Obi Lee Griffith

List of Publications by Year in Descending Order

176 papers	19,396 citations	59 h-index	139 g-index
207 ext. papers	23,096 ext. citations	10.6 avg, IF	5.93 L-index

#	Paper	IF	Citations
176	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**,	8.1	4
175	Bam-readcount - rapid generation of basepair-resolution sequence metrics. *Journal of Open Source Software*, **2022**, 7, 3722	5.2	2
174	Hematopoietic cell transplantation donor-derived memory-like NK cells functionally persist after transfer into patients with leukemia.. *Science Translational Medicine*, **2022**, 14, eabm1375	17.5	2
173	Integrative genomic analysis reveals low T-cell infiltration as the primary feature of tobacco use in HPV-positive oropharyngeal cancer.. *IScience*, **2022**, 25, 104216	6.1	0
172	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions.. *Cancer Genetics*, **2022**, 264-265, 50-59	2.3	1
171	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers.. *Cancer Genetics*, **2022**, 264-265, 90-99	2.3	1
170	A community approach to the cancer-variant-interpretation bottleneck. *Nature Cancer*, **2022**, 3, 522-525	15.4	0
169	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
168	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification.. *Cell Genomics*, **2021**, 1, 100027-100027		4
167	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). *Blood*, **2021**, 138, 4387-4387	2.2	
166	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	2.2	
165	In Silico Epitope Prediction Analyses Highlight the Potential for Distracting Antigen Immunodominance with Allogeneic Cancer Vaccines. *Cancer Research Communications*, **2021**, 1, 115-126		
164	Characterization of the Genomic and Immunological Diversity of Malignant Brain Tumors Through Multi-Sector Analysis. *Cancer Discovery*, **2021**,	24.4	4
163	Genetic Ancestry Correlations with Driver Mutations Suggest Complex Interactions between Somatic and Germline Variation in Cancer. *Cancer Discovery*, **2021**, 11, 534-536	24.4	0
162	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	12.9	7
161	Epigenomic regulation of human T-cell leukemia virus by chromatin-insulator CTCF. *PLoS Pathogens* , **2021**, 17, e1009577	7.6	1
160	Multitarget Stool RNA Test for Noninvasive Detection of Colorectal Neoplasias in a Multicenter, Prospective, and Retrospective Cohort. *Clinical and Translational Gastroenterology*, **2021**, 12, e00360	4.2	0

159	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	4.4	5
158	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	78
157	Integration of the Drug-Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. *Nucleic Acids Research*, **2021**, 49, D1144-D1151	20.1	71
156	Colonosight: Multitarget RNA-FIT assay for noninvasive detection of advanced colorectal neoplasia.. *Journal of Clinical Oncology*, **2021**, 39, 25-25	2.2	
155	Unraveling the chaotic genomic landscape of primary and metastatic canine appendicular osteosarcoma with current sequencing technologies and bioinformatic approaches. *PLoS ONE*, **2021**, 16, e0246443	3.7	0
154	Yap1 Mediates Trametinib Resistance in Head and Neck Squamous Cell Carcinomas. *Clinical Cancer Research*, **2021**, 27, 2326-2339	12.9	1
153	Exploring the Genomic Landscape of Cancer Patient Cohorts with GenVisR. *Current Protocols*, **2021**, 1, e252		2
152	Impact of a 40-Gene Targeted Panel Test on Physician Decision Making for Patients With Acute Myeloid Leukemia. *JCO Precision Oncology*, **2021**, 5,	3.6	2
151	Donor Memory-like NK cells Persist and Induce Remissions in Pediatric Patients with Relapsed AML after Transplant. *Blood*, **2021**,	2.2	5
150	Sex- and mutation-specific p53 gain-of-function activity in gliomagenesis.. *Cancer Research Communications*, **2021**, 1, 148-163		0
149	The clonal evolution of metastatic colorectal cancer. *Science Advances*, **2020**, 6, eaay9691	14.3	14
148	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. *JCO Clinical Cancer Informatics*, **2020**, 4, 245-253	5.2	5
147	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. *Nature Genetics*, **2020**, 52, 448-457	36.3	58
146	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	2.2	0
145	IMMU-53. CHARACTERIZATION OF THE GENOMIC AND IMMUNOLOGICAL DIVERSITY OF MALIGNANT BRAIN TUMORS THROUGH MULTI-SECTOR ANALYSIS. *Neuro-Oncology*, **2020**, 22, ii116-ii116	1	
144	Wikidata as a knowledge graph for the life sciences. *ELife*, **2020**, 9,	8.9	24
143	Reply. *Gastroenterology*, **2020**, 158, 793-794	13.3	
142	Splicing factor SF3B1 promotes endometrial cancer progression via regulating KSR2 RNA maturation. *Cell Death and Disease*, **2020**, 11, 842	9.8	10

141	Neoadjuvant and Adjuvant Pembrolizumab in Resectable Locally Advanced, Human Papillomavirus-Unrelated Head and Neck Cancer: A Multicenter, Phase II Trial. *Clinical Cancer Research*, **2020**, 26, 5140-5152	12.9	71
140	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. *JCO Clinical Cancer Informatics*, **2020**, 4, 602-613	5.2	11
139	pVACtools: A Computational Toolkit to Identify and Visualize Cancer Neoantigens. *Cancer Immunology Research*, **2020**, 8, 409-420	12.5	53
138	Targeting the Mevalonate Pathway to Overcome Acquired Anti-HER2 Treatment Resistance in Breast Cancer. *Molecular Cancer Research*, **2019**, 17, 2318-2330	6.6	22
137	Rapid progression of adult T-cell leukemia/lymphoma as tumor-infiltrating Tregs after PD-1 blockade. *Blood*, **2019**, 134, 1406-1414	2.2	50
136	Best practices for bioinformatic characterization of neoantigens for clinical utility. *Genome Medicine*, **2019**, 11, 56	14.4	73
135	A Spontaneous Aggressive ER⊞ Mammary Tumor Model Is Driven by Kras Activation. *Cell Reports*, **2019**, 28, 1526-1537.e4	10.6	10
134	Noninvasive Detection of High-Risk Adenomas Using Stool-Derived Eukaryotic RNA Sequences as Biomarkers. *Gastroenterology*, **2019**, 157, 884-887.e3	13.3	6
133	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	5.2	4
132	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	11.5	19
131	Standard operating procedure for curation and clinical interpretation of variants in cancer. *Genome Medicine*, **2019**, 11, 76	14.4	6
130	Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. *Genome Medicine*, **2019**, 11, 78	14.4	19
129	Accounting for proximal variants improves neoantigen prediction. *Nature Genetics*, **2019**, 51, 175-179	36.3	23
128	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor and□hormal samples. *Genetics in Medicine*, **2019**, 21, 972-981	8.1	31
127	DGIdb 3.0: a redesign and expansion of the drug-gene interaction database. *Nucleic Acids Research*, **2018**, 46, D1068-D1073	20.1	414
126	Single-agent ibrutinib in relapsed or refractory follicular lymphoma: a phase 2 consortium trial. *Blood*, **2018**, 131, 182-190	2.2	92
125	Oral Cavity Squamous Cell Carcinoma Xenografts Retain Complex Genotypes and Intertumor Molecular Heterogeneity. *Cell Reports*, **2018**, 24, 2167-2178	10.6	17
124	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	1.3	13

123	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	1.1	
122	A case of acute myeloid leukemia with promyelocytic features characterized by expression of a novel - fusion. *Blood Advances*, **2018**, 2, 1295-1299	7.8	18
121	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. *Nature Genetics*, **2018**, 50, 1735-1743	36.3	38
120	Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data community-driven standards. *Human Mutation*, **2018**, 39, 1721-1732	4.7	11
119	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. *Nature Communications*, **2018**, 9, 3787	17.4	63
118	The prognostic effects of somatic mutations in ER-positive breast cancer. *Nature Communications*, **2018**, 9, 3476	17.4	51
117	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. *Nature Genetics*, **2017**, 49, 170-174	36.3	308
116	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	12.9	160
115	Melorheostosis: Exome sequencing of an associated dermatosis implicates postzygotic mosaicism of mutated KRAS. *Bone*, **2017**, 101, 145-155	4.7	25
114	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	10.3	35
113	Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma. *Blood*, **2017**, 129, 473-483	2.2	98
112	Clinical implications of neoepitope landscapes for adult and pediatric cancers. *Genome Medicine*, **2017**, 9, 77	14.4	4
111	A Phase II Trial of Neoadjuvant MK-2206, an AKT Inhibitor, with Anastrozole in Clinical Stage II or III -Mutant ER-Positive and HER2-Negative Breast Cancer. *Clinical Cancer Research*, **2017**, 23, 6823-6832	12.9	51
110	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. *Experimental Hematology*, **2017**, 55, 19-33	3.1	8
109	Neoantigens in immunotherapy and personalized vaccines: Implications for head and neck squamous cell carcinoma. *Oral Oncology*, **2017**, 71, 169-176	4.4	13
108	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. *Nature Communications*, **2016**, 7, 12498	17.4	47
107	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. *Blood Cancer Journal*, **2016**, 6, e413	7	12
106	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. *Experimental Hematology*, **2016**, 44, 603-13	3.1	33

105	High-performance web services for querying gene and variant annotation. *Genome Biology*, **2016**, 17, 91	18.3	111
104	pVAC-Seq: A genome-guided in silico approach to identifying tumor neoantigens. *Genome Medicine*, **2016**, 8, 11	14.4	221
103	GenVisR: Genomic Visualizations in R. *Bioinformatics*, **2016**, 32, 3012-4	7.2	146
102	ORegAnno 3.0: a community-driven resource for curated regulatory annotation. *Nucleic Acids Research*, **2016**, 44, D126-32	20.1	89
101	A Phase I Trial of BKM120 (Buparlisib) in Combination with Fulvestrant in Postmenopausal Women with Estrogen Receptor-Positive Metastatic Breast Cancer. *Clinical Cancer Research*, **2016**, 22, 1583-91	12.9	77
100	Exome Sequencing of Hodgkin's and Non-Hodgkin Composite Lymphomas Identifies Shared Somatic Mutations Indicative of Common Founding Precursors. *Blood*, **2016**, 128, 5285-5285	2.2	
99	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	2.2	
98	Cancer Immunogenomics: Computational Neoantigen Identification and Vaccine Design. *Cold Spring Harbor Symposia on Quantitative Biology*, **2016**, 81, 105-111	3.9	15
97	A common founding clone with TP53 and PTEN mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. *Journal of Physical Education and Sports Management*, **2016**, 2, a000687	2.8	12
96	DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*, **2016**, 44, D1036-44	20.1	222
95	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. *Annals of Oncology*, **2016**, 27, 1148-1154	10.3	13
94	DoCM: a database of curated mutations in cancer. *Nature Methods*, **2016**, 13, 806-7	21.6	63
93	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. *Cell Reports*, **2016**, 17, 249-260	10.6	14
92	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	11.5	91
91	U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing. *Leukemia*, **2015**, 29, 909-17	10.7	79
90	Epigenetic and transcriptional determinants of the human breast. *Nature Communications*, **2015**, 6, 6351	17.4	44
89	RNA-sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. *Glia*, **2015**, 63, 531-548	9	26
88	Statistically identifying tumor suppressors and oncogenes from pan-cancer genome-sequencing data. *Bioinformatics*, **2015**, 31, 3561-8	7.2	30

87	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. *Cancer Cell*, **2015**, 27, 631-43	24.3	186
86	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. *JAMA - Journal of the American Medical Association*, **2015**, 314, 811-22	27.4	242
85	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. *Neoplasia*, **2015**, 17, 776-88	6.4	62
84	Convergent loss of PTEN leads to clinical resistance to a PI(3)K inhibitor. *Nature*, **2015**, 518, 240-4	50.4	366
83	Optimizing cancer genome sequencing and analysis. *Cell Systems*, **2015**, 1, 210-223	10.6	135
82	Genome Modeling System: A Knowledge Management Platform for Genomics. *PLoS Computational Biology*, **2015**, 11, e1004274	5	59
81	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. *PLoS Computational Biology*, **2015**, 11, e1004393	5	50
80	Recurrent Somatic Genomic Alterations in Follicular NHL (FL) Revealed By Exome and Custom-Capture Next Generation Sequencing. *Blood*, **2015**, 126, 574-574	2.2	2
79	Decoupling of the PI3K Pathway via Mutation Necessitates Combinatorial Treatment in HER2+ Breast Cancer. *PLoS ONE*, **2015**, 10, e0133219	3.7	16
78	Single exon-resolution targeted chromosomal microarray analysis of known and candidate intellectual disability genes. *European Journal of Human Genetics*, **2014**, 22, 792-800	5.3	30
77	Organizing knowledge to enable personalization of medicine in cancer. *Genome Biology*, **2014**, 15, 438	18.3	53
76	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, 2877-86	7.5	12
75	cDNA hybrid capture improves transcriptome analysis on low-input and archived samples. *Journal of Molecular Diagnostics*, **2014**, 16, 440-51	5.1	35
74	Clonal architectures and driver mutations in metastatic melanomas. *PLoS ONE*, **2014**, 9, e111153	3.7	53
73	SciClone: inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution. *PLoS Computational Biology*, **2014**, 10, e1003665	5	301
72	Hippo signaling influences HNF4A and FOXA2 enhancer switching during hepatocyte differentiation. *Cell Reports*, **2014**, 9, 261-271	10.6	59
71	Functional heterogeneity of genetically defined subclones in acute myeloid leukemia. *Cancer Cell*, **2014**, 25, 379-92	24.3	273
70	The cure: design and evaluation of a crowdsourcing game for gene selection for breast cancer survival prediction. *JMIR Serious Games*, **2014**, 2, e7	3.4	16

69	DGIdb: mining the druggable genome. *Nature Methods*, **2013**, 10, 1209-10	21.6	317
68	Novel mRNA isoforms and mutations of uridine monophosphate synthetase and 5-fluorouracil resistance in colorectal cancer. *Pharmacogenomics Journal*, **2013**, 13, 148-58	3.5	18
67	A robust prognostic signature for hormone-positive node-negative breast cancer. *Genome Medicine*, **2013**, 5, 92	14.4	17
66	Endocrine-therapy-resistant ESR1 variants revealed by genomic characterization of breast-cancer-derived xenografts. *Cell Reports*, **2013**, 4, 1116-30	10.6	447
65	c-Src modulates estrogen-induced stress and apoptosis in estrogen-deprived breast cancer cells. *Cancer Research*, **2013**, 73, 4510-20	10.1	65
64	Modeling precision treatment of breast cancer. *Genome Biology*, **2013**, 14, R110	18.3	204
63	F11R is a novel monocyte prognostic biomarker for malignant glioma. *PLoS ONE*, **2013**, 8, e77571	3.7	32
62	Cross-platform pathway-based analysis identifies markers of response to the PARP inhibitor olaparib. *Breast Cancer Research and Treatment*, **2012**, 135, 505-17	4.4	54
61	Lectin chromatography/mass spectrometry discovery workflow identifies putative biomarkers of aggressive breast cancers. *Journal of Proteome Research*, **2012**, 11, 2508-20	5.6	45
60	Genomic landscape of non-small cell lung cancer in smokers and never-smokers. *Cell*, **2012**, 150, 1121-34	56.2	860
59	Identification of PADI2 as a potential breast cancer biomarker and therapeutic target. *BMC Cancer*, **2012**, 12, 500	4.8	79
58	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. *Nature*, **2012**, 486, 395-9	50.4	1417
57	On the Deep Order-Preserving Submatrix Problem: A Best Effort Approach. *IEEE Transactions on Knowledge and Data Engineering*, **2012**, 24, 309-325	4.2	16
56	Loss of cell-surface laminin anchoring promotes tumor growth and is associated with poor clinical outcomes. *Cancer Research*, **2012**, 72, 2578-88	10.1	37
55	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, 4691-704	4.8	71
54	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. *Nature*, **2011**, 476, 298-303	50.4	1180
53	Immunophenotyping of thyroid tumors identifies molecular markers altered during transformation of differentiated into anaplastic carcinoma. *American Journal of Surgery*, **2011**, 201, 580-6	2.7	13
52	SOmic approaches to preventing or managing metastatic breast cancer. *Breast Cancer Research*, **2011**, 13, 230	8.3	19

51	Detection and management of hypothyroidism following thyroid lobectomy: evaluation of a clinical algorithm. *Annals of Surgical Oncology*, **2011**, 18, 2548-54	3.1	37
50	Lrig1 is an estrogen-regulated growth suppressor and correlates with longer relapse-free survival in ER□positive breast cancer. *Molecular Cancer Research*, **2011**, 9, 1406-17	6.6	51
49	Extensive relationship between antisense transcription and alternative splicing in the human genome. *Genome Research*, **2011**, 21, 1203-12	9.7	63
48	deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. *PLoS Computational Biology*, **2011**, 7, e1001138	5	409
47	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. *Nature Genetics*, **2010**, 42, 181-5	36.3	1273
46	Alternative expression analysis by RNA sequencing. *Nature Methods*, **2010**, 7, 843-7	21.6	227
45	De novo assembly and analysis of RNA-seq data. *Nature Methods*, **2010**, 7, 909-12	21.6	701
44	Diagnostic utility of galectin-3 in thyroid cancer. *American Journal of Pathology*, **2010**, 176, 2067-81	5.8	118
43	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. *Genome Biology*, **2010**, 11, R82	18.3	144
42	Personalized oncogenomics **2010**, 11, I5		78
41	Genomic analysis of a rare human tumor. *BMC Bioinformatics*, **2010**, 11,	3.6	78
40	Annotating the regulatory genome. *Methods in Molecular Biology*, **2010**, 674, 313-49	1.4	2
39	Thyroid Cancer: Identification of Gene Expression Markers for Diagnosis **2010**, 353-377		
38	The completion of the Mammalian Gene Collection (MGC). *Genome Research*, **2009**, 19, 2324-33	9.7	98
37	KiWi: A Scalable Subspace Clustering Algorithm for Gene Expression Analysis **2009**,		6
36	ALEXA: a microarray design platform for alternative expression analysis. *Nature Methods*, **2008**, 5, 118	21.6	19
35	Biomarker panel diagnosis of thyroid cancer: a critical review. *Expert Review of Anticancer Therapy*, **2008**, 8, 1399-413	3.5	35
34	Text-mining assisted regulatory annotation. *Genome Biology*, **2008**, 9, R31	18.3	29

33	Clinical utility of type 1 growth factor receptor expression in colon cancer. *American Journal of Surgery*, **2008**, 195, 604-10	2.7	16
32	Evaluation of type 1 growth factor receptor family expression in benign and malignant thyroid lesions. *American Journal of Surgery*, **2008**, 195, 667-73; discussion 673	2.7	15
31	In-depth characterization of the microRNA transcriptome in a leukemia progression model. *Genome Research*, **2008**, 18, 1787-97	9.7	148
30	Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. *Genome Research*, **2008**, 18, 610-21	9.7	879
29	Impact of whole genome amplification on analysis of copy number variants. *Nucleic Acids Research*, **2008**, 36, e80	20.1	70
28	Phosphorylated caveolin-1 regulates Rho/ROCK-dependent focal adhesion dynamics and tumor cell migration and invasion. *Cancer Research*, **2008**, 68, 8210-20	10.1	200
27	Meta-analysis of colorectal cancer gene expression profiling studies identifies consistently reported candidate biomarkers. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 543-52	4	120
26	Molecular phenotyping of thyroid tumors identifies a marker panel for differentiated thyroid cancer diagnosis. *Annals of Surgical Oncology*, **2008**, 15, 2811-26	3.1	43
25	ORegAnno: an open-access community-driven resource for regulatory annotation. *Nucleic Acids Research*, **2008**, 36, D107-13	20.1	199
24	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. *Nature Methods*, **2007**, 4, 651-7	21.6	1077
23	Cell cycle regulators show diagnostic and prognostic utility for differentiated thyroid cancer. *Annals of Surgical Oncology*, **2007**, 14, 3403-11	3.1	38
22	A survey of genomic properties for the detection of regulatory polymorphisms. *PLoS Computational Biology*, **2007**, 3, e106	5	22
21	Identification of molecular markers altered during transformation of differentiated into anaplastic thyroid carcinoma. *Archives of Surgery*, **2007**, 142, 717-27; discussion 727-9		72
20	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. *BMC Genomics*, **2006**, 7, 246	4.5	139
19	Sequence biases in large scale gene expression profiling data. *Nucleic Acids Research*, **2006**, 34, e83	20.1	44
18	Discovering significant OPSM subspace clusters in massive gene expression data **2006**,		19
17	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	9.7	59
16	Meta-analysis and meta-review of thyroid cancer gene expression profiling studies identifies important diagnostic biomarkers. *Journal of Clinical Oncology*, **2006**, 24, 5043-51	2.2	232

15	Assessment and integration of publicly available SAGE, cDNA microarray, and oligonucleotide microarray expression data for global coexpression analyses. *Genomics*, **2005**, 86, 476-88	4.3	40
14	Systematic recovery and analysis of full-ORF human cDNA clones. *Genome Research*, **2004**, 14, 2083-92	9.7	22
13	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). *Genome Research*, **2004**, 14, 2121-7	9.7	404
12	Novel avian influenza H7N3 strain outbreak, British Columbia. *Emerging Infectious Diseases*, **2004**, 10, 2192-5	10.2	154
11	Escherichia coli endA deletion strain for use in two-hybrid shuttle vector selection. *BioTechniques*, **2003**, 35, 272-4, 276, 278	2.5	6
10	The Genome sequence of the SARS-associated coronavirus. *Science*, **2003**, 300, 1399-404	33.3	1632
9	Clingen Cancer Somatic Working Group – standardizing and democratizing access to cancer molecular diagnostic data to drive translational research		1
8	CIViC: A knowledgebase for expert-crowdsourcing the clinical interpretation of variants in cancer		2
7	DGIdb 3.0: a redesign and expansion of the drug-gene interaction database		5
6	Integration of the Drug-Gene Interaction Database (DGIdb) with open crowdsource efforts		1
5	A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants		5
4	RegTools: Integrated analysis of genomic and transcriptomic data for the discovery of splicing variants in cancer		25
3	pVACtools: a computational toolkit to identify and visualize cancer neoantigens		5
2	Wikidata as a FAIR knowledge graph for the life sciences		1
1	The GA4GH Variation Representation Specification (VRS): a Computational Framework for the Precise Representation and Federated Identification of Molecular Variation		3