

# Obi Lee Griffith

## List of Publications by Year in descending order

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174  
papers

25,320  
citations

16451  
64  
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7518  
151  
g-index

208  
all docs

208  
docs citations

208  
times ranked

41740  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of the Genomic and Immunologic Diversity of Malignant Brain Tumors through Multisector Analysis. Cancer Discovery, 2022, 12, 154-171.	9.4	34
2	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
3	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
4	Checkpoint blockade-induced CD8+ T cell differentiation in head and neck cancer responders. , 2022, 10, e004034.		14
5	Bam-readcount - rapid generation of basepair-resolution sequence metrics. Journal of Open Source Software, 2022, 7, 3722.	4.6	36
6	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
7	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
8	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
9	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
10	Large scale genotypeâ€•and phenotypeâ€•driven machine learning in Von Hippelâ€•Lindau disease. Human Mutation, 2022, 43, 1268-1285.	2.5	6
11	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.4	3
12	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
13	Integration of the Drugâ€•Gene Interaction Database (DGIdb 4.0) with open crowdsourcing efforts. Nucleic Acids Research, 2021, 49, D1144-D1151.	14.5	439
14	Colonosight: Multitarget RNA-FIT assay for noninvasive detection of advanced colorectal neoplasia.. Journal of Clinical Oncology, 2021, 39, 25-25.	1.6	0
15	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
16	Yap1 Mediates Trametinib Resistance in Head and Neck Squamous Cell Carcinomas. Clinical Cancer Research, 2021, 27, 2326-2339.	7.0	16
17	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
18	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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19	Epigenomic regulation of human T-cell leukemia virus by chromatin-insulator CTCF. PLoS Pathogens, 2021, 17, e1009577.	4.7	12
20	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
21	Immunogenomic Profiling 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
22	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
23	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
24	Exploring the Genomic Landscape of Cancer Patient Cohorts with GenVisR. Current Protocols, 2021, 1, e252.	2.9	7
25	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
26	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
27	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	6.5	18
28	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
29	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
30	In Silico Epitope Prediction Analyses Highlight the Potential for Distracting Antigen Immunodominance with Allogeneic Cancer Vaccines. Cancer Research Communications, 2021, 1, 115-126.	1.7	1
31	Sex- and Mutation-Specific p53 Gain-of-Function Activity in Gliomagenesis. Cancer Research Communications, 2021, 1, 148-163.	1.7	6
32	Reply. Gastroenterology, 2020, 158, 793-794.	1.3	0
33	Splicing factor SF3B1 promotes endometrial cancer progression via regulating KSR2 RNA maturation. Cell Death and Disease, 2020, 11, 842.	6.3	30
34	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirus-Related Head and Neck Cancer: A Multicenter, Phase II Trial. Clinical Cancer Research, 2020, 26, 5140-5152.	7.0	163
35	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
36	The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.	10.3	41

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37	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
38	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
39	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. Cancer Immunology Research, 2020, 8, 409-420.	3.4	132
40	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	6.0	76
41	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
42	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
43	A Spontaneous Aggressive ER <sup>+</sup> Mammary Tumor Model Is Driven by Kras Activation. Cell Reports, 2019, 28, 1526-1537.e4.	6.4	19
44	Noninvasive Detection of High-Risk Adenomas Using Stool-Derived Eukaryotic RNA Sequences as Biomarkers. Gastroenterology, 2019, 157, 884-887.e3.	1.3	9
45	Targeting the Mevalonate Pathway to Overcome Acquired Anti-HER2 Treatment Resistance in Breast Cancer. Molecular Cancer Research, 2019, 17, 2318-2330.	3.4	41
46	Rapid progression of adult T-cell leukemia/lymphoma as tumor-infiltrating Tregs after PD-1 blockade. Blood, 2019, 134, 1406-1414.	1.4	80
47	Best practices for bioinformatic characterization of neoantigens for clinical utility. Genome Medicine, 2019, 11, 56.	8.2	146
48	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
49	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
50	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
51	Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. Genome Medicine, 2019, 11, 78.	8.2	35
52	Accounting for proximal variants improves neoantigen prediction. Nature Genetics, 2019, 51, 175-179.	21.4	43
53	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor and normal samples. Genetics in Medicine, 2019, 21, 972-981.	2.4	67
54	DGIdb 3.0: a redesign and expansion of the drug-gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.	14.5	686

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55	ClinGen Cancer Somatic Working Group “standardizing and democratizing access to cancer molecular diagnostic data to drive translational research.” 2018, .		12
56	Single-agent ibrutinib in relapsed or refractory follicular lymphoma: a phase 2 consortium trial. Blood, 2018, 131, 182-190.	1.4	130
57	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
58	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	21.4	62
59	Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data community-driven standards. Human Mutation, 2018, 39, 1721-1732.	2.5	15
60	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	12.8	112
61	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	12.8	89
62	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. Cell Reports, 2018, 24, 2167-2178.	6.4	26
63	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
64	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
65	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
66	NeoPalAna: Neoadjuvant Palbociclib, a Cyclin-Dependent Kinase 4/6 Inhibitor, and Anastrozole for Clinical Stage 2 or 3 Estrogen Receptor-Positive Breast Cancer. Clinical Cancer Research, 2017, 23, 4055-4065.	7.0	243
67	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. Bone, 2017, 101, 145-155.	2.9	37
68	Genomic characterization of HER2-positive breast cancer and response to neoadjuvant trastuzumab and chemotherapy—results from the ACOSOG Z1041 (Alliance) trial. Annals of Oncology, 2017, 28, 1070-1077.	1.2	55
69	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. Blood, 2017, 129, 473-483.	1.4	147
70	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. Clinical Cancer Research, 2017, 23, 6823-6832.	7.0	66
71	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
72	Neoantigens in immunotherapy and personalized vaccines: Implications for head and neck squamous cell carcinoma. Oral Oncology, 2017, 71, 169-176.	1.5	16

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73	Clinical implications of neoepitope landscapes for adult and pediatric cancers. <i>Genome Medicine</i> , 2017, 9, 77.	8.2	6
74	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2016, 81, 105-111.	1.1	22
75	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.	1.2	15
76	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	14.5	359
77	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. <i>Annals of Oncology</i> , 2016, 27, 1148-1154.	1.2	18
78	DoCM: a database of curated mutations in cancer. <i>Nature Methods</i> , 2016, 13, 806-807.	19.0	96
79	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	6.4	21
80	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.	7.1	119
81	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. <i>Nature Communications</i> , 2016, 7, 12498.	12.8	69
82	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. <i>Blood Cancer Journal</i> , 2016, 6, e413-e413.	6.2	18
83	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.	0.4	44
84	High-performance web services for querying gene and variant annotation. <i>Genome Biology</i> , 2016, 17, 91.	8.8	166
85	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. <i>Genome Medicine</i> , 2016, 8, 11.	8.2	350
86	GenVisR: Genomic Visualizations in R. <i>Bioinformatics</i> , 2016, 32, 3012-3014.	4.1	237
87	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. <i>Nucleic Acids Research</i> , 2016, 44, D126-D132.	14.5	142
88	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.	7.0	86
89	Exome Sequencing of Hodgkin's and Non-Hodgkin Composite Lymphomas Identifies Shared Somatic Mutations Indicative of Common Founding Precursors. <i>Blood</i> , 2016, 128, 5285-5285.	1.4	0
90	Clonal Evolution Revealed By Exome Sequencing in a Case of Primary Myelofibrosis Associated with Subsequent Development of Aggressive Systemic Mastocytosis/Mast Cell Leukemia. <i>Blood</i> , 2016, 128, 5496-5496.	1.4	0

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91	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
92	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
93	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. PLoS Computational Biology, 2015, 11, e1004393.	3.2	74
94	U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing. Leukemia, 2015, 29, 909-917.	7.2	107
95	Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351.	12.8	56
96	RNA-seq reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	4.9	44
97	Statistically identifying tumor suppressors and oncogenes from pan-cancer genome-sequencing data. Bioinformatics, 2015, 31, 3561-3568.	4.1	55
98	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. Cancer Cell, 2015, 27, 631-643.	16.8	259
99	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
100	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
101	Convergent loss of PTEN leads to clinical resistance to a PI(3)K inhibitor. Nature, 2015, 518, 240-244.	27.8	486
102	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
103	Decoupling of the PI3K Pathway via Mutation Necessitates Combinatorial Treatment in HER2+ Breast Cancer. PLoS ONE, 2015, 10, e0133219.	2.5	19
104	Clonal Architectures and Driver Mutations in Metastatic Melanomas. PLoS ONE, 2014, 9, e111153.	2.5	69
105	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
106	Hippo Signaling Influences HNF4A and FOXA2 Enhancer Switching during Hepatocyte Differentiation. Cell Reports, 2014, 9, 261-271.	6.4	89
107	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
108	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

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109	Organizing knowledge to enable personalization of medicine in cancer. <i>Genome Biology</i> , 2014, 15, 438.	8.8	81
110	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.	2.8	15
111	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	2.8	40
112	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.	3.1	31
113	DGldb: mining the druggable genome. <i>Nature Methods</i> , 2013, 10, 1209-1210.	19.0	443
114	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. <i>Pharmacogenomics Journal</i> , 2013, 13, 148-158.	2.0	29
115	A robust prognostic signature for hormone-positive node-negative breast cancer. <i>Genome Medicine</i> , 2013, 5, 92.	8.2	18
116	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. <i>Cell Reports</i> , 2013, 4, 1116-1130.	6.4	539
117	c-Src Modulates Estrogen-Induced Stress and Apoptosis in Estrogen-Deprived Breast Cancer Cells. <i>Cancer Research</i> , 2013, 73, 4510-4520.	0.9	77
118	Modeling precision treatment of breast cancer. <i>Genome Biology</i> , 2013, 14, R110.	9.6	264
119	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. <i>PLoS ONE</i> , 2013, 8, e77571.	2.5	40
120	On the Deep Order-Preserving Submatrix Problem: A Best Effort Approach. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2012, 24, 309-325.	5.7	19
121	Loss of Cell-Surface Laminin Anchoring Promotes Tumor Growth and Is Associated with Poor Clinical Outcomes. <i>Cancer Research</i> , 2012, 72, 2578-2588.	0.9	47
122	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.	2.3	93
123	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.	2.5	69
124	Lectin Chromatography/Mass Spectrometry Discovery Workflow Identifies Putative Biomarkers of Aggressive Breast Cancers. <i>Journal of Proteome Research</i> , 2012, 11, 2508-2520.	3.7	49
125	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. <i>Cell</i> , 2012, 150, 1121-1134.	28.9	1,038
126	Identification of PADI2 as a potential breast cancer biomarker and therapeutic target. <i>BMC Cancer</i> , 2012, 12, 500.	2.6	93



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127	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
128	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	27.8	1,428
129	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.	1.8	13
130	'Omic approaches to preventing or managing metastatic breast cancer. <i>Breast Cancer Research</i> , 2011, 13, 230.	5.0	21
131	Detection and Management of Hypothyroidism Following Thyroid Lobectomy: Evaluation of a Clinical Algorithm. <i>Annals of Surgical Oncology</i> , 2011, 18, 2548-2554.	1.5	46
132	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.	3.4	60
133	Extensive relationship between antisense transcription and alternative splicing in the human genome. <i>Genome Research</i> , 2011, 21, 1203-1212.	5.5	68
134	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001138.	3.2	477
135	Genomic analysis of a rare human tumor. <i>BMC Bioinformatics</i> , 2010, 11, .	2.6	0
136	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.	21.4	1,504
137	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	19.0	283
138	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	19.0	886
139	Diagnostic Utility of Galectin-3 in Thyroid Cancer. <i>American Journal of Pathology</i> , 2010, 176, 2067-2081.	3.8	137
140	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	9.6	159
141	Personalized oncogenomics. <i>Genome Biology</i> , 2010, 11, I5.	9.6	0
142	Annotating the Regulatory Genome. <i>Methods in Molecular Biology</i> , 2010, 674, 313-349.	0.9	2
143	Thyroid Cancer: Identification of Gene Expression Markers for Diagnosis. , 2010, , 353-377.		0
144	Personalized oncogenomics. <i>Genome Biology</i> , 2010, 11, I5.	9.6	0

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145	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
146	KiWi: A Scalable Subspace Clustering Algorithm for Gene Expression Analysis. , 2009, , .		7
147	Molecular Phenotyping of Thyroid Tumors Identifies a Marker Panel for Differentiated Thyroid Cancer Diagnosis. <i>Annals of Surgical Oncology</i> , 2008, 15, 2811-2826.	1.5	50
148	ALEXA: a microarray design platform for alternative expression analysis. <i>Nature Methods</i> , 2008, 5, 118-118.	19.0	19
149	Biomarker panel diagnosis of thyroid cancer: a critical review. <i>Expert Review of Anticancer Therapy</i> , 2008, 8, 1399-1413.	2.4	45
150	Text-mining assisted regulatory annotation. <i>Genome Biology</i> , 2008, 9, R31.	9.6	34
151	Clinical utility of type 1 growth factor receptor expression in colon cancer. <i>American Journal of Surgery</i> , 2008, 195, 604-610.	1.8	17
152	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.	1.8	16
153	M1982 Identification of Differentially Expressed Alternative mRNA Isoforms Associated with Chemotherapy Resistance in Colon Cancer Cell Lines. <i>Gastroenterology</i> , 2008, 134, A-444.	1.3	0
154	In-depth characterization of the microRNA transcriptome in a leukemia progression model. <i>Genome Research</i> , 2008, 18, 1787-1797.	5.5	162
155	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. <i>Genome Research</i> , 2008, 18, 610-621.	5.5	964
156	Impact of whole genome amplification on analysis of copy number variants. <i>Nucleic Acids Research</i> , 2008, 36, e80-e80.	14.5	74
157	Phosphorylated Caveolin-1 Regulates Rho/ROCK-Dependent Focal Adhesion Dynamics and Tumor Cell Migration and Invasion. <i>Cancer Research</i> , 2008, 68, 8210-8220.	0.9	228
158	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.	2.5	132
159	A Survey of Genomic Properties for the Detection of Regulatory Polymorphisms. <i>PLoS Computational Biology</i> , 2007, 3, e106.	3.2	24
160	ORegAnno: an open-access community-driven resource for regulatory annotation. <i>Nucleic Acids Research</i> , 2007, 36, D107-D113.	14.5	227
161	Identification of Molecular Markers Altered During Transformation of Differentiated Into Anaplastic Thyroid Carcinoma. <i>Archives of Surgery</i> , 2007, 142, 717.	2.2	88
162	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657.	19.0	1,254

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163	Cell Cycle Regulators Show Diagnostic and Prognostic Utility for Differentiated Thyroid Cancer. <i>Annals of Surgical Oncology</i> , 2007, 14, 3403-3411.	1.5	42
164	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.	1.6	279
165	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.	2.8	173
166	Sequence biases in large scale gene expression profiling data. <i>Nucleic Acids Research</i> , 2006, 34, e83-e83.	14.5	51
167	Discovering significant OPSM subspace clusters in massive gene expression data. , 2006, , .		23
168	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.	5.5	73
169	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.	2.9	44
170	Systematic Recovery and Analysis of Full-ORF Human cDNA Clones. <i>Genome Research</i> , 2004, 14, 2083-2092.	5.5	28
171	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.	5.5	486
172	Novel Avian Influenza H7N3 Strain Outbreak, British Columbia. <i>Emerging Infectious Diseases</i> , 2004, 10, 2192-2195.	4.3	182
173	The Genome Sequence of the SARS-Associated Coronavirus. <i>Science</i> , 2003, 300, 1399-1404.	12.6	1,842
174	<i>Escherichia coli</i> endA deletion strain for use in two-hybrid shuttle vector selection. <i>BioTechniques</i> , 2003, 35, 272-278.	1.8	6