2017, 8, 15451.	5.8	216
100	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	9.4	107
101	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	9.4	57
102	Orthotopic patient-derived xenografts of paediatric solid tumours. <i>Nature</i> , 2017, 549, 96-100.	13.7	223
103	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.2	9
104	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
105	Dynamic changes in the clonal structure of MDS and AML in response to epigenetic therapy. <i>Leukemia</i> , 2017, 31, 872-881.	3.3	87
106	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017, 27, 677-685.	2.4	323
107	Glutaraldehyde Cross-linking of HIV-1 Env Trimers Skews the Antibody Subclass Response in Mice. <i>Frontiers in Immunology</i> , 2017, 8, 1654.	2.2	9
108	Acute Illness Among Surfers After Exposure to Seawater in Dry- and Wet-Weather Conditions. <i>American Journal of Epidemiology</i> , 2017, 186, 866-875.	1.6	50

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109	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.	2.1	58
110	The Contribution of GWAS Loci in Familial Dyslipidemias. <i>PLoS Genetics</i> , 2016, 12, e1006078.	1.5	48
111	Tumor Evolution in Two Patients with Basal-like Breast Cancer: A Retrospective Genomics Study of Multiple Metastases. <i>PLoS Medicine</i> , 2016, 13, e1002174.	3.9	86
112	<i>IRF6</i> mutation screening in non-syndromic orofacial clefting: analysis of 1521 families. <i>Clinical Genetics</i> , 2016, 90, 28-34.	1.0	50
113	Visualizing tumor evolution with the fishplot package for R. <i>BMC Genomics</i> , 2016, 17, 880.	1.2	131
114	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <i>Scientific Reports</i> , 2016, 6, 20316.	1.6	23
115	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	6.0	368
116	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, 939-950.	6.6	85
117	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.	1.1	50
118	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	6.5	359
119	Rapid expansion of preexisting nonleukemic hematopoietic clones frequently follows induction therapy for de novo AML. <i>Blood</i> , 2016, 127, 893-897.	0.6	94
120	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016, 13, 806-807.	9.0	96
121	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	2.9	21
122	Interchromosomal core duplicons drive both evolutionary instability and disease susceptibility of the Chromosome 8p23.1 region. <i>Genome Research</i> , 2016, 26, 1453-1467.	2.4	37
123	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	2.4	95
124	Targeted sequencing informs the evaluation of normal karyotype cytopenic patients for low-grade myelodysplastic syndrome. <i>Leukemia</i> , 2016, 30, 2422-2426.	3.3	6
125	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.	1.1	22
126	<i>TP53</i> and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.	13.9	663



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127	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	9.4	231
128	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, 12997.	5.8	32
129	An HIV-1 Env Antibody Complex Focuses Antibody Responses to Conserved Neutralizing Epitopes. <i>Journal of Immunology</i> , 2016, 197, 3982-3998.	0.4	17
130	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016, 7, 12498.	5.8	69
131	The genomic landscape of core-binding factor acute myeloid leukemias. <i>Nature Genetics</i> , 2016, 48, 1551-1556.	9.4	215
132	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633.	4.7	64
133	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.	0.8	41
134	Research note: Natural environments and prescribing in England. <i>Landscape and Urban Planning</i> , 2016, 151, 103-108.	3.4	12
135	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.	0.2	44
136	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.	3.9	288
137	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, 3729-3743.	0.4	26
138	The impact of chromosomal translocation locus and fusion oncogene coding sequence in synovial sarcomagenesis. <i>Oncogene</i> , 2016, 35, 5021-5032.	2.6	36
139	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016, 26, 108-118.	2.4	120
140	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.	1.1	87
141	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.	0.8	8
142	Thermostability of Well-Ordered HIV Spikes Correlates with the Elicitation of Autologous Tier 2 Neutralizing Antibodies. <i>PLoS Pathogens</i> , 2016, 12, e1005767.	2.1	72
143	Inactivation of RASA1 promotes melanoma tumorigenesis via R-Ras activation. <i>Oncotarget</i> , 2016, 7, 23885-23896.	0.8	23
144	Abstract LB-326: Identification of novel recurrent mutations in follicular lymphoma. , 2016, , .		0

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145	Abstract 1863: Inactivation of RASA1 promotes melanoma tumorigenesis via R-Ras activation. , 2016, , .		0
146	Rare Pre-Existing MDS Subclones Contribute to Secondary AML Progression. Blood, 2016, 128, 959-959.	0.6	12
147	Dynamic Changes in MDS Clonal Architecture Following Allogeneic Stem Cell Transplant. Blood, 2016, 128, 5506-5506.	0.6	0
148	Clonal Evolution of Acute Myeloid Leukemia Following Allogeneic Stem Cell Transplantation. Blood, 2016, 128, 1528-1528.	0.6	4
149	DNMT3A-Dependent DNA Methylation May Act As a Tumor Suppressor-Not a Tumor Promoter-during AML Progression. Blood, 2016, 128, 1050-1050.	0.6	3
150	North Carolina macular dystrophy (MCDR1) caused by a novel tandem duplication of the gene. Molecular Vision, 2016, 22, 1239-1247.	1.1	28
151	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	2.9	174
152	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood, 2015, 126, 2484-2490.	0.6	207
153	Genetic Heterogeneity of Induced Pluripotent Stem Cells: Results from 24 Clones Derived from a Single C57BL/6 Mouse. PLoS ONE, 2015, 10, e0120585.	1.1	12
154	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
155	The Effects of the Endocannabinoids Anandamide and 2-Arachidonoylglycerol on Human Osteoblast Proliferation and Differentiation. PLoS ONE, 2015, 10, e0136546.	1.1	23
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