Obi Lee Griffith

List of Publications by Year
in descending order

174 papers	25,320 citations	16451 64 h-index	7518 151 g-index
208 all docs	208 docs citations	208 times ranked	41740 citing authors

#	Article	IF	Citations
1	The Genome Sequence of the SARS-Associated Coronavirus. Science, 2003, 300, 1399-1404.	12.6	1,842
2	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
3	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
4	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
5	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. Nature Methods, 2007, 4, 651-657.	19.0	1,254
6	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
7	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. Genome Research, 2008, 18, 610-621.	5.5	964
8	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886
9	DGIdb 3.0: a redesign and expansion of the drug–gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.	14.5	686
10	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
11	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
12	Convergent loss of PTEN leads to clinical resistance to a PI(3)Kα inhibitor. Nature, 2015, 518, 240-244.	27.8	486
13	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	3.2	477
14	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
15	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
16	Integration of the Drug–Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. Nucleic Acids Research, 2021, 49, D1144-D1151.	14.5	439
17	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
18	DGIdb 2.0: mining clinically relevant drug–gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359

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19	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. Genome Medicine, 2016, 8, 11.	8.2	350
20	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
21	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
22	Alternative expression analysis by RNA sequencing. Nature Methods, 2010, 7, 843-847.	19.0	283
23	Meta-Analysis and Meta-Review of Thyroid Cancer Gene Expression Profiling Studies Identifies Important Diagnostic Biomarkers. Journal of Clinical Oncology, 2006, 24, 5043-5051.	1.6	279
24	Modeling precision treatment of breast cancer. Genome Biology, 2013, 14, R110.	9.6	264
25	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing InÂVivo. Cancer Cell, 2015, 27, 631-643.	16.8	259
26	NeoPalAna: Neoadjuvant Palbociclib, a Cyclin-Dependent Kinase 4/6 Inhibitor, and Anastrozole for Clinical Stage 2 or 3 Estrogen Receptorâ€"Positive Breast Cancer. Clinical Cancer Research, 2017, 23, 4055-4065.	7.0	243
27	GenVisR: Genomic Visualizations in R. Bioinformatics, 2016, 32, 3012-3014.	4.1	237
28	Phosphorylated Caveolin-1 Regulates Rho/ROCK-Dependent Focal Adhesion Dynamics and Tumor Cell Migration and Invasion. Cancer Research, 2008, 68, 8210-8220.	0.9	228
29	ORegAnno: an open-access community-driven resource for regulatory annotation. Nucleic Acids Research, 2007, 36, D107-D113.	14.5	227
30	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. Emerging Infectious Diseases, 2004, 10, 2192-2195.	4.3	182
31	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
32	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246.	2.8	173
33	High-performance web services for querying gene and variant annotation. Genome Biology, 2016, 17, 91.	8.8	166
34	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirusâ€"Unrelated Head and Neck Cancer: A Multicenter, Phase II Trial. Clinical Cancer Research, 2020, 26, 5140-5152.	7.0	163
35	In-depth characterization of the microRNA transcriptome in a leukemia progression model. Genome Research, 2008, 18, 1787-1797.	5.5	162
36	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159

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37	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. Blood, 2017, 129, 473-483.	1.4	147
38	Best practices for bioinformatic characterization of neoantigens for clinical utility. Genome Medicine, 2019, 11, 56.	8.2	146
39	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. Nucleic Acids Research, 2016, 44, D126-D132.	14.5	142
40	Diagnostic Utility of Galectin-3 in Thyroid Cancer. American Journal of Pathology, 2010, 176, 2067-2081.	3.8	137
41	Meta-analysis of Colorectal Cancer Gene Expression Profiling Studies Identifies Consistently Reported Candidate Biomarkers. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 543-552.	2.5	132
42	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	3.4	132
43	Single-agent ibrutinib in relapsed or refractory follicular lymphoma: a phase 2 consortium trial. Blood, 2018, 131, 182-190.	1.4	130
44	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
45	FOXA1 overexpression mediates endocrine resistance by altering the ER transcriptome and IL-8 expression in ER-positive breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6600-E6609.	7.1	119
46	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	12.8	112
47	U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing. Leukemia, 2015, 29, 909-917.	7.2	107
48	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
49	DoCM: a database of curated mutations in cancer. Nature Methods, 2016, 13, 806-807.	19.0	96
50	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
51	Interaction of Cyclin-Dependent Kinase 12/CrkRS with Cyclin K1 Is Required for the Phosphorylation of the C-Terminal Domain of RNA Polymerase II. Molecular and Cellular Biology, 2012, 32, 4691-4704.	2.3	93
52	Identification of PADI2 as a potential breast cancer biomarker and therapeutic target. BMC Cancer, 2012, 12, 500.	2.6	93
53	Hippo Signaling Influences HNF4A and FOXA2 Enhancer Switching during Hepatocyte Differentiation. Cell Reports, 2014, 9, 261-271.	6.4	89
54	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	12.8	89

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55	Identification of Molecular Markers Altered During Transformation of Differentiated Into Anaplastic Thyroid Carcinoma. Archives of Surgery, 2007, 142, 717.	2.2	88
56	A Phase I Trial of BKM120 (Buparlisib) in Combination with Fulvestrant in Postmenopausal Women with Estrogen Receptorâ€"Positive Metastatic Breast Cancer. Clinical Cancer Research, 2016, 22, 1583-1591.	7.0	86
57	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
58	Organizing knowledge to enable personalization of medicine in cancer. Genome Biology, 2014, 15, 438.	8.8	81
59	Rapid progression of adult T-cell leukemia/lymphoma as tumor-infiltrating Tregs after PD-1 blockade. Blood, 2019, 134, 1406-1414.	1.4	80
60	c-Src Modulates Estrogen-Induced Stress and Apoptosis in Estrogen-Deprived Breast Cancer Cells. Cancer Research, 2013, 73, 4510-4520.	0.9	77
61	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	6.0	76
62	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. Neoplasia, 2015, 17, 776-788.	5.3	75
63	Impact of whole genome amplification on analysis of copy number variants. Nucleic Acids Research, 2008, 36, e80-e80.	14.5	74
64	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. PLoS Computational Biology, 2015, 11, e1004393.	3.2	74
65	Sequencing and analysis of 10,967 full-length cDNA clones from Xenopus laevis and Xenopus tropicalis reveals post-tetraploidization transcriptome remodeling. Genome Research, 2006, 16, 796-803.	5.5	73
66	Cross-platform pathway-based analysis identifies markers of response to the PARP inhibitor olaparib. Breast Cancer Research and Treatment, 2012, 135, 505-517.	2.5	69
67	Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS ONE, 2014, 9, e111153.	2.5	69
68	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 2016, 7, 12498.	12.8	69
69	Extensive relationship between antisense transcription and alternative splicing in the human genome. Genome Research, 2011, 21, 1203-1212.	5.5	68
70	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor andÂnormal samples. Genetics in Medicine, 2019, 21, 972-981.	2.4	67
71	A Phase II Trial of Neoadjuvant MK-2206, an AKT Inhibitor, with Anastrozole in Clinical Stage II or III<i>PIK3CA</i>-Mutant ER-Positive and HER2-Negative Breast Cancer. Clinical Cancer Research, 2017, 23, 6823-6832.	7.0	66
72	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	21.4	62

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73	Lrig1 Is an Estrogen-Regulated Growth Suppressor and Correlates with Longer Relapse-Free Survival in ERÎ±-Positive Breast Cancer. Molecular Cancer Research, 2011, 9, 1406-1417.	3.4	60
74	Donor memory-like NK cells persist and induce remissions in pediatric patients with relapsed AML after transplant. Blood, 2022, 139, 1670-1683.	1.4	57
75	Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351.	12.8	56
76	Statistically identifying tumor suppressors and oncogenes from pan-cancer genome-sequencing data. Bioinformatics, 2015, 31, 3561-3568.	4.1	55
77	Genomic characterization of HER2-positive breast cancer and response to neoadjuvant trastuzumab and chemotherapyâ€"results from the ACOSOG Z1041 (Alliance) trial. Annals of Oncology, 2017, 28, 1070-1077.	1.2	55
78	Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC). Genetics in Medicine, 2022, 24, 986-998.	2.4	55
79	Sequence biases in large scale gene expression profiling data. Nucleic Acids Research, 2006, 34, e83-e83.	14.5	51
80	Molecular Phenotyping of Thyroid Tumors Identifies a Marker Panel for Differentiated Thyroid Cancer Diagnosis. Annals of Surgical Oncology, 2008, 15, 2811-2826.	1.5	50
81	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. Journal of Proteome Research, 2012, 11, 2508-2520.	3.7	49
82	Hematopoietic cell transplantation donor-derived memory-like NK cells functionally persist after transfer into patients with leukemia. Science Translational Medicine, 2022, 14, eabm1375.	12.4	49
83	Loss of Cell-Surface Laminin Anchoring Promotes Tumor Growth and Is Associated with Poor Clinical Outcomes. Cancer Research, 2012, 72, 2578-2588.	0.9	47
84	Detection and Management of Hypothyroidism Following Thyroid Lobectomy: Evaluation of a Clinical Algorithm. Annals of Surgical Oncology, 2011, 18, 2548-2554.	1.5	46
85	Biomarker panel diagnosis of thyroid cancer: a critical review. Expert Review of Anticancer Therapy, 2008, 8, 1399-1413.	2.4	45
86	Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. Genomics, 2005, 86, 476-488.	2.9	44
87	RNAâ€sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	4.9	44
88	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.4	44
89	Accounting for proximal variants improves neoantigen prediction. Nature Genetics, 2019, 51, 175-179.	21.4	43
90	Cell Cycle Regulators Show Diagnostic and Prognostic Utility for Differentiated Thyroid Cancer. Annals of Surgical Oncology, 2007, 14, 3403-3411.	1.5	42

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91	Targeting the Mevalonate Pathway to Overcome Acquired Anti-HER2 Treatment Resistance in Breast Cancer. Molecular Cancer Research, 2019, 17, 2318-2330.	3.4	41
92	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	10.3	41
93	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. PLoS ONE, 2013, 8, e77571.	2.5	40
94	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	2.8	40
95	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23662-23670.	7.1	40
96	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. Bone, 2017, 101, 145-155.	2.9	37
97	Bam-readcount - rapid generation of basepair-resolution sequence metrics. Journal of Open Source Software, 2022, 7, 3722.	4.6	36
98	Single exon-resolution targeted chromosomal microarray analysis of known and candidate intellectual disability genes. European Journal of Human Genetics, 2014, 22, 792-800.	2.8	35
99	Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. Genome Medicine, 2019, 11, 78.	8.2	35
100	Text-mining assisted regulatory annotation. Genome Biology, 2008, 9, R31.	9.6	34
101	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. Cancer Discovery, 2022, 12, 154-171.	9.4	34
102	The Cure: Design and Evaluation of a Crowdsourcing Game for Gene Selection for Breast Cancer Survival Prediction. JMIR Serious Games, 2014, 2, e7.	3.1	31
103	Splicing factor SF3B1 promotes endometrial cancer progression via regulating KSR2 RNA maturation. Cell Death and Disease, 2020, 11, 842.	6.3	30
104	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. Pharmacogenomics Journal, 2013, 13, 148-158.	2.0	29
105	Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. Genome Research, 2004, 14, 2083-2092.	5.5	28
106	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. Cell Reports, 2018, 24, 2167-2178.	6.4	26
107	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
108	Phase I Trial of N-803, an IL15 Receptor Agonist, with Rituximab in Patients with Indolent Non-Hodgkin Lymphoma. Clinical Cancer Research, 2021, 27, 3339-3350.	7.0	26

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109	A case of acute myeloid leukemia with promyelocytic features characterized by expression of a novel RARG-CPSF6 fusion. Blood Advances, 2018, 2, 1295-1299.	5.2	25
110	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. PLoS Computational Biology, 2007, 3, e106.	3.2	24
111	ImmunogenomicÂprofiling and pathological response results from a clinical trial of docetaxel and carboplatin in triple-negative breast cancer. Breast Cancer Research and Treatment, 2021, 189, 187-202.	2.5	24
112	Discovering significant OPSM subspace clusters in massive gene expression data. , 2006, , .		23
113	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 105-111.	1.1	22
114	'Omic approaches to preventing or managing metastatic breast cancer. Breast Cancer Research, 2011, 13, 230.	5.0	21
115	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.	6.4	21
116	ALEXA: a microarray design platform for alternative expression analysis. Nature Methods, 2008, 5, 118-118.	19.0	19
117	On the Deep Order-Preserving Submatrix Problem: A Best Effort Approach. IEEE Transactions on Knowledge and Data Engineering, 2012, 24, 309-325.	5.7	19
118	A Spontaneous Aggressive ERÎ±+ Mammary Tumor Model Is Driven by Kras Activation. Cell Reports, 2019, 28, 1526-1537.e4.	6.4	19
119	Decoupling of the PI3K Pathway via Mutation Necessitates Combinatorial Treatment in HER2+ Breast Cancer. PLoS ONE, 2015, 10, e0133219.	2.5	19
120	A robust prognostic signature for hormone-positive node-negative breast cancer. Genome Medicine, 2013, 5, 92.	8.2	18
121	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. Annals of Oncology, 2016, 27, 1148-1154.	1.2	18
122	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. Blood Cancer Journal, 2016, 6, e413-e413.	6.2	18
123	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	6.5	18
124	Clinical utility of type 1 growth factor receptor expression in colon cancer. American Journal of Surgery, 2008, 195, 604-610.	1.8	17
125	Phase 1/dose expansion trial of brentuximab vedotin andÂlenalidomide in relapsed or refractory diffuse large B-cell lymphoma. Blood, 2022, 139, 1999-2010.	1.4	17
126	Evaluation of type 1 growth factor receptor family expression in benign and malignant thyroid lesions. American Journal of Surgery, 2008, 195, 667-673.	1.8	16

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127	Neoantigens in immunotherapy and personalized vaccines: Implications for head and neck squamous cell carcinoma. Oral Oncology, 2017, 71, 169-176.	1.5	16
128	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
129	Yap1 Mediates Trametinib Resistance in Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2021, 27, 2326-2339.	7.0	16
130	Identification of gene regulation patterns underlying both oestrogen- and tamoxifen-stimulated cell growth through global gene expression profiling in breast cancer cells. European Journal of Cancer, 2014, 50, 2877-2886.	2.8	15
131	A common founding clone with <i>TP53</i> and <i>PTEN</i> mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. Journal of Physical Education and Sports Management, 2016, 2, a000687.	1.2	15
132	Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data communityâ€driven standards. Human Mutation, 2018, 39, 1721-1732.	2.5	15
133	Checkpoint blockade-induced CD8+ T cell differentiation in head and neck cancer responders. , 2022, 10, e004034.		14
134	Immunophenotyping of thyroid tumors identifies molecular markers altered during transformation of differentiated into anaplastic carcinoma. American Journal of Surgery, 2011, 201, 580-586.	1.8	13
135	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 247-258.	0.7	13
136	ClinGen Cancer Somatic Working Group â€" standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. , 2018, , .		12
137	Epigenomic regulation of human T-cell leukemia virus by chromatin-insulator CTCF. PLoS Pathogens, 2021, 17, e1009577.	4.7	12
138	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
139	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
140	Noninvasive Detection of High-Risk Adenomas Using Stool-Derived Eukaryotic RNA Sequences as Biomarkers. Gastroenterology, 2019, 157, 884-887.e3.	1.3	9
141	KiWi: A Scalable Subspace Clustering Algorithm for Gene Expression Analysis. , 2009, , .		7
142	Unraveling the chaotic genomic landscape of primary and metastatic canine appendicular osteosarcoma with current sequencing technologies and bioinformatic approaches. PLoS ONE, 2021, 16, e0246443.	2.5	7
143	Exploring the Genomic Landscape of Cancer Patient Cohorts with GenVisR. Current Protocols, 2021, 1, e252.	2.9	7
144	Escherichia coli endA deletion strain for use in two-hybrid shuttle vector selection. BioTechniques, 2003, 35, 272-278.	1.8	6

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145	Clinical implications of neoepitope landscapes for adult and pediatric cancers. Genome Medicine, 2017, 9, 77.	8.2	6
146	Open-Sourced CIViC Annotation Pipeline to Identify and Annotate Clinically Relevant Variants Using Single-Molecule Molecular Inversion Probes. JCO Clinical Cancer Informatics, 2019, 3, 1-12.	2.1	6
147	Integrative genomic analysis reveals low T-cell infiltration as the primary feature of tobacco use in HPV-positive oropharyngeal cancer. IScience, 2022, 25, 104216.	4.1	6
148	Sex- and Mutation-Specific p53 Gain-of-Function Activity in Gliomagenesis. Cancer Research Communications, 2021, 1, 148-163.	1.7	6
149	Large scale genotypeâ€•and phenotypeâ€•driven machine learning in Von Hippelâ€•Lindau disease. Human Mutation, 2022, 43, 1268-1285.	2.5	6
150	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
151	Impact of a 40-Gene Targeted Panel Test on Physician Decision Making for Patients With Acute Myeloid Leukemia. JCO Precision Oncology, 2021, 5, 191-203.	3.0	4
152	B-Cell Acute Lymphoblastic Leukemia Arising in Patients with a Preexisting Diagnosis of Multiple Myeloma Is a Novel Cancer with High Incidence of TP53 Mutations. Blood, 2020, 136, 20-20.	1.4	3
153	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.4	3
154	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
155	Genetic Ancestry Correlations with Driver Mutations Suggest Complex Interactions between Somatic and Germline Variation in Cancer. Cancer Discovery, 2021, 11, 534-536.	9.4	2
156	Multitarget Stool RNA Test for Noninvasive Detection of Colorectal Neoplasia in a Multicenter, Prospective, and Retrospective Cohort. Clinical and Translational Gastroenterology, 2021, 12, e00360.	2.5	2
157	Annotating the Regulatory Genome. Methods in Molecular Biology, 2010, 674, 313-349.	0.9	2
158	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. Blood, 2015, 126, 574-574.	1.4	2
159	Cytokine-Induced Memory-like NK Cells Have a Distinct Single Cell Transcriptional Profile and Persist for Months in Adult and Pediatric Leukemia Patients after Adoptive Transfer. Blood, 2021, 138, 3825-3825.	1.4	1
160	<i>In Silico</i> Epitope Prediction Analyses Highlight the Potential for Distracting Antigen Immunodominance with Allogeneic Cancer Vaccines. Cancer Research Communications, 2021, 1, 115-126.	1.7	1
161	M1982 Identification of Differentially Expressed Alternative mRNA Isoforms Associated with Chemotherapy Resistance in Colon Cancer Cell Lines. Gastroenterology, 2008, 134, A-444.	1.3	0
162	Genomic analysis of a rare human tumor. BMC Bioinformatics, 2010, 11, .	2.6	0

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163	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0
164	Reply. Gastroenterology, 2020, 158, 793-794.	1.3	0
165	Colonosight: Multitarget RNA-FIT assay for noninvasive detection of advanced colorectal neoplasia.. Journal of Clinical Oncology, 2021, 39, 25-25.	1.6	0
166	OMIC-13. THE ROLE OF COPY NUMBER ALTERATIONS IN PREDICTING SURVIVAL AND INFLUENCING TREATMENT OF CHILDHOOD BRAIN TUMORS. Neuro-Oncology, 2021, 23, i40-i40.	1.2	0
167	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
168	Thyroid Cancer: Identification of Gene Expression Markers for Diagnosis. , 2010, , 353-377.		0
169	Exome Sequencing of Hodgkin's and Non-Hodgkin Composite Lymphomas Identifies Shared Somatic Mutations Indicative of Common Founding Precursors. Blood, 2016, 128, 5285-5285.	1.4	0
170	Clonal Evolution Revealed By Exome Sequencing in a Case of Primary Myelofibrosis Associated with Subsequent Development of Aggressive Systemic Mastocytosis/Mast Cell Leukemia. Blood, 2016, 128, 5496-5496.	1.4	0
171	Standardizing And Democratizing Access To Cancer Molecular Diagnostic Test Data From Patients To Drive Translational Research. AMIA Summits on Translational Science Proceedings, 2018, 2017, 152-159.	0.4	0
172	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
173	IMMU-53. CHARACTERIZATION OF THE GENOMIC AND IMMUNOLOGICAL DIVERSITY OF MALIGNANT BRAIN TUMORS THROUGH MULTI-SECTOR ANALYSIS. Neuro-Oncology, 2020, 22, ii116-ii116.	1.2	0
174	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0