David A Wheeler

List of Publications by Year in Descending Order

240 papers	94,994 citations	105 h-index	254 g-index
254 ext. papers	115,532 ext. citations	18.4 avg, IF	8.89 L-index

#	Paper	IF	Citations
240	The mitochondrial and chloroplast genomes of the kelp, Ecklonia radiata. *Aquatic Botany*, **2022**, 178, 103485	1.8	0
239	Abstract PD15-03: Overlapping molecular features (proliferation, immune signatures andTP53mutations) associated with palbociclib resistance inER+HER2- primary breast cancer. *Cancer Research*, **2022**, 82, PD15-03-PD15-03	10.1	
238	A CTNNB1-altered medulloblastoma shows the immunophenotypic, DNA methylation, and transcriptomic profiles of SHH-activated, and not WNT-activated, medulloblastoma.. *Neuropathology and Applied Neurobiology*, **2022**, e12815	5.2	
237	ID/HIV Physician Ambassadors: Advancing Policy to Improve Health. *Journal of the Pediatric Infectious Diseases Society*, **2021**, 10, 432-439	4.8	1
236	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	10.4	3
235	Infectious Diseases/Human Immunodeficiency Virus Physician Ambassadors: Advancing Policy to Improve Health. *Clinical Infectious Diseases*, **2021**, 73, e2243-e2250	11.6	
234	Responses of Chlamydomonas reinhardtii during the transition from P-deficient to P-sufficient growth (the P-overplus response): The roles of the vacuolar transport chaperones and polyphosphate synthesis. *Journal of Phycology*, **2021**, 57, 988-1003	3	2
233	Conservation genomics of a critically endangered brown seaweed. *Journal of Phycology*, **2021**, 57, 1345-1355	3	1
232	Genotype-Environment mismatch of kelp forests under climate change. *Molecular Ecology*, **2021**, 30, 3730-3746	5.7	7
231	Novel Anaplastic Thyroid Cancer PDXs and Cell Lines: Expanding Preclinical Models of Genetic Diversity. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, e4652-e4665	5.6	2
230	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	5.6	0
229	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. *Cancer Discovery*, **2021**,	24.4	21
228	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. *Journal of the National Cancer Institute*, **2021**, 113, 27-37	9.7	9
227	The Proximal Airway Is a Reservoir for Adaptive Immunologic Memory in Idiopathic Subglottic Stenosis. *Laryngoscope*, **2021**, 131, 610-617	3.6	3
226	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	2.4	3
225	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. *Cancer Cell*, **2021**, 39, 38-53.e7	24.3	18
224	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. *Communications Biology*, **2021**, 4, 155	6.7	11

223	TOR targets an RNA processing network to regulate facultative heterochromatin, developmental gene expression and cell proliferation. *Nature Cell Biology*, **2021**, 23, 243-256	23.4	5
222	indelPost: harmonizing ambiguities in simple and complex indel alignments. *Bioinformatics*, **2021**,	7.2	1
221	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. *Cancer Research*, **2020**, 80, 3810-3819	10.1	9
220	Proteogenomic Characterization of Endometrial Carcinoma. *Cell*, **2020**, 180, 729-748.e26	56.2	122
219	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
218	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
217	Analyses of non-coding somatic drivers in 2,658´cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
216	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. *Nature Communications*, **2020**, 11, 3644	17.4	16
215	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. *Acta Neuropathologica*, **2020**, 140, 963-965	14.3	8
214	Identification of novel fusion transcripts in meningioma. *Journal of Neuro-Oncology*, **2020**, 149, 219-230	4.8	2
213	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
212	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. *Cancer Research*, **2020**, 80, 2663-2675	10.1	25
211	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	11.5	49
210	An enhanced genetic model of colorectal cancer progression history. *Genome Biology*, **2019**, 20, 168	18.3	21
209	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. *Cell Reports*, **2019**, 28, 1370-1384.e5	10.6	161
208	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. *Cell Reports*, **2019**, 29, 1675-1689.e9	10.6	51
207	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. *Cell*, **2019**, 179, 964-983.e31	56.2	173
206	Framework for microRNA variant annotation and prioritization using human population and disease datasets. *Human Mutation*, **2019**, 40, 73-89	4.7	11

205	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	11.6	2
204	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. *Cancer Discovery*, **2018**, 8, 730-749	24.4	235
203	Iron homeostasis regulates facultative heterochromatin assembly in adaptive genome control. *Nature Structural and Molecular Biology*, **2018**, 25, 372-383	17.6	20
202	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. *Cell*, **2018**, 173, 864-878.e29	56.2	58
201	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
200	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
199	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
198	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
197	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
196	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
195	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
194	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
193	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
192	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
191	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
190	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
189	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
188	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405

187	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
186	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
185	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
184	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
183	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor-Pathway. *Gastroenterology*, **2018**, 154, 195-210	13.3	68
182	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	2.1	7
181	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	7.2	16
180	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. *Journal of Thoracic Oncology*, **2018**, 13, 1483-1495	8.9	12
179	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
178	Whole Exome Analysis Reveals Key Genomic Differences between Sporadic and Endemic Pediatric Burkitt Lymphoma. *Blood*, **2018**, 132, 4117-4117	2.2	
177	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
176	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. *Neuro-Oncology*, **2018**, 20, i184-i184	1	78
175	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. *Nature Communications*, **2017**, 8, 14098	17.4	54
174	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. *Journal of Neuropathology and Experimental Neurology*, **2017**, 76, 126-134	3.1	41
173	Whole-genome landscape of pancreatic neuroendocrine tumours. *Nature*, **2017**, 543, 65-71	50.4	482
172	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
171	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. *European Urology*, **2017**, 72, 641-649	10.2	111
170	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247

169	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	3.3	16
168	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. *Nature Genetics*, **2017**, 49, 1487-1494	36.3	160
167	Effect of Oral Methylprednisolone on Clinical Outcomes in Patients With IgA Nephropathy: The TESTING Randomized Clinical Trial. *JAMA - Journal of the American Medical Association*, **2017**, 318, 432-442	27.4	214
166	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.5	896
165	Renal cell carcinoma harboring somatic TSC2 mutations in a child with methylmalonic acidemia. *Pediatric Blood and Cancer*, **2017**, 64, e26286	3	6
164	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. *Hepatology*, **2017**, 65, 104-121	11.2	104
163	SVachra: a tool to identify genomic structural variation in mate pair sequencing data containing inward and outward facing reads. *BMC Genomics*, **2017**, 18, 691	4.5	3
162	Activating MAPK1 (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. *Oncotarget*, **2017**, 8, 46065-46070	3.3	18
161	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	18.3	120
160	An open access pilot freely sharing cancer genomic data from participants in Texas. *Scientific Data*, **2016**, 3, 160010	8.2	12
159	SV-STAT accurately detects structural variation via alignment to reference-based assemblies. *Source Code for Biology and Medicine*, **2016**, 11, 8	1.9	3
158	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. *Cell Reports*, **2016**, 14, 2476-89	10.6	228
157	Acquired uniparental disomy of chromosome 9p in hematologic malignancies. *Experimental Hematology*, **2016**, 44, 644-52	3.1	3
156	ITD assembler: an algorithm for internal tandem duplication discovery from short-read sequencing data. *BMC Bioinformatics*, **2016**, 17, 188	3.6	11
155	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. *JAMA Oncology*, **2016**, 2, 616-624	13.4	276
154	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. *Cell*, **2016**, 164, 538-49	56.2	239
153	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. *Cell Reports*, **2016**, 14, 907-919	10.6	75
152	Clonal Dynamics In Vivo of Virus Integration Sites of T Cells Expressing a Safety Switch. *Molecular Therapy*, **2016**, 24, 736-45	11.7	7

151	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. *Journal of Thoracic Oncology*, **2016**, 11, 52-61	8.9	18
150	Genomic analyses identify molecular subtypes of pancreatic cancer. *Nature*, **2016**, 531, 47-52	50.4	1785
149	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. *Cancer Research*, **2016**, 76, 2197-205	10.1	95
148	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
147	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. *Journal of Clinical Investigation*, **2016**, 126, 2881-92	15.9	52
146	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	2.2	
145	Pharmacogenetic characterization of naturally occurring germline NT5C1A variants to chemotherapeutic nucleoside analogs. *Pharmacogenetics and Genomics*, **2016**, 26, 271-9	1.9	1
144	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. *Blood*, **2016**, 128, 2533-2537	2.2	93
143	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. *Nature Communications*, **2016**, 7, 12601	17.4	88
142	Coexistence of gain-of-function JAK2 germ line mutations with JAK2V617F in polycythemia vera. *Blood*, **2016**, 128, 2266-2270	2.2	17
141	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. *Experimental Hematology*, **2016**, 44, 740-4	3.1	33
140	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
139	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	12.9	49
138	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	2.8	17
137	Identifying gene disruptions in novel balanced de novo constitutional translocations in childhood cancer patients by whole-genome sequencing. *Genetics in Medicine*, **2015**, 17, 831-5	8.1	4
136	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. *Nature Communications*, **2015**, 6, 6604	17.4	215
135	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. *Blood*, **2015**, 125, 629-38	2.2	163
134	Assessing structural variation in a personal genome-towards a human reference diploid genome. *BMC Genomics*, **2015**, 16, 286	4.5	117

133	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. *Nature Communications*, **2015**, 6, 8891	17.4	92
132	Genomic profiling of S□ary syndrome identifies alterations of key T cell signaling and differentiation genes. *Nature Genetics*, **2015**, 47, 1426-34	36.3	199
131	Comparison of Positive End-Expiratory Pressure of 8 versus 5 cm H2O on Outcome After Cardiac Operations. *Journal of Intensive Care Medicine*, **2015**, 30, 338-43	3.3	6
130	BCOR-CCNB3 fusions are frequent in undifferentiated sarcomas of male children. *Modern Pathology*, **2015**, 28, 575-86	9.8	93
129	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, 91-8	3	55
128	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
127	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. *Nature Communications*, **2015**, 6, 10013	17.4	41
126	Recurrent DGCR8, DROSHA, and SIX homeodomain mutations in favorable histology Wilms tumors. *Cancer Cell*, **2015**, 27, 286-97	24.3	175
125	The relationship of JAK2(V617F) and acquired UPD at chromosome 9p in polycythemia vera. *Leukemia*, **2014**, 28, 938-41	10.7	15
124	Genomic sequencing for cancer diagnosis and therapy. *Annual Review of Medicine*, **2014**, 65, 33-48	17.4	30
123	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. *Nature Genetics*, **2014**, 46, 1267-73	36.3	491
122	Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. *Leukemia*, **2014**, 28, 935-8	10.7	19
121	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, 15544-9	11.5	229
120	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3□UTR landscape across seven tumour types. *Nature Communications*, **2014**, 5, 5274	17.4	260
119	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. *Genome Research*, **2014**, 24, 1740-50	9.7	187
118	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
117	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
116	Squamous cell carcinoma of the oral tongue in young non-smokers is genomically similar to tumors in older smokers. *Clinical Cancer Research*, **2014**, 20, 3842-8	12.9	96

115	Case series of patients with acute myeloid leukemia receiving hypomethylation therapy and retrospectively found to have IDH1 or IDH2 mutations. *Leukemia and Lymphoma*, **2014**, 55, 1431-4	1.9	3
114	Novel somatic and germline mutations in intracranial germ cell tumours. *Nature*, **2014**, 511, 241-5	50.4	131
113	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. *Blood*, **2014**, 124, 3007-15	2.2	272
112	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. *Genome Biology*, **2014**, 15, 443	18.3	47
111	Mutational landscape of aggressive cutaneous squamous cell carcinoma. *Clinical Cancer Research*, **2014**, 20, 6582-92	12.9	362
110	Heterochromatin protein 1 expression is reduced in human thyroid malignancy. *Laboratory Investigation*, **2014**, 94, 788-95	5.9	6
109	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
108	Effects of TP53 mutational status on gene expression patterns across 10 human cancer types. *Journal of Pathology*, **2014**, 232, 522-33	9.4	52
107	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	2.2	2
106	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. *Nature Genetics*, **2013**, 45, 1226-1231	36.3	205
105	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. *Nature Communications*, **2013**, 4, 2730	17.4	91
104	Identification of TP53 as an acute lymphocytic leukemia susceptibility gene through exome sequencing. *Pediatric Blood and Cancer*, **2013**, 60, E1-3	3	40
103	MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. *Journal of Pathology*, **2013**, 229, 99-110	9.4	58
102	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
101	Deep resequencing and association analysis of schizophrenia candidate genes. *Molecular Psychiatry*, **2013**, 18, 138-40	15.1	13
100	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genetics*, **2013**, 45, 767-75	36.3	131
99	From human genome to cancer genome: the first decade. *Genome Research*, **2013**, 23, 1054-62	9.7	103
98	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184

97	Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers. *Cancer Discovery*, **2013**, 3, 770-81	24.4	391
96	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	2.2	3
95	Whole Exome Sequencing and Analysis Of Mutations In S□ary Syndrome. *Blood*, **2013**, 122, 2558-2558	2.2	
94	Molecular Characterization Of Polycythemia Vera Based On The Relationship Of JAK2V617F and 9pUPD. *Blood*, **2013**, 122, 1607-1607	2.2	
93	Dietary Determinants Of The White Blood Cell Count. *Blood*, **2013**, 122, 1705-1705	2.2	
92	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. *Nature*, **2012**, 491, 399-405	50.4	1427
91	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
90	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
89	Integrated analyses of microRNAs demonstrate their widespread influence on gene expression in high-grade serous ovarian carcinoma. *PLoS ONE*, **2012**, 7, e34546	3.7	94
88	Landscape of somatic retrotransposition in human cancers. *Science*, **2012**, 337, 967-71	33.3	507
87	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 □n NCI/COG Target AML Study. *Blood*, **2012**, 120, 123-123	2.2	1
86	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	2.2	2
85	Whole Genome Sequencing of Four CD34+-Derived iPSC Polycythemia Vera Clones From a Single Female. *Blood*, **2012**, 120, 1755-1755	2.2	1
84	Whole Exome Sequencing of Polycythemia Vera Reveals Novel Recurrent Somatic and Germline Variation. *Blood*, **2012**, 120, 705-705	2.2	1
83	Several Grassland Soil Nematode Species Are Insensitive to RNA-Mediated Interference. *Journal of Nematology*, **2012**, 44, 92-101	1.1	4
82	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	2.2	
81	Integrated genomic analyses of ovarian carcinoma. *Nature*, **2011**, 474, 609-15	50.4	5210
80	Activation of multiple proto-oncogenic tyrosine kinases in breast cancer via loss of the PTPN12 phosphatase. *Cell*, **2011**, 144, 703-18	56.2	214

79	Exome sequencing of ion channel genes reveals complex profiles confounding personal risk assessment in epilepsy. *Cell*, **2011**, 145, 1036-48	56.2	240
78	Identification of genetic susceptibility to childhood cancer through analysis of genes in parallel. *Cancer Genetics*, **2011**, 204, 19-25	2.3	14
77	Resequencing of IRS2 reveals rare variants for obesity but not fasting glucose homeostasis in Hispanic children. *Physiological Genomics*, **2011**, 43, 1029-37	3.6	3
76	High incidence of IDH mutations in acute myeloid leukaemia with cuplike nuclei. *British Journal of Haematology*, **2011**, 155, 125-8	4.5	13
75	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. *Nature Genetics*, **2011**, 43, 189-96	36.3	271
74	Exome sequencing of head and neck squamous cell carcinoma reveals inactivating mutations in NOTCH1. *Science*, **2011**, 333, 1154-7	33.3	1331
73	A primer on a hepatocellular carcinoma bioresource bank using the cancer genome atlas guidelines: practical issues and pitfalls. *World Journal of Surgery*, **2011**, 35, 1732-7	3.3	4
72	Building a comprehensive genomic program for hepatocellular carcinoma. *World Journal of Surgery*, **2011**, 35, 1746-50	3.3	13
71	Overview of the development of personalized genomic medicine and surgery. *World Journal of Surgery*, **2011**, 35, 1693-9	3.3	13
70	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). *BMC Genomics*, **2011**, 12, 311	4.5	27
69	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. *Human Mutation*, **2011**, 32, 661-8	4.7	161
68	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	11.5	163
67	Disruptive TP53 mutation is associated with aggressive disease characteristics in an orthotopic murine model of oral tongue cancer. *Clinical Cancer Research*, **2011**, 17, 6658-70	12.9	79
66	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
65	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
64	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
63	A SNP discovery method to assess variant allele probability from next-generation resequencing data. *Genome Research*, **2010**, 20, 273-80	9.7	130
62	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. *Nature Communications*, **2010**, 1, 131	17.4	183

61	Whole-genome sequencing in a patient with Charcot-Marie-Tooth neuropathy. *New England Journal of Medicine*, **2010**, 362, 1181-91	59.2	613
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