

# Nikolaus D Schultz

## List of Publications by Citations

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237  
papers

94,864  
citations

105  
h-index

256  
g-index

256  
ext. papers

122,579  
ext. citations

17.7  
avg, IF

8.88  
L-index

#	Paper	IF	Citations
237	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. <i>Cancer Discovery</i> , <b>2012</b> , 2, 401-4	24.4	8578
236	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , <b>2012</b> , 490, 61-70	50.4	8025
235	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. <i>Science Signaling</i> , <b>2013</b> , 6, p11	8.8	7715
234	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , <b>2011</b> , 474, 609-15	50.4	5210
233	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , <b>2013</b> , 45, 1113-20	36.3	3933
232	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , <b>2014</b> , 511, 543-50	50.4	3310
231	The somatic genomic landscape of glioblastoma. <i>Cell</i> , <b>2013</b> , 155, 462-77	56.2	2900
230	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , <b>2012</b> , 489, 519-25	50.4	2820
229	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , <b>2013</b> , 497, 67-73	50.4	2800
228	Integrative genomic profiling of human prostate cancer. <i>Cancer Cell</i> , <b>2010</b> , 18, 11-22	24.3	2666
227	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , <b>2013</b> , 499, 43-9	50.4	2184
226	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 2481-98	59.2	1828
225	Integrative clinical genomics of advanced prostate cancer. <i>Cell</i> , <b>2015</b> , 161, 1215-1228	56.2	1765
224	The Immune Landscape of Cancer. <i>Immunity</i> , <b>2018</b> , 48, 812-830.e14	32.3	1754
223	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , <b>2015</b> , 163, 1011-25	56.2	1713
222	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , <b>2014</b> , 159, 676-90	56.2	1660
221	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , <b>2017</b> , 23, 703-713	50.5	1638

220	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , <b>2017</b> , 169, 1327-1341.e23	56.2	1125
219	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124
218	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , <b>2018</b> , 173, 400-416.e11	56.2	1072
217	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , <b>2015</b> , 163, 506-19	56.2	1055
216	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , <b>2017</b> , 171, 540-556.e25	56.2	961
215	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , <b>2013</b> , 45, 1127-33	36.3	889
214	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , <b>2018</b> , 173, 291-304.e6	56.2	888
213	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
212	Evaluating cell lines as tumour models by comparison of genomic profiles. <i>Nature Communications</i> , <b>2013</b> , 4, 2126	17.4	831
211	Inherited DNA-Repair Gene Mutations in Men with Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , <b>2016</b> , 375, 443-53	59.2	791
210	Pathway Commons, a web resource for biological pathway data. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D685-90	20.1	786
209	Molecular Determinants of Response to Anti-Programmed Cell Death (PD)-1 and Anti-Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Non-Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. <i>Journal of Clinical Oncology</i> , <b>2018</b> , 36, 633-641	2.2	730
208	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	699
207	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. <i>Journal of Clinical Investigation</i> , <b>2016</b> , 126, 1052-66	15.9	576
206	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , <b>2018</b> , 173, 338-354.e15	56.2	560
205	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 155-63	44.5	465
204	A multitude of genes expressed solely in meiotic or postmeiotic spermatogenic cells offers a myriad of contraceptive targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 12201-6	11.5	463
203	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , <b>2012</b> , 22, 398-406	9.7	452

202	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , <b>2017</b> , 171, 950-965.e28	56.2	451
201	Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. <i>Nature Medicine</i> , <b>2016</b> , 22, 369-78	50.5	425
200	Response to MET inhibitors in patients with stage IV lung adenocarcinomas harboring MET mutations causing exon 14 skipping. <i>Cancer Discovery</i> , <b>2015</b> , 5, 842-9	24.4	409
199	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 239-254.e6	10.6	405
198	Genomic correlates of clinical outcome in advanced prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 11428-11436	11.5	383
197	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , <b>2018</b> , 50, 645-651	36.3	380
196	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , <b>2018</b> , 33, 676-689.e3	24.3	377
195	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 1160-5	36.3	367
194	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , <b>2018</b> , 23, 181-193.e7	10.6	366
193	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , <b>2018</b> , 173, 355-370.e14	56.2	342
192	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 34, 427-438.e6	24.3	339
191	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 125-136.e3	24.3	338
190	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6	24.3	327
189	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , <b>2016</b> , 29, 723-736.e3	24.3	324
188	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , <b>2017</b> , 7, 596-609	24.4	317
187	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , <b>2013</b> , 45, 791-8	36.3	311
186	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2018</b> , 23, 313-326.e5	10.6	295
185	Somatic mutations of the Parkinson's disease-associated gene PARK2 in glioblastoma and other human malignancies. <i>Nature Genetics</i> , <b>2010</b> , 42, 77-82	36.3	280

184	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 33, 690-705.e9	24.3	277
183	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 706-720.e9	24.3	275
182	Automated network analysis identifies core pathways in glioblastoma. <i>PLoS ONE</i> , <b>2010</b> , 5, e8918	3.7	268
181	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. <i>JAMA Oncology</i> , <b>2019</b> , 5, 471-478	13.4	257
180	Pattern discovery and cancer gene identification in integrated cancer genomic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 4245-50	11.5	250
179	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 227-238.e3	10.6	235
178	Adverse outcomes in clear cell renal cell carcinoma with mutations of 3p21 epigenetic regulators BAP1 and SETD2: a report by MSKCC and the KIRC TCGA research network. <i>Clinical Cancer Research</i> , <b>2013</b> , 19, 3259-67	12.9	233
177	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. <i>Nature Genetics</i> , <b>2014</b> , 46, 424-6	36.3	231
176	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , <b>2018</b> , 33, 721-735.e8	24.3	228
175	Prevalence and co-occurrence of actionable genomic alterations in high-grade bladder cancer. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 3133-40	2.2	226
174	Prospective Genotyping of Hepatocellular Carcinoma: Clinical Implications of Next-Generation Sequencing for Matching Patients to Targeted and Immune Therapies. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 2116-2126	12.9	219
173	Copy number alteration burden predicts prostate cancer relapse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 11139-44	11.5	218
172	Genome doubling shapes the evolution and prognosis of advanced cancers. <i>Nature Genetics</i> , <b>2018</b> , 50, 1189-1195	36.3	208
171	MLL3 is a haploinsufficient 7q tumor suppressor in acute myeloid leukemia. <i>Cancer Cell</i> , <b>2014</b> , 25, 652-65	24.3	206
170	Loss of NF1 in cutaneous melanoma is associated with RAS activation and MEK dependence. <i>Cancer Research</i> , <b>2014</b> , 74, 2340-50	10.1	204
169	Ibrutinib Unmasks Critical Role of Bruton Tyrosine Kinase in Primary CNS Lymphoma. <i>Cancer Discovery</i> , <b>2017</b> , 7, 1018-1029	24.4	201
168	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , <b>2018</b> , 23, 3392-3406	10.6	200
167	The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 9435-40	11.5	196

166	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 282-296.e4	10.6	188
165	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , <b>2014</b> , 24, 1740-50	9.7	187
164	Comprehensive Molecular Profiling of Intrahepatic and Extrahepatic Cholangiocarcinomas: Potential Targets for Intervention. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 4154-4161	12.9	182
163	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 49-58	24.4	180
162	Tumor genetic analyses of patients with metastatic renal cell carcinoma and extended benefit from mTOR inhibitor therapy. <i>Clinical Cancer Research</i> , <b>2014</b> , 20, 1955-64	12.9	173
161	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , <b>2019</b> , 571, 576-579	50.4	170
160	Next-generation Sequencing of Nonmuscle Invasive Bladder Cancer Reveals Potential Biomarkers and Rational Therapeutic Targets. <i>European Urology</i> , <b>2017</b> , 72, 952-959	10.2	168
159	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
158	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. <i>Cancer Cell</i> , <b>2018</b> , 34, 893-905.e8	24.3	166
157	PIK3CA mutations are associated with decreased benefit to neoadjuvant human epidermal growth factor receptor 2-targeted therapies in breast cancer. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 1334-9	2.2	164
156	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 174-183	24.4	162
155	An epidemiologic and genomic investigation into the obesity paradox in renal cell carcinoma. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 1862-70	9.7	161
154	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , <b>2018</b> , 6, 282-300.e2	10.6	159
153	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with -Mutant Lung Cancers. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 1063-1069	12.9	156
152	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 1325-32	17.6	153
151	Distinct patterns of dysregulated expression of enzymes involved in androgen synthesis and metabolism in metastatic prostate cancer tumors. <i>Cancer Research</i> , <b>2012</b> , 72, 6142-52	10.1	152
150	The expanding landscape of Synchronismutations in human cancers. <i>Nature</i> , <b>2019</b> , 567, 473-478	50.4	151
149	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , <b>2017</b> , 2017,	3.6	151

148	Genomic Characterization of Upper Tract Urothelial Carcinoma. <i>European Urology</i> , <b>2015</b> , 68, 970-7	10.2	147
147	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. <i>Nature</i> , <b>2016</b> , 531, 471-475	50.4	142
146	Integrative subtype discovery in glioblastoma using iCluster. <i>PLoS ONE</i> , <b>2012</b> , 7, e35236	3.7	140
145	The metabolic co-regulator PGC1 $\beta$ suppresses prostate cancer metastasis. <i>Nature Cell Biology</i> , <b>2016</b> , 18, 645-656	23.4	140
144	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , <b>2018</b> , 173, 386-399.e12	36.2	133
143	Identification of PHLPP1 as a tumor suppressor reveals the role of feedback activation in PTEN-mutant prostate cancer progression. <i>Cancer Cell</i> , <b>2011</b> , 20, 173-86	24.3	131
142	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , <b>2017</b> , 9, 4	14.4	117
141	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 450-462.e10	24.3	114
140	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. <i>ELife</i> , <b>2018</b> , 7,	8.9	114
139	Comprehensive Molecular Characterization of Salivary Duct Carcinoma Reveals Actionable Targets and Similarity to Apocrine Breast Cancer. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 4623-33	12.9	114
138	Defining the spermatogonial stem cell. <i>Developmental Biology</i> , <b>2004</b> , 269, 393-410	3.1	112
137	SQSTM1 is a pathogenic target of 5q copy number gains in kidney cancer. <i>Cancer Cell</i> , <b>2013</b> , 24, 738-50	24.3	111
136	Genetic Determinants of Cisplatin Resistance in Patients With Advanced Germ Cell Tumors. <i>Journal of Clinical Oncology</i> , <b>2016</b> , 34, 4000-4007	2.2	110
135	Genomic Alterations Observed in Colitis-Associated Cancers Are Distinct From Those Found in Sporadic Colorectal Cancers and Vary by Type of Inflammatory Bowel Disease. <i>Gastroenterology</i> , <b>2016</b> , 151, 278-287.e6	13.3	109
134	Real-Time Genomic Profiling of Pancreatic Ductal Adenocarcinoma: Potential Actionability and Correlation with Clinical Phenotype. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 6094-6100	12.9	107
133	Genomic predictors of survival in patients with high-grade urothelial carcinoma of the bladder. <i>European Urology</i> , <b>2015</b> , 67, 198-201	10.2	105
132	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. <i>Lancet Oncology</i> , <b>2020</b> , 21, 821-831	21.7	104
131	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , <b>2015</b> , 16, 45	18.3	101



130	18F-fluorodeoxy-glucose positron emission tomography marks MYC-overexpressing human basal-like breast cancers. <i>Cancer Research</i> , <b>2011</b> , 71, 5164-74	10.1	101
129	A cluster of cooperating tumor-suppressor gene candidates in chromosomal deletions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 8212-7	11.5	101
128	Synthetic lethality in ATM-deficient RAD50-mutant tumors underlies outlier response to cancer therapy. <i>Cancer Discovery</i> , <b>2014</b> , 4, 1014-21	24.4	98
127	Cancer cells preferentially lose small chromosomes. <i>International Journal of Cancer</i> , <b>2013</b> , 132, 2316-26	7.5	98
126	Integrated analyses of microRNAs demonstrate their widespread influence on gene expression in high-grade serous ovarian carcinoma. <i>PLoS ONE</i> , <b>2012</b> , 7, e34546	3.7	94
125	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. <i>Nature Communications</i> , <b>2016</b> , 7, 13131	17.4	90
124	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , <b>2013</b> , 141, 409-20	4.4	90
123	Genomic complexity and AKT dependence in serous ovarian cancer. <i>Cancer Discovery</i> , <b>2012</b> , 2, 56-67	24.4	89
122	Frequent alterations and epigenetic silencing of differentiation pathway genes in structurally rearranged liposarcomas. <i>Cancer Discovery</i> , <b>2011</b> , 1, 587-97	24.4	88
121	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , <b>2018</b> , 7, 422-437.e7	10.6	85
120	Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer. <i>Journal of Clinical Investigation</i> , <b>2018</b> , 128, 4441-4453	15.9	84
119	and Amplifications Determine Response to HER2 Inhibition in -Amplified Esophagogastric Cancer. <i>Cancer Discovery</i> , <b>2019</b> , 9, 199-209	24.4	79
118	Somatic POLE mutations cause an ultramutated giant cell high-grade glioma subtype with better prognosis. <i>Neuro-Oncology</i> , <b>2015</b> , 17, 1356-64	1	76
117	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , <b>2015</b> , 1, 197-209	10.6	72
116	Time to recurrence and survival in serous ovarian tumors predicted from integrated genomic profiles. <i>PLoS ONE</i> , <b>2011</b> , 6, e24709	3.7	72
115	Chemotherapy Resistance in Diffuse-Type Gastric Adenocarcinoma Is Mediated by RhoA Activation in Cancer Stem-Like Cells. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 971-83	12.9	70
114	Identification of low abundance microbiome in clinical samples using whole genome sequencing. <i>Genome Biology</i> , <b>2015</b> , 16, 265	18.3	67
113	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- $\beta$ pathway and reveal microRNA regulation of TGFBR2. <i>Silence: A Journal of RNA Regulation</i> , <b>2011</b> , 2, 3		67



112	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , <b>2018</b> , 5, 180061-2	6.2	66
111	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
110	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 4276-4289	15.9	64
109	Mitochondrial respiratory gene expression is suppressed in many cancers. <i>ELife</i> , <b>2017</b> , 6,	8.9	64
108	Comprehensive analysis of long non-coding RNAs in ovarian cancer reveals global patterns and targeted DNA amplification. <i>PLoS ONE</i> , <b>2013</b> , 8, e80306	3.7	63
107	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. <i>Cancer Cell</i> , <b>2017</b> , 32, 155-168.e6	24.3	61
106	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , <b>2020</b> , 52, 448-457	36.3	58
105	Analytic and clinical validation of a prostate cancer-enhanced messenger RNA detection assay in whole blood as a prognostic biomarker for survival. <i>European Urology</i> , <b>2014</b> , 65, 1191-7	10.2	58
104	MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. <i>Journal of Pathology</i> , <b>2013</b> , 229, 99-110	9.4	58
103	Genomic Methods Identify Homologous Recombination Deficiency in Pancreas Adenocarcinoma and Optimize Treatment Selection. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 3239-3247	12.9	58
102	Loss of the tyrosine phosphatase PTPRD leads to aberrant STAT3 activation and promotes gliomagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 8149-54	11.5	57
101	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. <i>Cancer Cell</i> , <b>2018</b> , 33, 527-541.e855	34.3	55
100	Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma: A Phase 2 Clinical Trial. <i>JAMA Oncology</i> , <b>2020</b> , 6, 60-67	13.4	55
99	Genomic Differences Between "Primary" and "Secondary" Muscle-invasive Bladder Cancer as a Basis for Disparate Outcomes to Cisplatin-based Neoadjuvant Chemotherapy. <i>European Urology</i> , <b>2019</b> , 75, 231-239	10.2	53
98	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. <i>Clinical Cancer Research</i> , <b>2018</b> , 24, 1965-1973	12.9	51
97	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 1893-1898	7.6	50
96	Oncogenic Genomic Alterations, Clinical Phenotypes, and Outcomes in Metastatic Castration-Sensitive Prostate Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 3230-3238	12.9	49
95	KMT2C mediates the estrogen dependence of breast cancer through regulation of ER $\alpha$ enhancer function. <i>Oncogene</i> , <b>2018</b> , 37, 4692-4710	9.2	48

94	ERF mutations reveal a balance of ETS factors controlling prostate oncogenesis. <i>Nature</i> , <b>2017</b> , 546, 671-674	6.7	47
93	BRCA1 immunohistochemistry in a molecularly characterized cohort of ovarian high-grade serous carcinomas. <i>American Journal of Surgical Pathology</i> , <b>2013</b> , 37, 138-46	6.7	47
92	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. <i>Oncotarget</i> , <b>2014</b> , 5, 8083-92	3.3	46
91	Clinical and Molecular Predictors of Response to Immune Checkpoint Inhibitors in Patients with Advanced Esophagogastric Cancer. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 6160-6169	12.9	45
90	Recurrent patterns of DNA copy number alterations in tumors reflect metabolic selection pressures. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 914	12.2	44
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