

Trevor J Pugh

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

149
papers

24,259
citations

57
h-index

155
g-index

168
ext. papers

29,921
ext. citations

17.2
avg, IF

7.18
L-index

#	Paper	IF	Citations
149	Tryptophan-derived microbial metabolites activate the aryl hydrocarbon receptor in tumor-associated macrophages to suppress anti-tumor immunity.. <i>Immunity</i> , 2022 , 55, 324-340.e8	32.3	14
148	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency.. <i>Nature Medicine</i> , 2022 ,	50.5	2
147	REFLECTIONs on Combination Therapies Empowered by Data Sharing. <i>Cancer Discovery</i> , 2022 , 12, 1416-1418	14.8	0
146	Coenzyme A fuels T cell anti-tumor immunity. <i>Cell Metabolism</i> , 2021 , 33, 2415-2427.e6	24.6	4
145	Longitudinal single-cell analysis of a myeloma mouse model identifies subclonal molecular programs associated with progression. <i>Nature Communications</i> , 2021 , 12, 6322	17.4	1
144	CanDIG: Federated network across Canada for multi-omic and health data discovery and analysis. <i>Cell Genomics</i> , 2021 , 1, 100033		2
143	Selective Cell State in the Clonally Expanded T-Cell Compartment of VβMYC Mice Responding to Treatment with Checkpoint Inhibitors. <i>Blood</i> , 2021 , 138, 1581-1581	2.2	
142	Predicting Toxicity and Response to Pembrolizumab Through Germline Genomic HLA Class 1 Analysis. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkaa115	4.6	3
141	Transplant Oncology in Primary and Metastatic Liver Tumors: Principles, Evidence, and Opportunities. <i>Annals of Surgery</i> , 2021 , 273, 483-493	7.8	11
140	The DEAD-box helicase DDX56 is a conserved stemness regulator in normal and cancer stem cells. <i>Cell Reports</i> , 2021 , 34, 108903	10.6	2
139	Understanding the clinical implication of mismatch repair deficiency in endometrioid endometrial cancer through a prospective study. <i>Gynecologic Oncology</i> , 2021 , 161, 221-227	4.9	0
138	Tumor genomic, transcriptomic, and immune profiling characterizes differential response to first-line platinum chemotherapy in high grade serous ovarian cancer. <i>Cancer Medicine</i> , 2021 , 10, 3045-3058	4.8	6
137	Maximizing cancer prevention through genetic navigation for Lynch syndrome detection in women with newly diagnosed endometrial and nonserous/nonmucinous epithelial ovarian cancer. <i>Cancer</i> , 2021 , 127, 3082-3091	6.4	2
136	IMMU-14. COMPUTATIONAL DECONVOLUTION OF TUMOR-INFILTRATING IMMUNE COMPONENTS IN PEDIATRIC NERVOUS SYSTEM TUMORS. <i>Neuro-Oncology</i> , 2021 , 23, i30-i30	1	78
135	Whole-genome profiling of nasopharyngeal carcinoma reveals viral-host co-operation in inflammatory NF- κ B activation and immune escape. <i>Nature Communications</i> , 2021 , 12, 4193	17.4	10
134	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. <i>Leukemia</i> , 2021 , 35, 796-808	10.7	6
133	Epigenomic, genomic, and transcriptomic landscape of schwannomatosis. <i>Acta Neuropathologica</i> , 2021 , 141, 101-116	14.3	11

132	An Integrative DNA Sequencing and Methylation Panel to Assess Mismatch Repair Deficiency. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 242-252	5.1	5
131	Applications of Circulating Tumor DNA in a Cohort of Phase I Solid Tumor Patients Treated With Immunotherapy. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkaa122	4.6	5
130	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , 2021 , 2, 157-173	15.4	31
129	Adavosertib plus gemcitabine for platinum-resistant or platinum-refractory recurrent ovarian cancer: a double-blind, randomised, placebo-controlled, phase 2 trial. <i>Lancet, The</i> , 2021 , 397, 281-292	4.0	32
128	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , 2021 , 184, 226-247.e2168	17.4	21
127	Mutations in the RAS/MAPK Pathway Drive Replication Repair-Deficient Hypermutated Tumors and Confer Sensitivity to MEK Inhibition. <i>Cancer Discovery</i> , 2021 , 11, 1454-1467	24.4	6
126	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021 , 12, 979	17.4	23
125	Elevation in viral entry genes and innate immunity compromise underlying increased infectivity and severity of COVID-19 in cancer patients. <i>Scientific Reports</i> , 2021 , 11, 4533	4.9	1
124	Prospective observational study and serosurvey of SARS-CoV-2 infection in asymptomatic healthcare workers at a Canadian tertiary care center. <i>PLoS ONE</i> , 2021 , 16, e0247258	3.7	9
123	Minimal Residual Disease in Myeloma: Application for Clinical Care and New Drug Registration. <i>Clinical Cancer Research</i> , 2021 ,	12.9	4
122	Pan-cancer analysis of longitudinal metastatic tumors reveals genomic alterations and immune landscape dynamics associated with pembrolizumab sensitivity. <i>Nature Communications</i> , 2021 , 12, 5137	17.4	5
121	Implementation of serological and molecular tools to inform COVID-19 patient management: protocol for the GENCOV prospective cohort study. <i>BMJ Open</i> , 2021 , 11, e052842	3	0
120	DNA Methylation-Based Classification of Small B-Cell Lymphomas: A Proof-of-Principle Study. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 1774-1786	5.1	
119	HPV Sequencing Facilitates Ultrasensitive Detection of HPV Circulating Tumor DNA. <i>Clinical Cancer Research</i> , 2021 , 27, 5857-5868	12.9	6
118	Genomic Landscape of Malignant Peripheral Nerve Sheath Tumor-Like Melanoma. <i>Journal of Investigative Dermatology</i> , 2021 , 141, 2470-2479	4.3	1
117	Antitumor immune effects of preoperative sitravatinib and nivolumab in oral cavity cancer: SNOW window-of-opportunity study 2021 , 9,		4
116	Integration of intra-sample contextual error modeling for improved detection of somatic mutations from deep sequencing. <i>Science Advances</i> , 2020 , 6,	14.3	2
115	CReSCENT: Cancer Single Cell Expression Toolkit. <i>Nucleic Acids Research</i> , 2020 , 48, W372-W379	20.1	5

114	Minimalist approaches to cancer tissue-of-origin classification by DNA methylation. <i>Modern Pathology</i> , 2020 , 33, 1874-1888	9.8	8
113	Rare driver mutations in head and neck squamous cell carcinomas converge on NOTCH signaling. <i>Science</i> , 2020 , 367, 1264-1269	33.3	112
112	IL6 Induces an IL22 CD8 T-cell Subset with Potent Antitumor Function. <i>Cancer Immunology Research</i> , 2020 , 8, 321-333	12.5	10
111	Noncoding mutations target cis-regulatory elements of the FOXA1 plexus in prostate cancer. <i>Nature Communications</i> , 2020 , 11, 441	17.4	21
110	Centromeric cohesion failure invokes a conserved choreography of chromosomal mis-segregations in pancreatic neuroendocrine tumor. <i>Genome Medicine</i> , 2020 , 12, 38	14.4	1
109	Early Detection of Multiple Resistance Mechanisms by ctDNA Profiling in a Patient With EGFR-mutant Lung Adenocarcinoma Treated With Osimertinib. <i>Clinical Lung Cancer</i> , 2020 , 21, e488-e492	4.9	2
108	Clinical impact of combined epigenetic and molecular analysis of pediatric low-grade gliomas. <i>Neuro-Oncology</i> , 2020 , 22, 1474-1483	1	14
107	Tumor site discordance in mismatch repair deficiency in synchronous endometrial and ovarian cancers. <i>International Journal of Gynecological Cancer</i> , 2020 , 30, 1951-1958	3.5	2
106	EVOLVE: A Multicenter Open-Label Single-Arm Clinical and Translational Phase II Trial of Cediranib Plus Olaparib for Ovarian Cancer after PARP Inhibition Progression. <i>Clinical Cancer Research</i> , 2020 , 26, 4206-4215	12.9	30
105	Landscape mapping of shared antigenic epitopes and their cognate TCRs of tumor-infiltrating T lymphocytes in melanoma. <i>ELife</i> , 2020 , 9,	8.9	6
104	Unsupervised Resolution of Histomorphologic Heterogeneity in Renal Cell Carcinoma Using a Brain Tumor-Educated Neural Network. <i>JCO Clinical Cancer Informatics</i> , 2020 , 4, 811-821	5.2	5
103	Considerations for the use of circulating tumor DNA sequencing as a screening tool in cancer predisposition syndromes. <i>Pediatric Blood and Cancer</i> , 2020 , 67, e28758	3	1
102	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirus-Unrelated Head and Neck Cancer: A Multicenter, Phase II Trial. <i>Clinical Cancer Research</i> , 2020 , 26, 5140-5152	12.9	71
101	Assessment of Genetic Drift in Large Pharmacogenomic Studies. <i>Cell Systems</i> , 2020 , 11, 393-401.e2	10.6	3
100	Personalized circulating tumor DNA analysis as a predictive biomarker in solid tumor patients treated with pembrolizumab.. <i>Nature Cancer</i> , 2020 , 1, 873-881	15.4	89
99	An open-label, phase II multicohort study of an oral hypomethylating agent CC-486 and durvalumab in advanced solid tumors 2020 , 8,		12
98	Phase I/II Trial of the Combination of Lutetium Prostate specific Membrane Antigen 617 and Idroneoxil (NOX66) in Men with End-stage Metastatic Castration-resistant Prostate Cancer (LuPIN). <i>European Urology Oncology</i> , 2020 , 4, 963-963	6.7	14
97	Brain Tumor Stem Cell Dependence on Glutaminase Reveals a Metabolic Vulnerability through the Amino Acid Deprivation Response Pathway. <i>Cancer Research</i> , 2020 , 80, 5478-5490	10.1	5

96	Performance characteristics of screening strategies to identify Lynch syndrome in women with ovarian cancer. <i>Cancer</i> , 2020 , 126, 4886-4894	6.4	5
95	Wnt activation as a therapeutic strategy in medulloblastoma. <i>Nature Communications</i> , 2020 , 11, 4323	17.4	13
94	Translational genomics of nasopharyngeal cancer. <i>Seminars in Cancer Biology</i> , 2020 , 61, 84-100	12.7	35
93	High efficiency error suppression for accurate detection of low-frequency variants. <i>Nucleic Acids Research</i> , 2019 , 47, e87	20.1	12
92	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019 , 572, 67-73	50.4	149
91	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. <i>Cancer Research</i> , 2019 , 79, 2111-2123	10.1	14
90	An interim report on the investigator-initiated phase 2 study of pembrolizumab immunological response evaluation (INSPIRE) 2019 , 7, 72		16
89	Molecular characteristics and therapeutic vulnerabilities across paediatric solid tumours. <i>Nature Reviews Cancer</i> , 2019 , 19, 420-438	31.3	52
88	Safety and tolerability of CFI-400945, a first-in-class, selective PLK4 inhibitor in advanced solid tumours: a phase 1 dose-escalation trial. <i>British Journal of Cancer</i> , 2019 , 121, 318-324	8.7	18
87	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , 2019 , 29, 1211-1222	9.7	31
86	OCTANE (Ontario-wide Cancer Targeted Nucleic Acid Evaluation): a platform for intraprovincial, national, and international clinical data-sharing. <i>Current Oncology</i> , 2019 , 26, e618-e623	2.8	1
85	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019 , 8,	3.6	28
84	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNA-sequencing data. <i>F1000Research</i> , 2019 , 8, 296	3.6	23
83	Heterogeneous alteration of the ERBB3-MYC axis associated with MEK inhibitor resistance in a -mutated low-grade serous ovarian cancer patient. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	4
82	GCN2 drives macrophage and MDSC function and immunosuppression in the tumor microenvironment. <i>Science Immunology</i> , 2019 , 4,	28	34
81	DNA hypermethylation within TERT promoter upregulates TERT expression in cancer. <i>Journal of Clinical Investigation</i> , 2019 , 129, 223-229	15.9	62
80	Circulating Tumour DNA for Detecting Minimal Residual Disease in Multiple Myeloma. <i>Seminars in Hematology</i> , 2018 , 55, 38-40	4	22
79	Regulatory T Cells in Ovarian Cancer Are Characterized by a Highly Activated Phenotype Distinct from that in Melanoma. <i>Clinical Cancer Research</i> , 2018 , 24, 5685-5696	12.9	46

78	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , 2018 , 559, 400-404	50.4	368
77	Bamgineer: Introduction of simulated allele-specific copy number variants into exome and targeted sequence data sets. <i>PLoS Computational Biology</i> , 2018 , 14, e1006080	5	3
76	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. <i>Nature</i> , 2018 , 563, 579-583	50.4	344
75	Assessing genome-wide copy number aberrations and copy-neutral loss-of-heterozygosity as best practice: An evidence-based review from the Cancer Genomics Consortium working group for plasma cell disorders. <i>Cancer Genetics</i> , 2018 , 228-229, 184-196	2.3	8
74	Patient-Derived Xenografts for Prognostication and Personalized Treatment for Head and Neck Squamous Cell Carcinoma. <i>Cell Reports</i> , 2018 , 25, 1318-1331.e4	10.6	41
73	Landscape of genomic alterations in high-grade serous ovarian cancer from exceptional long- and short-term survivors. <i>Genome Medicine</i> , 2018 , 10, 81	14.4	46
72	CapTCR-seq: hybrid capture for T-cell receptor repertoire profiling. <i>Blood Advances</i> , 2018 , 2, 3506-3514	7.8	9
71	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. <i>Cancer Research</i> , 2017 , 77, 509-519	10.1	60
70	Somatic BRCA1/2 Recovery as a Resistance Mechanism After Exceptional Response to Poly (ADP-ribose) Polymerase Inhibition. <i>Journal of Clinical Oncology</i> , 2017 , 35, 1240-1249	2.2	59
69	A distinct innate lymphoid cell population regulates tumor-associated T cells. <i>Nature Medicine</i> , 2017 , 23, 368-375	50.5	97
68	The Role of Minimal Residual Disease Testing in Myeloma Treatment Selection and Drug Development: Current Value and Future Applications. <i>Clinical Cancer Research</i> , 2017 , 23, 3980-3993	12.9	51
67	Circulating tumour DNA sequence analysis as an alternative to multiple myeloma bone marrow aspirates. <i>Nature Communications</i> , 2017 , 8, 15086	17.4	77
66	Integration of Technical, Bioinformatic, and Variant Assessment Approaches in the Validation of a Targeted Next-Generation Sequencing Panel for Myeloid Malignancies. <i>Archives of Pathology and Laboratory Medicine</i> , 2017 , 141, 759-775	5	21
65	AACR Project GENIE: Powering Precision Medicine through an International Consortium. <i>Cancer Discovery</i> , 2017 , 7, 818-831	24.4	629
64	Data resources for the identification and interpretation of actionable mutations by clinicians. <i>Annals of Oncology</i> , 2017 , 28, 946-957	10.3	18
63	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. <i>Nature</i> , 2017 , 549, 227-232	50.4	197
62	Therapeutic radiation for childhood cancer drives structural aberrations of NF2 in meningiomas. <i>Nature Communications</i> , 2017 , 8, 186	17.4	45
61	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017 , 547, 55-60	50.4	192

60	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. <i>Nature Genetics</i> , 2016 , 48, 1260-6	36.3	53
59	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. <i>Nature Genetics</i> , 2016 , 48, 1142-50	36.3	158
58	Molecular profiling of advanced solid tumors and patient outcomes with genotype-matched clinical trials: the Princess Margaret IMPACT/COMPACT trial. <i>Genome Medicine</i> , 2016 , 8, 109	14.4	149
57	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016 , 529, 351-7	50.4	206
56	Human Papillomavirus Genotype Association With Survival in Head and Neck Squamous Cell Carcinoma. <i>JAMA Oncology</i> , 2016 , 2, 823-6	13.4	66
55	Next generation sequencing-based copy number analysis reveals low prevalence of deletions and duplications in 46 genes associated with genetic cardiomyopathies. <i>Molecular Genetics & Genomic Medicine</i> , 2016 , 4, 143-51	2.3	27
54	VisCap: inference and visualization of germ-line copy-number variants from targeted clinical sequencing data. <i>Genetics in Medicine</i> , 2016 , 18, 712-9	8.1	46
53	Institutional implementation of clinical tumor profiling on an unselected cancer population. <i>JCI Insight</i> , 2016 , 1, e87062	9.9	245
52	Whole Exome Sequencing Identifies TSC1/TSC2 Biallelic Loss as the Primary and Sufficient Driver Event for Renal Angiomyolipoma Development. <i>PLoS Genetics</i> , 2016 , 12, e1006242	6	62
51	An Anaplastic Lymphoma Kinase Immunohistochemistry-Negative but Fluorescence In Situ Hybridization-Positive Lung Adenocarcinoma Is Resistant to Crizotinib. <i>Journal of Thoracic Oncology</i> , 2016 , 11, 2248-2252	8.9	2
50	The genomic landscape of schwannoma. <i>Nature Genetics</i> , 2016 , 48, 1339-1348	36.3	74
49	Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations. <i>Nature Genetics</i> , 2015 , 47, 864-868	36.3	313
48	Pugh et al. reply. <i>Nature</i> , 2015 , 520, E12-4	50.4	8
47	DNA-Demethylating Agents Target Colorectal Cancer Cells by Inducing Viral Mimicry by Endogenous Transcripts. <i>Cell</i> , 2015 , 162, 961-73	56.2	705
46	Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. <i>Clinical Cancer Research</i> , 2015 , 21, 632-41	12.9	398
45	Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. <i>Human Mutation</i> , 2015 , 36, 1080-7	4.7	51
44	Oncotator: cancer variant annotation tool. <i>Human Mutation</i> , 2015 , 36, E2423-9	4.7	332
43	A shower of second hit events as the cause of multifocal renal cell carcinoma in tuberous sclerosis complex. <i>Human Molecular Genetics</i> , 2015 , 24, 1836-42	5.6	39

42	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
41	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014 , 506, 445-50	50.4	434
40	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , 2014 , 25, 393-405	24.3	469
39	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014 , 506, 371-5	50.4	541
38	Comprehensive diagnostic testing for stereocilin: an approach for analyzing medically important genes with high homology. <i>Journal of Molecular Diagnostics</i> , 2014 , 16, 639-47	5.1	41
37	The landscape of genetic variation in dilated cardiomyopathy as surveyed by clinical DNA sequencing. <i>Genetics in Medicine</i> , 2014 , 16, 601-8	8.1	215
36	Exome sequencing of pleuropulmonary blastoma reveals frequent biallelic loss of TP53 and two hits in DICER1 resulting in retention of 5p-derived miRNA hairpin loop sequences. <i>Oncogene</i> , 2014 , 33, 5295-302	9.2	105
35	WNT activation by lithium abrogates TP53 mutation associated radiation resistance in medulloblastoma. <i>Acta Neuropathologica Communications</i> , 2014 , 2, 174	7.3	32
34	Inhibitor-sensitive FGFR2 and FGFR3 mutations in lung squamous cell carcinoma. <i>Cancer Research</i> , 2013 , 73, 5195-205	10.1	136
33	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. <i>Pharmacogenomics Journal</i> , 2013 , 13, 148-58	3.5	18
32	A systematic approach to assessing the clinical significance of genetic variants. <i>Clinical Genetics</i> , 2013 , 84, 453-63	4	124
31	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013 , 45, 1483-6	36.3	219
30	Activation of the PD-1 pathway contributes to immune escape in EGFR-driven lung tumors. <i>Cancer Discovery</i> , 2013 , 3, 1355-63	24.4	831
29	Discovery and characterization of artifactual mutations in deep coverage targeted capture sequencing data due to oxidative DNA damage during sample preparation. <i>Nucleic Acids Research</i> , 2013 , 41, e67	20.1	301
28	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013 , 499, 214-218	50.4	3616
27	A comprehensive assay for CFTR mutational analysis using next-generation sequencing. <i>Clinical Chemistry</i> , 2013 , 59, 1481-8	5.5	40
26	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013 , 45, 279-84	36.3	717
25	Subgroup-specific prognostic implications of TP53 mutation in medulloblastoma. <i>Journal of Clinical Oncology</i> , 2013 , 31, 2927-35	2.2	290

24	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. <i>Cell</i> , 2012 , 150, 1107-1110	50.4	1304
23	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <i>Nature</i> , 2012 , 488, 106-10	50.4	552
22	Melanoma genome sequencing reveals frequent PREX2 mutations. <i>Nature</i> , 2012 , 485, 502-6	50.4	555
21	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. <i>BMC Proceedings</i> , 2012 , 6,	2.3	1
20	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012 , 488, 100-5	50.4	623
19	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. <i>Nature Genetics</i> , 2011 , 43, 964-968	36.3	242
18	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011 , 470, 214-20	50.4	984
17	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011 , 471, 467-72	50.4	1117
16	Development and validation of a computational method for assessment of missense variants in hypertrophic cardiomyopathy. <i>American Journal of Human Genetics</i> , 2011 , 88, 183-92	11	60
15	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010 , 7, 843-7	21.6	227
14	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010 , 11, R82	18.3	144
13	Sequence variant discovery in DNA repair genes from radiosensitive and radiotolerant prostate brachytherapy patients. <i>Clinical Cancer Research</i> , 2009 , 15, 5008-16	12.9	39
12	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009 , 461, 809-13	50.4	879
11	Impact of whole genome amplification on analysis of copy number variants. <i>Nucleic Acids Research</i> , 2008 , 36, e80	20.1	70
10	Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing. <i>BioTechniques</i> , 2008 , 45, 81-94	2.5	322
9	A patient with vertebral, cognitive and behavioural abnormalities and a de novo deletion of NRXN1alpha. <i>Journal of Medical Genetics</i> , 2008 , 45, 239-43	5.8	104
8	Correlations of EGFR mutations and increases in EGFR and HER2 copy number to gefitinib response in a retrospective analysis of lung cancer patients. <i>BMC Cancer</i> , 2007 , 7, 128	4.8	32
7	Epidermal growth factor receptor (EGFR) is transcriptionally induced by the Y-box binding protein-1 (YB-1) and can be inhibited with Iressa in basal-like breast cancer, providing a potential target for therapy. <i>Breast Cancer Research</i> , 2007 , 9, R61	8.3	112

6	A BAC clone fingerprinting approach to the detection of human genome rearrangements. <i>Genome Biology</i> , 2007 , 8, R224	18.3	10
5	Oligonucleotide microarray analysis of genomic imbalance in children with mental retardation. <i>American Journal of Human Genetics</i> , 2006 , 79, 500-13	11	247
4	Facilitated loading of horizontal gels using a capillary comb loader. <i>BioTechniques</i> , 2003 , 34, 814-8	2.5	
3	CReSCENT: Cancer Single Cell Expression Toolkit		1
2	Childhood Cerebellar Tumors Mirror Conserved Fetal Transcriptional Programs		5
1	Evaluation of methods to assign cell type labels to cell clusters from single-cell RNAsequencing data		4