

# David A Wheeler

## List of Publications by Year in descending order

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209  
papers

78,161  
citations

949

109  
h-index

1446

208  
g-index

245  
all docs

245  
docs citations

245  
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	indelPost: harmonizing ambiguities in simple and complex indel alignments. <i>Bioinformatics</i> , 2022, 38, 549-551.	5.0	9
2	A <i>CTNNB1</i> -altered medulloblastoma shows the immunophenotypic, DNA methylation and transcriptomic profiles of SHH-activated, and not WNT-activated, medulloblastoma. <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	3.4	1
3	Consensus subtypes of hepatocellular carcinoma associated with clinical outcomes and genomic phenotypes. <i>Hepatology</i> , 2022, 76, 1634-1648.	11.6	14
4	RNAseqCNV: analysis of large-scale copy number variations from RNA-seq data. <i>Leukemia</i> , 2022, 36, 1492-1498.	8.1	22
5	Infectious Diseases/Human Immunodeficiency Virus Physician Ambassadors: Advancing Policy to Improve Health. <i>Clinical Infectious Diseases</i> , 2021, 73, e2243-e2250.	5.6	1
6	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. <i>Journal of the National Cancer Institute</i> , 2021, 113, 27-37.	5.1	21
7	The Proximal Airway Is a Reservoir for Adaptive Immunologic Memory in Idiopathic Subglottic Stenosis. <i>Laryngoscope</i> , 2021, 131, 610-617.	1.6	17
8	Multiomic analysis identifies natural inpatient temporal variability and changes in response to systemic corticosteroid therapy in chronic rhinosinusitis. <i>Immunity, Inflammation and Disease</i> , 2021, 9, 90-107.	2.5	6
9	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	33.4	66
10	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, .	4.5	28
11	Responses of <i>Chlamydomonas reinhardtii</i> during the transition from P-deficient to P-sufficient growth (the P-overplus response): The roles of the vacuolar transport chaperones and polyphosphate synthesis. <i>Journal of Phycology</i> , 2021, 57, 988-1003.	3.4	23
12	Conservation genomics of a critically endangered brown seaweed. <i>Journal of Phycology</i> , 2021, 57, 1345-1355.	3.4	4
13	Novel Anaplastic Thyroid Cancer PDXs and Cell Lines: Expanding Preclinical Models of Genetic Diversity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e4652-e4665.	4.4	8
14	A High-throughput Approach to Identify Effective Systemic Agents for the Treatment of Anaplastic Thyroid Carcinoma. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 2962-2978.	4.4	10
15	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. <i>Cancer Discovery</i> , 2021, 11, 3008-3027.	26.4	122
16	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
17	Differences in Breast and Colorectal Cancer Screening Adherence Among Women Residing in Urban and Rural Communities in the United States. <i>JAMA Network Open</i> , 2021, 4, e2128000.	7.2	47
18	ID/HIV Physician Ambassadors: Advancing Policy to Improve Health. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2021, 10, 432-439.	1.5	3

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19	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , 2020, 11, .	14.1	57
20	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. <i>Acta Neuropathologica</i> , 2020, 140, 963-965.	7.9	17
21	Identification of novel fusion transcripts in meningioma. <i>Journal of Neuro-Oncology</i> , 2020, 149, 219-230.	2.7	7
22	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, .	14.1	33
23	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. <i>Cancer Research</i> , 2020, 80, 3810-3819.	0.6	22
24	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	35.1	289
25	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, .	14.1	74
26	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	40.1	2,047
27	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	40.1	383
28	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. <i>Cancer Research</i> , 2020, 80, 2663-2675.	0.6	65
29	An enhanced genetic model of colorectal cancer progression history. <i>Genome Biology</i> , 2019, 20, .	8.4	31
30	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	6.4	407
31	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019, 29, 1675-1689.e9.	6.4	112
32	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	35.1	438
33	Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21715-21726.	7.7	126
34	Framework for microRNA variant annotation and prioritization using human population and disease datasets. <i>Human Mutation</i> , 2019, 40, 73-89.	4.1	15
35	How Do You Measure Up: Quality Measurement for Improving Patient Care and Establishing the Value of Infectious Diseases Specialists. <i>Clinical Infectious Diseases</i> , 2019, 68, 1946-1951.	5.6	6
36	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	26.4	375

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37	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	35.1	102
38	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	35.1	2,212
39	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	35.1	1,486
40	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.	35.1	1,566
41	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	35.1	256
42	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	35.1	1,407
43	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	35.1	2,023
44	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	35.1	568
45	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	303
46	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	401
47	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	534
48	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	668
49	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	22.7	3,724
50	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	106
51	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	752
52	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	179
53	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.0	518
54	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	33.4	669

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55	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	33.4	424
56	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- $\beta$ Pathway. <i>Gastroenterology</i> , 2018, 154, 195-210.	1.0	114
57	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.0	138
58	TBIO-20. CLINICAL TUMOR WHOLE EXOME SEQUENCING FOR PEDIATRIC NEURO-ONCOLOGY PATIENTS – RESULTS FROM THE BAYLOR ADVANCING SEQUENCING IN CHILDHOOD CANCER CARE (BASIC3) CLINICAL SEQUENCING STUDY. <i>Neuro-Oncology</i> , 2018, 20, i184-i184.	0.9	0
59	National Cancer Institute Biospecimen Evidence-Based Practices: Harmonizing Procedures for Nucleic Acid Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. <i>Biopreservation and Biobanking</i> , 2018, 16, 247-250.	1.5	8
60	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2018, 13, 1483-1495.	1.1	24
61	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	331
62	Whole Exome Analysis Reveals Key Genomic Differences between Sporadic and Endemic Pediatric Burkitt Lymphoma. <i>Blood</i> , 2018, 132, 4117-4117.	1.0	0
63	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. <i>Nature Communications</i> , 2017, 8, .	14.1	82
64	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2017, , nlw116.	1.9	47
65	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	40.1	694
66	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	35.1	1,756
67	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. <i>European Urology</i> , 2017, 72, 641-649.	1.4	176
68	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	440
69	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. <i>Nature Genetics</i> , 2017, 49, 1487-1494.	16.3	257
70	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	33.4	1,371
71	Renal cell carcinoma harboring somatic <i>TSC2</i> mutations in a child with methylmalonic acidemia. <i>Pediatric Blood and Cancer</i> , 2017, 64, .	1.5	10
72	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. <i>Hepatology</i> , 2017, 65, 104-121.	11.6	168

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73	SVachra: a tool to identify genomic structural variation in mate pair sequencing data containing inward and outward facing reads. BMC Genomics, 2017, 18, .	3.2	7
74	Non-malignant respiratory epithelial cells preferentially proliferate from resected non-small cell lung cancer specimens cultured under conditionally reprogrammed conditions. Oncotarget, 2017, 8, 11114-11126.	1.7	22
75	Activating <i>MAPK1</i> (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. Oncotarget, 2017, 8, 46065-46070.	1.7	30
76	Pharmacogenetic characterization of naturally occurring germline NT5C1A variants to chemotherapeutic nucleoside analogs. Pharmacogenetics and Genomics, 2016, 26, 271-279.	1.3	1
77	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. Blood, 2016, 128, 2533-2537.	1.0	132
78	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. Nature Communications, 2016, 7, .	14.1	120
79	Coexistence of gain-of-function JAK2 germ line mutations with JAK2V617F in polycythemia vera. Blood, 2016, 128, 2266-2270.	1.0	22
80	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. Experimental Hematology, 2016, 44, 740-744.	0.4	47
81	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	33.4	448
82	Significance of <i>TP53</i> Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591.	6.4	84
83	Integrated tumor and germline whole-exome sequencing identifies mutations in MAPK and PI3K pathway genes in an adolescent with rosette-forming glioneuronal tumor of the fourth ventricle. Journal of Physical Education and Sports Management, 2016, 2, a001057.	1.4	24
84	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. Genome Biology, 2016, 17, .	8.4	177
85	An open access pilot freely sharing cancer genomic data from participants in Texas. Scientific Data, 2016, 3, .	6.4	19
86	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	6.4	283
87	Acquired uniparental disomy of chromosome 9p in hematologic malignancies. Experimental Hematology, 2016, 44, 644-652.	0.4	10
88	ITD assembler: an algorithm for internal tandem duplication discovery from short-read sequencing data. BMC Bioinformatics, 2016, 17, .	3.3	14
89	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. JAMA Oncology, 2016, 2, 616.	13.6	391
90	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	35.1	293

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91	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	6.4	108
92	Clonal Dynamics In Vivo of Virus Integration Sites of T Cells Expressing a Safety Switch. <i>Molecular Therapy</i> , 2016, 24, 736-745.	10.5	11
93	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2016, 11, 52-61.	1.1	26
94	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	40.1	2,593
95	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. <i>Cancer Research</i> , 2016, 76, 2197-2205.	0.6	128
96	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	25.5	1,017
97	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. <i>Journal of Clinical Investigation</i> , 2016, 126, 2881-2892.	9.1	67
98	Integrated Genomic Analysis of Down Syndrome Acute Lymphoblastic Leukemia Reveals Recurrent Cancer Gene Alterations and Evidence of Frequent Subclonal Driver Events. <i>Blood</i> , 2016, 128, 4083-4083.	1.0	0
99	Initial testing (stage 1) of the PARP inhibitor BMN 673 by the pediatric preclinical testing program: <i>BRCA1</i> mutation predicts exceptional <i>in vivo</i> response to BMN 673. <i>Pediatric Blood and Cancer</i> , 2015, 62, 91-98.	1.5	68
100	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, .	14.1	221
101	MLL1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. <i>Nature Communications</i> , 2015, 6, .	14.1	69
102	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. <i>Cancer Cell</i> , 2015, 27, 286-297.	33.4	226
103	Identifying gene disruptions in novel balanced de novo constitutional translocations in childhood cancer patients by whole-genome sequencing. <i>Genetics in Medicine</i> , 2015, 17, 831-835.	2.3	11
104	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2015, 6, .	14.1	274
105	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. <i>Blood</i> , 2015, 125, 629-638.	1.0	198
106	Assessing structural variation in a personal genome towards a human reference diploid genome. <i>BMC Genomics</i> , 2015, 16, .	3.2	117
107	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, .	14.1	126
108	Genomic profiling of SÃ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. <i>Nature Genetics</i> , 2015, 47, 1426-1434.	16.3	273

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109	Comparison of Positive End-Expiratory Pressure of 8 versus 5 cm H <sub>2</sub> O on Outcome After Cardiac Operations. <i>Journal of Intensive Care Medicine</i> , 2015, 30, 338-343.	2.4	7
110	Abstract 2976: Comprehensive Pan-Genomic characterization of adrenocortical carcinoma. <i>Cancer Research</i> , 2015, 75, 2976-2976.	0.6	2
111	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. <i>Genome Biology</i> , 2014, 15, .	8.4	48
112	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 6582-6592.	6.4	492
113	Heterochromatin protein 1 expression is reduced in human thyroid malignancy. <i>Laboratory Investigation</i> , 2014, 94, 788-795.	3.5	7
114	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	35.1	2,295
115	Effects of TP53 mutational status on gene expression patterns across 10 human cancer types. <i>Journal of Pathology</i> , 2014, 232, 522-533.	5.2	69
116	Genomic Sequencing for Cancer Diagnosis and Therapy. <i>Annual Review of Medicine</i> , 2014, 65, 33-48.	20.4	36
117	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , 2014, 46, 1267-1273.	16.3	611
118	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, 15544-15549.	7.7	307
119	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3' UTR landscape across seven tumour types. <i>Nature Communications</i> , 2014, 5, .	14.1	384
120	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014, 24, 1740-1750.	4.6	219
121	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	33.4	632
122	Squamous Cell Carcinoma of the Oral Tongue in Young Non-Smokers Is Genomically Similar to Tumors in Older Smokers. <i>Clinical Cancer Research</i> , 2014, 20, 3842-3848.	6.4	125
123	Case series of patients with acute myeloid leukemia receiving hypomethylation therapy and retrospectively found to have IDH1 or IDH2 mutations. <i>Leukemia and Lymphoma</i> , 2014, 55, 1431-1434.	1.6	4
124	Novel somatic and germline mutations in intracranial germ cell tumours. <i>Nature</i> , 2014, 511, 241-245.	40.1	185
125	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. <i>Blood</i> , 2014, 124, 3007-3015.	1.0	358
126	BCOR and CCNB3 fusions are frequent in undifferentiated sarcomas of male children. <i>Modern Pathology</i> , 2014, 28, 575-586.	5.0	123

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127	Genomic Characterization of Sinonasal Undifferentiated Carcinoma. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , 2014, 75, .	1.2	1
128	Mixed Phenotype Acute Leukemia (MPAL) Has a High Frequency of Mutations in Epigenetic Regulatory Genes: Results from Whole Exome Sequencing. <i>Blood</i> , 2014, 124, 3560-3560.	1.0	3
129	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1226-1231.	16.3	264
130	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. <i>Nature Communications</i> , 2013, 4, .	14.1	95
131	Identification of <i>TP53</i> as an acute lymphocytic leukemia susceptibility gene through exome sequencing. <i>Pediatric Blood and Cancer</i> , 2013, 60, .	1.5	44
132	<i>MLH1</i> silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. <i>Journal of Pathology</i> , 2013, 229, 99-110.	5.2	59
133	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775.	16.3	133
134	From human genome to cancer genome: The first decade. <i>Genome Research</i> , 2013, 23, 1054-1062.	4.6	123
135	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. <i>Cancer Discovery</i> , 2013, 3, 770-781.	26.4	463
136	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. <i>Blood</i> , 2013, 122, 824-824.	1.0	4
137	Whole Exome Sequencing and Analysis Of Mutations In SÅ©zary Syndrome. <i>Blood</i> , 2013, 122, 2558-2558.	1.0	0
138	Molecular Characterization Of Polycythemia Vera Based On The Relationship Of JAK2V617F and 9pUPD. <i>Blood</i> , 2013, 122, 1607-1607.	1.0	0
139	Dietary Determinants Of The White Blood Cell Count. <i>Blood</i> , 2013, 122, 1705-1705.	1.0	0
140	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	40.1	1,657
141	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	2.5	98
142	Identification of Novel Somatic Mutations, Regions of Recurrent Loss of Heterozygosity (LOH) and Significant Clonal Evolution From Diagnosis to Relapse in Childhood AML Determined by Exome Capture Sequencing – an NCI/COG Target AML Study. <i>Blood</i> , 2012, 120, 123-123.	1.0	3
143	Genome Wide Promoter Methylation Patterns Predict AML Subtype Outcomes and Identify Novel Pathways Characterizing Diagnostic and Relapsed Disease in Children. <i>Blood</i> , 2012, 120, 1287-1287.	1.0	3
144	Whole Genome Sequencing of Four CD34+-Derived iPSC Polycythemia Vera Clones From a Single Female. <i>Blood</i> , 2012, 120, 1755-1755.	1.0	2

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145	Whole Exome Sequencing of Polycythemia Vera Reveals Novel Recurrent Somatic and Germline Variation. <i>Blood</i> , 2012, 120, 705-705.	1.0	3
146	Clinically Significant Mutations, Deletions and Translocations Involving ETV6 Identified by Whole Genome and Whole Exome Sequencing; Report From NCI/COG Target AML Initiative. <i>Blood</i> , 2012, 120, 125-125.	1.0	0
147	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. <i>Cell</i> , 2011, 144, 703-718.	35.1	236
148	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. <i>Cell</i> , 2011, 145, 1036-1048.	35.1	255
149	Identification of genetic susceptibility to childhood cancer through analysis of genes in parallel. <i>Cancer Genetics</i> , 2011, 204, 19-25.	0.5	12
150	Resequencing of <i>IRS2</i> reveals rare variants for obesity but not fasting glucose homeostasis in Hispanic children. <i>Physiological Genomics</i> , 2011, 43, 1029-1037.	2.5	6
151	High incidence of <i>IDH</i> mutations in acute myeloid leukaemia with cuplike nuclei. <i>British Journal of Haematology</i> , 2011, 155, 125-128.	2.7	13
152	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. <i>Nature Genetics</i> , 2011, 43, 189-196.	16.3	286
153	A Primer on a Hepatocellular Carcinoma Bioresource Bank Using the Cancer Genome Atlas Guidelines: Practical Issues and Pitfalls. <i>World Journal of Surgery</i> , 2011, 35, 1732-1737.	1.9	2
154	Building a Comprehensive Genomic Program for Hepatocellular Carcinoma. <i>World Journal of Surgery</i> , 2011, 35, 1746-1750.	1.9	9
155	Overview of the Development of Personalized Genomic Medicine and Surgery. <i>World Journal of Surgery</i> , 2011, 35, 1693-1699.	1.9	16
156	Characterization of single-nucleotide variation in Indian-origin rhesus macaques ( <i>Macaca mulatta</i> ). <i>BMC Genomics</i> , 2011, 12, .	3.2	28
157	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. <i>Human Mutation</i> , 2011, 32, 661-668.	4.1	175
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