

Obi Lee Griffith

List of Publications by Year in descending order

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Version: 2024-02-01

173
papers

25,320
citations

18887

64
h-index

8627

151
g-index

208
all docs

208
docs citations

208
times ranked

45985
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	6.0	1,842
2	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	13.7	1,778
3	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	9.4	1,504
4	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
5	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657.	9.0	1,254
6	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. <i>Cell</i> , 2012, 150, 1121-1134.	13.5	1,038
7	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. <i>Genome Research</i> , 2008, 18, 610-621.	2.4	964
8	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	9.0	886
9	DrugDB 3.0: a redesign and expansion of the drug-gene interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D1068-D1073.	6.5	686
10	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. <i>Cell Reports</i> , 2013, 4, 1116-1130.	2.9	539
11	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	2.4	486
12	Convergent loss of PTEN leads to clinical resistance to a PI(3)K inhibitor. <i>Nature</i> , 2015, 518, 240-244.	13.7	486
13	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001138.	1.5	477
14	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	9.4	460
15	DrugDB: mining the druggable genome. <i>Nature Methods</i> , 2013, 10, 1209-1210.	9.0	443
16	Integration of the Drug-Gene Interaction Database (DrugDB 4.0) with open crowdsource efforts. <i>Nucleic Acids Research</i> , 2021, 49, D1144-D1151.	6.5	439
17	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. <i>PLoS Computational Biology</i> , 2014, 10, e1003665.	1.5	400
18	DrugDB 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	6.5	359

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19	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. <i>Genome Medicine</i> , 2016, 8, 11.	3.6	350
20	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2014, 25, 379-392.	7.7	330
21	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 811.	3.8	302
22	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	9.0	283
23	Meta-Analysis and Meta-Review of Thyroid Cancer Gene Expression Profiling Studies Identifies Important Diagnostic Biomarkers. <i>Journal of Clinical Oncology</i> , 2006, 24, 5043-5051.	0.8	279
24	Modeling precision treatment of breast cancer. <i>Genome Biology</i> , 2013, 14, R110.	13.9	264
25	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. <i>Cancer Cell</i> , 2015, 27, 631-643.	7.7	259
26	NeoPalAna: Neoadjuvant Palbociclib, a Cyclin-Dependent Kinase 4/6 Inhibitor, and Anastrozole for Clinical Stage 2 or 3 Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4055-4065.	3.2	243
27	GenVisR: Genomic Visualizations in R. <i>Bioinformatics</i> , 2016, 32, 3012-3014.	1.8	237
28	Phosphorylated Caveolin-1 Regulates Rho/ROCK-Dependent Focal Adhesion Dynamics and Tumor Cell Migration and Invasion. <i>Cancer Research</i> , 2008, 68, 8210-8220.	0.4	228
29	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	6.5	227
30	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.	2.0	182
31	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	2.9	174
32	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.	1.2	173
33	High-performance web services for querying gene and variant annotation. <i>Genome Biology</i> , 2016, 17, 91.	3.8	166
34	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirus-Related Head and Neck Cancer: A Multicenter, Phase II Trial. <i>Clinical Cancer Research</i> , 2020, 26, 5140-5152.	3.2	163
35	In-depth characterization of the microRNA transcriptome in a leukemia progression model. <i>Genome Research</i> , 2008, 18, 1787-1797.	2.4	162
36	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	159

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37	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. <i>Blood</i> , 2017, 129, 473-483.	0.6	147
38	Best practices for bioinformatic characterization of neoantigens for clinical utility. <i>Genome Medicine</i> , 2019, 11, 56.	3.6	146
39	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. <i>Nucleic Acids Research</i> , 2016, 44, D126-D132.	6.5	142
40	Diagnostic Utility of Galectin-3 in Thyroid Cancer. <i>American Journal of Pathology</i> , 2010, 176, 2067-2081.	1.9	137
41	Meta-analysis of Colorectal Cancer Gene Expression Profiling Studies Identifies Consistently Reported Candidate Biomarkers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 543-552.	1.1	132
42	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. <i>Cancer Immunology Research</i> , 2020, 8, 409-420.	1.6	132
43	Single-agent ibrutinib in relapsed or refractory follicular lymphoma: a phase 2 consortium trial. <i>Blood</i> , 2018, 131, 182-190.	0.6	130
44	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	2.4	125
45	FOXA1 overexpression mediates endocrine resistance by altering the ER transcriptome and IL-8 expression in ER-positive breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6600-E6609.	3.3	119
46	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. <i>Nature Communications</i> , 2018, 9, 3787.	5.8	112
47	U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing. <i>Leukemia</i> , 2015, 29, 909-917.	3.3	107
48	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	9.4	104
49	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016, 13, 806-807.	9.0	96
50	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	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. <i>Molecular and Cellular Biology</i> , 2012, 32, 4691-4704.	1.1	93
52	Identification of PADI2 as a potential breast cancer biomarker and therapeutic target. <i>BMC Cancer</i> , 2012, 12, 500.	1.1	93
53	Hippo Signaling Influences HNF4A and FOXA2 Enhancer Switching during Hepatocyte Differentiation. <i>Cell Reports</i> , 2014, 9, 261-271.	2.9	89
54	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	5.8	89

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55	Identification of Molecular Markers Altered During Transformation of Differentiated Into Anaplastic Thyroid Carcinoma. <i>Archives of Surgery</i> , 2007, 142, 717.	2.3	88
56	A Phase I Trial of BKM120 (Buparlisib) in Combination with Fulvestrant in Postmenopausal Women with Estrogen Receptor-Positive Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 1583-1591.	3.2	86
57	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	1.5	83
58	Organizing knowledge to enable personalization of medicine in cancer. <i>Genome Biology</i> , 2014, 15, 438.	3.8	81
59	Rapid progression of adult T-cell leukemia/lymphoma as tumor-infiltrating Tregs after PD-1 blockade. <i>Blood</i> , 2019, 134, 1406-1414.	0.6	80
60	c-Src Modulates Estrogen-Induced Stress and Apoptosis in Estrogen-Deprived Breast Cancer Cells. <i>Cancer Research</i> , 2013, 73, 4510-4520.	0.4	77
61	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020, 9, .	2.8	76
62	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. <i>Neoplasia</i> , 2015, 17, 776-788.	2.3	75
63	Impact of whole genome amplification on analysis of copy number variants. <i>Nucleic Acids Research</i> , 2008, 36, e80-e80.	6.5	74
64	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. <i>PLoS Computational Biology</i> , 2015, 11, e1004393.	1.5	74
65	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	2.4	73
66	Cross-platform pathway-based analysis identifies markers of response to the PARP inhibitor olaparib. <i>Breast Cancer Research and Treatment</i> , 2012, 135, 505-517.	1.1	69
67	Clonal Architectures and Driver Mutations in Metastatic Melanomas. <i>PLoS ONE</i> , 2014, 9, e111153.	1.1	69
68	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016, 7, 12498.	5.8	69
69	Extensive relationship between antisense transcription and alternative splicing in the human genome. <i>Genome Research</i> , 2011, 21, 1203-1212.	2.4	68
70	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor and normal samples. <i>Genetics in Medicine</i> , 2019, 21, 972-981.	1.1	67
71	A Phase II Trial of Neoadjuvant MK-2206, an AKT Inhibitor, with Anastrozole in Clinical Stage II or III PIK3CA-Mutant ER-Positive and HER2-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6823-6832.	3.2	66
72	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. <i>Nature Genetics</i> , 2018, 50, 1735-1743.	9.4	62

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73	Lrig1 Is an Estrogen-Regulated Growth Suppressor and Correlates with Longer Relapse-Free Survival in ER \pm -Positive Breast Cancer. <i>Molecular Cancer Research</i> , 2011, 9, 1406-1417.	1.5	60
74	Donor memory-like NK cells persist and induce remissions in pediatric patients with relapsed AML after transplant. <i>Blood</i> , 2022, 139, 1670-1683.	0.6	57
75	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351.	5.8	56
76	Statistically identifying tumor suppressors and oncogenes from pan-cancer genome-sequencing data. <i>Bioinformatics</i> , 2015, 31, 3561-3568.	1.8	55
77	Genomic characterization of HER2-positive breast cancer and response to neoadjuvant trastuzumab and chemotherapy—results from the ACOSOG Z1041 (Alliance) trial. <i>Annals of Oncology</i> , 2017, 28, 1070-1077.	0.6	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). <i>Genetics in Medicine</i> , 2022, 24, 986-998.	1.1	55
79	Sequence biases in large scale gene expression profiling data. <i>Nucleic Acids Research</i> , 2006, 34, e83-e83.	6.5	51
80	Molecular Phenotyping of Thyroid Tumors Identifies a Marker Panel for Differentiated Thyroid Cancer Diagnosis. <i>Annals of Surgical Oncology</i> , 2008, 15, 2811-2826.	0.7	50
81	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. <i>Journal of Proteome Research</i> , 2012, 11, 2508-2520.	1.8	49
82	Hematopoietic cell transplantation donor-derived memory-like NK cells functionally persist after transfer into patients with leukemia. <i>Science Translational Medicine</i> , 2022, 14, eabm1375.	5.8	49
83	Loss of Cell-Surface Laminin Anchoring Promotes Tumor Growth and Is Associated with Poor Clinical Outcomes. <i>Cancer Research</i> , 2012, 72, 2578-2588.	0.4	47
84	Detection and Management of Hypothyroidism Following Thyroid Lobectomy: Evaluation of a Clinical Algorithm. <i>Annals of Surgical Oncology</i> , 2011, 18, 2548-2554.	0.7	46
85	Biomarker panel diagnosis of thyroid cancer: a critical review. <i>Expert Review of Anticancer Therapy</i> , 2008, 8, 1399-1413.	1.1	45
86	Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. <i>Genomics</i> , 2005, 86, 476-488.	1.3	44
87	RNA-seq reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. <i>Glia</i> , 2015, 63, 531-548.	2.5	44
88	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.2	44
89	Accounting for proximal variants improves neoantigen prediction. <i>Nature Genetics</i> , 2019, 51, 175-179.	9.4	43
90	Cell Cycle Regulators Show Diagnostic and Prognostic Utility for Differentiated Thyroid Cancer. <i>Annals of Surgical Oncology</i> , 2007, 14, 3403-3411.	0.7	42

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91	Targeting the Mevalonate Pathway to Overcome Acquired Anti-HER2 Treatment Resistance in Breast Cancer. <i>Molecular Cancer Research</i> , 2019, 17, 2318-2330.	1.5	41
92	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	4.7	41
93	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. <i>PLoS ONE</i> , 2013, 8, e77571.	1.1	40
94	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	1.2	40
95	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23662-23670.	3.3	40
96	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. <i>Bone</i> , 2017, 101, 145-155.	1.4	37
97	Bam-readcount - rapid generation of basepair-resolution sequence metrics. <i>Journal of Open Source Software</i> , 2022, 7, 3722.	2.0	36
98	Single exon-resolution targeted chromosomal microarray analysis of known and candidate intellectual disability genes. <i>European Journal of Human Genetics</i> , 2014, 22, 792-800.	1.4	35
99	Text-mining clinically relevant cancer biomarkers for curation into the CIVIC database. <i>Genome Medicine</i> , 2019, 11, 78.	3.6	35
100	Text-mining assisted regulatory annotation. <i>Genome Biology</i> , 2008, 9, R31.	13.9	34
101	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. <i>Cancer Discovery</i> , 2022, 12, 154-171.	7.7	34
102	The Cure: Design and Evaluation of a Crowdsourcing Game for Gene Selection for Breast Cancer Survival Prediction. <i>JMIR Serious Games</i> , 2014, 2, e7.	1.7	31
103	Splicing factor SF3B1 promotes endometrial cancer progression via regulating KSR2 RNA maturation. <i>Cell Death and Disease</i> , 2020, 11, 842.	2.7	30
104	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. <i>Pharmacogenomics Journal</i> , 2013, 13, 148-158.	0.9	29
105	Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. <i>Genome Research</i> , 2004, 14, 2083-2092.	2.4	28
106	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. <i>Cell Reports</i> , 2018, 24, 2167-2178.	2.9	26
107	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 602-613.	1.0	26
108	Phase I Trial of N-803, an IL15 Receptor Agonist, with Rituximab in Patients with Indolent Non-Hodgkin Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 3339-3350.	3.2	26

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109	A case of acute myeloid leukemia with promyelocytic features characterized by expression of a novel RARG-CPSF6 fusion. <i>Blood Advances</i> , 2018, 2, 1295-1299.	2.5	25
110	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. <i>PLoS Computational Biology</i> , 2007, 3, e106.	1.5	24
111	Immunogenomic Profiling and pathological response results from a clinical trial of docetaxel and carboplatin in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 189, 187-202.	1.1	24
112	Discovering significant OPSM subspace clusters in massive gene expression data. , 2006, , .		23
113	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2016, 81, 105-111.	2.0	22
114	'Omic approaches to preventing or managing metastatic breast cancer. <i>Breast Cancer Research</i> , 2011, 13, 230.	2.2	21
115	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	2.9	21
116	ALEXA: a microarray design platform for alternative expression analysis. <i>Nature Methods</i> , 2008, 5, 118-118.	9.0	19
117	On the Deep Order-Preserving Submatrix Problem: A Best Effort Approach. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2012, 24, 309-325.	4.0	19
118	A Spontaneous Aggressive ER ⁺ Mammary Tumor Model Is Driven by Kras Activation. <i>Cell Reports</i> , 2019, 28, 1526-1537.e4.	2.9	19
119	Decoupling of the PI3K Pathway via Mutation Necessitates Combinatorial Treatment in HER2+ Breast Cancer. <i>PLoS ONE</i> , 2015, 10, e0133219.	1.1	19
120	A robust prognostic signature for hormone-positive node-negative breast cancer. <i>Genome Medicine</i> , 2013, 5, 92.	3.6	18
121	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. <i>Annals of Oncology</i> , 2016, 27, 1148-1154.	0.6	18
122	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. <i>Blood Cancer Journal</i> , 2016, 6, e413-e413.	2.8	18
123	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. <i>Cell Genomics</i> , 2021, 1, 100027.	3.0	18
124	Clinical utility of type 1 growth factor receptor expression in colon cancer. <i>American Journal of Surgery</i> , 2008, 195, 604-610.	0.9	17
125	Phase 1/dose expansion trial of brentuximab vedotin and lenalidomide in relapsed or refractory diffuse large B-cell lymphoma. <i>Blood</i> , 2022, 139, 1999-2010.	0.6	17
126	Evaluation of type 1 growth factor receptor family expression in benign and malignant thyroid lesions. <i>American Journal of Surgery</i> , 2008, 195, 667-673.	0.9	16

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127	Neoantigens in immunotherapy and personalized vaccines: Implications for head and neck squamous cell carcinoma. <i>Oral Oncology</i> , 2017, 71, 169-176.	0.8	16
128	Standard operating procedure for curation and clinical interpretation of variants in cancer. <i>Genome Medicine</i> , 2019, 11, 76.	3.6	16
129	Yap1 Mediates Trametinib Resistance in Head and Neck Squamous Cell Carcinomas. <i>Clinical Cancer Research</i> , 2021, 27, 2326-2339.	3.2	16
130	Identification of gene regulation patterns underlying both oestrogen- and tamoxifen-stimulated cell growth through global gene expression profiling in breast cancer cells. <i>European Journal of Cancer</i> , 2014, 50, 2877-2886.	1.3	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. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000687.	0.5	15
132	Adapting crowdsourced clinical cancer curation in CIVIC to the ClinGen minimum variant level data community-driven standards. <i>Human Mutation</i> , 2018, 39, 1721-1732.	1.1	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. <i>American Journal of Surgery</i> , 2011, 201, 580-586.	0.9	13
135	ClinGen Cancer Somatic Working Group - standardizing and democratizing access to cancer molecular diagnostic data to drive translational research. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 247-258.	0.7	13
136	ClinGen Cancer Somatic Working Group "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. <i>PLoS Pathogens</i> , 2021, 17, e1009577.	2.1	12
138	CIVICpy: A Python Software Development and Analysis Toolkit for the CIVIC Knowledgebase. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 245-253.	1.0	10
139	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.2	9
140	Noninvasive Detection of High-Risk Adenomas Using Stool-Derived Eukaryotic RNA Sequences as Biomarkers. <i>Gastroenterology</i> , 2019, 157, 884-887.e3.	0.6	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. <i>PLoS ONE</i> , 2021, 16, e0246443.	1.1	7
143	Exploring the Genomic Landscape of Cancer Patient Cohorts with GenVisR. <i>Current Protocols</i> , 2021, 1, e252.	1.3	7
144	<i>Escherichia coli</i> endA deletion strain for use in two-hybrid shuttle vector selection. <i>BioTechniques</i> , 2003, 35, 272-278.	0.8	6

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145	Clinical implications of neopeptide landscapes for adult and pediatric cancers. <i>Genome Medicine</i> , 2017, 9, 77.	3.6	6
146	Open-Sourced CIViC Annotation Pipeline to Identify and Annotate Clinically Relevant Variants Using Single-Molecule Molecular Inversion Probes. <i>JCO Clinical Cancer Informatics</i> , 2019, 3, 1-12.	1.0	6
147	Integrative genomic analysis reveals low T-cell infiltration as the primary feature of tobacco use in HPV-positive oropharyngeal cancer. <i>IScience</i> , 2022, 25, 104216.	1.9	6
148	Sex- and Mutation-Specific p53 Gain-of-Function Activity in Gliomagenesis. <i>Cancer Research Communications</i> , 2021, 1, 148-163.	0.7	6
149	Large scale genotype- and phenotype- driven machine learning in Von Hippel-Lindau disease. <i>Human Mutation</i> , 2022, 43, 1268-1285.	1.1	6
150	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. <i>Cancer Genetics</i> , 2022, 264-265, 50-59.	0.2	5
151	Impact of a 40-Gene Targeted Panel Test on Physician Decision Making for Patients With Acute Myeloid Leukemia. <i>JCO Precision Oncology</i> , 2021, 5, 191-203.	1.5	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. <i>Blood</i> , 2020, 136, 20-20.	0.6	3
153	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.2	3
154	A community approach to the cancer-variant-interpretation bottleneck. <i>Nature Cancer</i> , 2022, 3, 522-525.	5.7	3
155	Genetic Ancestry Correlations with Driver Mutations Suggest Complex Interactions between Somatic and Germline Variation in Cancer. <i>Cancer Discovery</i> , 2021, 11, 534-536.	7.7	2
156	Multitarget Stool RNA Test for Noninvasive Detection of Colorectal Neoplasia in a Multicenter, Prospective, and Retrospective Cohort. <i>Clinical and Translational Gastroenterology</i> , 2021, 12, e00360.	1.3	2
157	Annotating the Regulatory Genome. <i>Methods in Molecular Biology</i> , 2010, 674, 313-349.	0.4	2
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