David A Wheeler

List of Publications by Year
in descending order

Version: 2024-02-01

243 papers	129,066 citations	1229 113 h-index	1238 233 g-index
254 all docs	254 docs citations	254 times ranked	140986 citing authors

#	Article	IF	Citations
1	indelPost: harmonizing ambiguities in simple and complex indel alignments. Bioinformatics, 2022, 38, 549-551.	1.8	10
2	The mitochondrial and chloroplast genomes of the kelp, Ecklonia radiata. Aquatic Botany, 2022, 178, 103485.	0.8	1
3	Abstract PD15-03: Overlapping molecular features (proliferation, immune signatures) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 6 Cancer Research, 2022, 82, PD15-03-PD15-03.	0.4	0
4	A CTNNB1â€altered medulloblastoma shows the immunophenotypic, DNA methylation and transcriptomic profiles of SHHâ€activated, and not WNTâ€activated, medulloblastoma. Neuropathology and Applied Neurobiology, 2022, 48, e12815.	1.8	0
5	Consensus subtypes of hepatocellular carcinoma associated with clinical outcomes and genomic phenotypes. Hepatology, 2022, 76, 1634-1648.	3.6	10
6	RNAseqCNV: analysis of large-scale copy number variations from RNA-seq data. Leukemia, 2022, 36, 1492-1498.	3.3	16
7	Consensus subtypes associated with clinical outcomes, response to therapies, and multiple biomarkers in early-stage hepatocellular carcinoma. International Journal of Surgery, 2022, 100, 106365.	1.1	0
8	Infectious Diseases/Human Immunodeficiency Virus Physician Ambassadors: Advancing Policy to Improve Health. Clinical Infectious Diseases, 2021, 73, e2243-e2250.	2.9	1
9	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. Journal of the National Cancer Institute, 2021, 113, 27-37.	3.0	17
10	The Proximal Airway Is a Reservoir for Adaptive Immunologic Memory in Idiopathic Subglottic Stenosis. Laryngoscope, 2021, 131, 610-617.	1.1	12
11	Multiomic analysis identifies natural intrapatient temporal variability and changes in response to systemic corticosteroid therapy in chronic rhinosinusitis. Immunity, Inflammation and Disease, 2021, 9, 90-107.	1.3	5
12	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. Cancer Cell, 2021, 39, 38-53.e7.	7.7	65
13	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
14	TOR targets an RNA processing network to regulate facultative heterochromatin, developmental gene expression and cell proliferation. Nature Cell Biology, 2021, 23, 243-256.	4.6	20
15	Responses of Chlamydomonas reinhardtii during the transition from Pâ€deficient to Pâ€sufficient growth (the Pâ€overplus response): The roles of the vacuolar transport chaperones and polyphosphate synthesis. Journal of Phycology, 2021, 57, 988-1003.	1.0	15
16	Conservation genomics of a critically endangered brown seaweed. Journal of Phycology, 2021, 57, 1345-1355.	1.0	4
17	Genotypeâ€“Environment mismatch of kelp forests under climate change. Molecular Ecology, 2021, 30, 3730-3746.	2.0	39
18	Novel Anaplastic Thyroid Cancer PDXs and Cell Lines: Expanding Preclinical Models of Genetic Diversity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e4652-e4665.	1.8	8

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19	A High-throughput Approach to Identify Effective Systemic Agents for the Treatment of Anaplastic Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 2962-2978.	1.8	10
20	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	7.7	88
21	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
22	Differences in Breast and Colorectal Cancer Screening Adherence Among Women Residing in Urban and Rural Communities in the United States. JAMA Network Open, 2021, 4, e2128000.	2.8	34
23	ID/HIV Physician Ambassadors: Advancing Policy to Improve Health. Journal of the Pediatric Infectious Diseases Society, 2021, 10, 432-439.	0.6	3
24	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	5.8	55
25	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. Acta Neuropathologica, 2020, 140, 963-965.	3.9	14
26	Identification of novel fusion transcripts in meningioma. Journal of Neuro-Oncology, 2020, 149, 219-230.	1.4	6
27	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
28	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. Cancer Research, 2020, 80, 3810-3819.	0.4	18
29	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
30	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
31	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
32	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
33	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. Cancer Research, 2020, 80, 2663-2675.	0.4	55
34	An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168.	3.8	34
35	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5.	2.9	382
36	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9.	2.9	103

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37	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
38	Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21715-21726.	3.3	122
39	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	1.1	18
40	How Do You Measure Up: Quality Measurement for Improving Patient Care and Establishing the Value of Infectious Diseases Specialists. Clinical Infectious Diseases, 2019, 68, 1946-1951.	2.9	4
41	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	7.7	367
42	Iron homeostasis regulates facultative heterochromatin assembly in adaptive genome control. Nature Structural and Molecular Biology, 2018, 25, 372-383.	3.6	28
43	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. Cell, 2018, 173, 864-878.e29.	13.5	102
44	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
45	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
46	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
47	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
48	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
49	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
50	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
51	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
52	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
53	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
54	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

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55	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
56	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
57	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
58	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
59	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
60	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
61	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
62	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor-Î² Pathway. Gastroenterology, 2018, 154, 195-210.	0.6	105
63	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
64	TBIO-20. CLINICAL TUMOR WHOLE EXOME SEQUENCING FOR PEDIATRIC NEURO-ONCOLOGY PATIENTS â€“ RESULTS FROM THE BAYLOR ADVANCING SEQUENCING IN CHILDHOOD CANCER CARE (BASIC3) CLINICAL SEQUENCING STUDY. Neuro-Oncology, 2018, 20, i184-i184.	0.6	0
65	National Cancer Institute Biospecimen Evidence-Based Practices: Harmonizing Procedures for Nucleic Acid Extraction from Formalin-Fixed, Paraffin-Embedded Tissue. Biopreservation and Biobanking, 2018, 16, 247-250.	0.5	11
66	Gene expression profiling and immune cell-type deconvolution highlight robust disease progression and survival markers in multiple cohorts of CTCL patients. OncoImmunology, 2018, 7, e1467856.	2.1	24
67	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. Journal of Thoracic Oncology, 2018, 13, 1483-1495.	0.5	22
68	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
69	Whole Exome Analysis Reveals Key Genomic Differences between Sporadic and Endemic Pediatric Burkitt Lymphoma. Blood, 2018, 132, 4117-4117.	0.6	0
70	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. Nature Communications, 2017, 8, 14098.	5.8	80
71	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. Journal of Neuropathology and Experimental Neurology, 2017, 76, nlw116.	0.9	54
72	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716

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73	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
74	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2017, 72, 641-649.	0.9	170
75	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
76	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	9.4	255
77	Effect of Oral Methylprednisolone on Clinical Outcomes in Patients With IgA Nephropathy. JAMA - Journal of the American Medical Association, 2017, 318, 432.	3.8	376
78	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
79	Renal cell carcinoma harboring somatic TSC2 mutations in a child with methylmalonic acidemia. Pediatric Blood and Cancer, 2017, 64, e26286.	0.8	9
80	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. Hepatology, 2017, 65, 104-121.	3.6	192
81	SVachra: a tool to identify genomic structural variation in mate pair sequencing data containing inward and outward facing reads. BMC Genomics, 2017, 18, 691.	1.2	7
82	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.	0.8	22
83	Activating MAPK1 (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. Oncotarget, 2017, 8, 46065-46070.	0.8	24
84	Pharmacogenetic characterization of naturally occurring germline NT5C1A variants to chemotherapeutic nucleoside analogs. Pharmacogenetics and Genomics, 2016, 26, 271-279.	0.7	1
85	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. Blood, 2016, 128, 2533-2537.	0.6	122
86	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. Nature Communications, 2016, 7, 12601.	5.8	123
87	Coexistence of gain-of-function JAK2 germ line mutations with JAK2V617F in polycythemia vera. Blood, 2016, 128, 2266-2270.	0.6	21
88	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. Experimental Hematology, 2016, 44, 740-744.	0.2	48
89	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
90	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591.	3.2	82

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91	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.	0.5	21
92	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, 178.	3.8	231
93	An open access pilot freely sharing cancer genomic data from participants in Texas. Scientific Data, 2016, 3, 160010.	2.4	19
94	SV-STAT accurately detects structural variation via alignment to reference-based assemblies. Source Code for Biology and Medicine, 2016, 11, 8.	1.7	3
95	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	2.9	298
96	Acquired uniparental disomy of chromosome 9p in hematologic malignancies. Experimental Hematology, 2016, 44, 644-652.	0.2	12
97	ITD assembler: an algorithm for internal tandem duplication discovery from short-read sequencing data. BMC Bioinformatics, 2016, 17, 188.	1.2	16
98	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. JAMA Oncology, 2016, 2, 616.	3.4	378
99	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	13.5	363
100	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	2.9	107
101	Clonal Dynamics In Vivo of Virus Integration Sites of T Cells Expressing a Safety Switch. Molecular Therapy, 2016, 24, 736-745.	3.7	11
102	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. Journal of Thoracic Oncology, 2016, 11, 52-61.	0.5	27
103	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
104	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. Cancer Research, 2016, 76, 2197-2205.	0.4	133
105	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
106	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. Journal of Clinical Investigation, 2016, 126, 2881-2892.	3.9	65
107	Integrated Genomic Analysis of Down Syndrome Acute Lymphoblastic Leukemia Reveals Recurrent Cancer Gene Alterations and Evidence of Frequent Subclonal Driver Events. Blood, 2016, 128, 4083-4083.	0.6	0
108	Initial testing (stage 1) of the PARP inhibitor BMN 673 by the pediatric preclinical testing program: PALB2 mutation predicts exceptional in vivo response to BMN 673. Pediatric Blood and Cancer, 2015, 62, 91-98.	0.8	65

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109	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
110	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013.	5.8	64
111	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	7.7	244
112	Identifying gene disruptions in novel balanced de novo constitutional translocations in childhood cancer patients by whole-genome sequencing. Genetics in Medicine, 2015, 17, 831-835.	1.1	7
113	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	5.8	281
114	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. Blood, 2015, 125, 629-638.	0.6	206
115	Assessing structural variation in a personal genomeâ€"towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	1.2	153
116	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. Nature Communications, 2015, 6, 8891.	5.8	126
117	Genomic profiling of SÃ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. Nature Genetics, 2015, 47, 1426-1434.	9.4	276
118	Comparison of Positive End-Expiratory Pressure of 8 versus 5 cm H₂O on Outcome After Cardiac Operations. Journal of Intensive Care Medicine, 2015, 30, 338-343.	1.3	7
119	BCORâ€"CCNB3 fusions are frequent in undifferentiated sarcomas of male children. Modern Pathology, 2015, 28, 575-586.	2.9	122
120	Abstract 2976: Comprehensive Pan-Genomic characterization of adrenocortical carcinoma. , 2015, , .		2
121	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. Genome Biology, 2014, 15, 443.	3.8	59
122	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. Clinical Cancer Research, 2014, 20, 6582-6592.	3.2	493
123	Heterochromatin protein 1 expression is reduced in human thyroid malignancy. Laboratory Investigation, 2014, 94, 788-795.	1.7	7
124	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
125	Effects of <scp>TP53</scp> mutational status on gene expression patterns across 10 human cancer types. Journal of Pathology, 2014, 232, 522-533.	2.1	65
126	The relationship of JAK2V617F and acquired UPD at chromosome 9p in polycythemia vera. Leukemia, 2014, 28, 938-941.	3.3	18

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127	Genomic Sequencing for Cancer Diagnosis and Therapy. Annual Review of Medicine, 2014, 65, 33-48.	5.0	35
128	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. Nature Genetics, 2014, 46, 1267-1273.	9.4	655
129	Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. Leukemia, 2014, 28, 935-938.	3.3	22
130	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	3.3	317
131	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3â€²-UTR landscape across seven tumour types. Nature Communications, 2014, 5, 5274.	5.8	430
132	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750.	2.4	244
133	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
134	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
135	Squamous Cell Carcinoma of the Oral Tongue in Young Non-Smokers Is Genomically Similar to Tumors in Older Smokers. Clinical Cancer Research, 2014, 20, 3842-3848.	3.2	124
136	Case series of patients with acute myeloid leukemia receiving hypomethylation therapy and retrospectively found to haveIDH1orIDH2mutations. Leukemia and Lymphoma, 2014, 55, 1431-1434.	0.6	4
137	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	13.7	181
138	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. Blood, 2014, 124, 3007-3015.	0.6	352
139	Genomic Characterization of Sinonasal Undifferentiated Carcinoma. Journal of Neurological Surgery, Part B: Skull Base, 2014, 75, .	0.4	1
140	Mixed Phenotype Acute Leukemia (MPAL) Has a High Frequency of Mutations in Epigenetic Regulatory Genes: Results from Whole Exome Sequencing. Blood, 2014, 124, 3560-3560.	0.6	3
141	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	9.4	270
142	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. Nature Communications, 2013, 4, 2730.	5.8	104
143	Identification of TP53 as an acute lymphocytic leukemia susceptibility gene through exome sequencing. Pediatric Blood and Cancer, 2013, 60, E1-3.	0.8	44
144	MLH1â€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	2.1	67

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145	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
146	Deep resequencing and association analysis of schizophrenia candidate genes. Molecular Psychiatry, 2013, 18, 138-140.	4.1	15
147	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	9.4	176
148	From human genome to cancer genome: The first decade. Genome Research, 2013, 23, 1054-1062.	2.4	132
149	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	13.7	2,839
150	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. Cancer Discovery, 2013, 3, 770-781.	7.7	484
151	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. Blood, 2013, 122, 824-824.	0.6	4
152	Whole Exome Sequencing and Analysis Of Mutations In SÃ©zary Syndrome. Blood, 2013, 122, 2558-2558.	0.6	0
153	Molecular Characterization Of Polycythemia Vera Based On The Relationship Of JAK2V617F and 9pUPD. Blood, 2013, 122, 1607-1607.	0.6	0
154	Dietary Determinants Of The White Blood Cell Count. Blood, 2013, 122, 1705-1705.	0.6	0
155	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
156	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
157	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	13.7	3,483
158	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.	1.1	104
159	Landscape of Somatic Retrotransposition in Human Cancers. Science, 2012, 337, 967-971.	6.0	631
160	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 â€“ an NCI/COG Target AML Study. Blood, 2012, 120, 123-123.	0.6	2
161	Genome Wide Promoter Methylation Patterns Predict AML Subtype Outcomes and Identify Novel Pathways Characterizing Diagnostic and Relapsed Disease in Children. Blood, 2012, 120, 1287-1287.	0.6	2
162	Whole Genome Sequencing of Four CD34+-Derived iPSC Polycythemia Vera Clones From a Single Female. Blood, 2012, 120, 1755-1755.	0.6	2

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163	Whole Exome Sequencing of Polycythemia Vera Reveals Novel Recurrent Somatic and Germline Variation. Blood, 2012, 120, 705-705.	0.6	3
164	Clinically Significant Mutations, Deletions and Translocations Involving ETV6 Identified by Whole Genome and Whole Exome Sequencing; Report From NCI/COG Target AML Initiative. Blood, 2012, 120, 125-125.	0.6	0
165	Several Grassland Soil Nematode Species Are Insensitive to RNA-Mediated Interference. Journal of Nematology, 2012, 44, 92-101.	0.4	4
166	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
167	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. Cell, 2011, 144, 703-718.	13.5	246
168	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. Cell, 2011, 145, 1036-1048.	13.5	274
169	Identification of genetic susceptibility to childhood cancer through analysis of genes in parallel. Cancer Genetics, 2011, 204, 19-25.	0.2	14
170	Resequencing ofIRS2reveals rare variants for obesity but not fasting glucose homeostasis in Hispanic children. Physiological Genomics, 2011, 43, 1029-1037.	1.0	6
171	High incidence of IDH mutations in acute myeloid leukaemia with cuplike nuclei. British Journal of Haematology, 2011, 155, 125-128.	1.2	16
172	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. Nature Genetics, 2011, 43, 189-196.	9.4	326
173	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in NOTCH1. Science, 2011, 333, 1154-1157.	6.0	1,568
174	A Primer on a Hepatocellular Carcinoma Bioresource Bank Using the Cancer Genome Atlas Guidelines: Practical Issues and Pitfalls. World Journal of Surgery, 2011, 35, 1732-1737.	0.8	4
175	Building a Comprehensive Genomic Program for Hepatocellular Carcinoma. World Journal of Surgery, 2011, 35, 1746-1750.	0.8	15
176	Overview of the Development of Personalized Genomic Medicine and Surgery. World Journal of Surgery, 2011, 35, 1693-1699.	0.8	18
177	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). BMC Genomics, 2011, 12, 311.	1.2	30
178	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. Human Mutation, 2011, 32, 661-668.	1.1	195
179	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1128-36.	3.3	200
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